Access DB# 43730



SEARCH REQUEST FORM

Scientific and Technical Information Center

Art Unit:	- N.L. 1 20	Exammer #:	_ Date:	·
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If more than one search is suf-	mitted place	prioritize searches in order of ne		
Include the elected species or structures	he search topic, and s, keywords, synony ns that may have a s	describe as specifically as possible the sub ms, acronyms, and registry numbers, and c	ject matter to b	e searched.
Title of Invention:				
Inventors (please provide full names)				
Earliest Priority Filing Date:				
For Sequence Searches Only Please inc	lude all pertinent info	rmation (parent, child, divisional, or issued pa	rtant numb	
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STIC-Biotech/ChemLib

Fro n: Sent: To: Subject:

Prouty, Rebecca Friday, June 01, 2001 2:40 PM STIC-Biotech/ChemLib sequence Search

Art Unit 1652, 10A13 308-4000 Serial Number: 09/382,242

Please search and interference search SEQ ID NOS: 24-32

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Email: d402hu@sakura.cc.tsukuba.ac.jp
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AU034952 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
discoideum cDNA clone SLE392, mrNA sequence.
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The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
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56.6; DB 106;
No. 1.4e-05;
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BF112633 EST440223
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AL077773 Drosophil
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441 CAGTAACTCACCTAAGAATTCAAGCAATGGTTCATGATTTCGT 483
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
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[ (bases 1 to 1101)
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                                                                                                                                                                                                                                 at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
/organism="Drosophila
/db_xref="taxon:727"
/clone_lib="RPCI-98"
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                                                                                                                                         Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AU052396 510 bp mRNA EST 28-APR-1999 AU052396 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium discoideum cDNA clone SLD248, mRNA sequence.
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                                                                                  d402hu@sakura.cc.tsukuba.ac.jp
r - Dictyostelium discoideum cDNA
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Pred. No. 7.8e-05;
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D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, developm
of the cotton fiber
Unpublished (2000)
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AW666750
                                                                                                                                                                    Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
                                                                                                                                                                                                                        Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gossypium arboreum
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/db_xref="taxon:44689"
/clone="SLD248"
/clone_lib="Dictyostelium discoideum
/clone_lib="Slug"
/dev_stage="slug"
/dev_stage="slug"
/dev_stage="slug"
/clone="GA__Ea0005001"
/clone_lib="Gossypium arboreum 7-10
                   /db_xref="taxon:29729"
/clone="GA__Ea0005001"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124;
                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Maria J. Harrison
Plant Biology Division
Phe Samuel Roberts Noble Foundation
The Samuel Roberts Ardmore, OK 73401, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW587200 EST U/-SEF-20 EST318823 MHAM Medicago truncatula/Glomus versiforme mixed library cDNA clone pMHAM-57P8, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.I
Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.!
ESTs from roots of Medicago truncatula after colonization with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medicago truncatula/Glomus versiforme mixed Medicago truncatula/Glomus versiforme mixed EURATYOta; mixed EST libraries.
                                                                                                                                                                                                                                                                             Email: mjharrison@noble.org
Noble EST name:N255450e
                                                                                                                                                                                                                                         More information is available at.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                            sequence name:MTDBF88TK
                                                                                                                                                                                                                                                                                                                 580-221-7380
                                                                                                                                                                               versiforme
/tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 day.
post-inoculation with Glomus versiforme. The library was
                                                       /cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="pwhAM-5798"
/clone_11b="MHAM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. coli"
/note="Vector: pBK-CMV; Site_1:
117 c 213 g 170 t
                                                                                                                                               /organism="Medicago truncatula/Glomus versiforme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue_type="Fibers"
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49.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,T., Ochiai,H. and Tanaka,Y. The Dictyostelium developmental cDNA project: generation and manalysis of expressed sequence tags from the first-finger stage of analysis of expressed sequence tags from the first-finger stage of the control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AU034062 568 bp mRNA EST 28-APR-1999
AU034062 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 5 (6), 335-340 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                   PROJECT = 'Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: d402hu@sakura.cc.tsukuba.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Tsukuba
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                           /strain="AX4"
/db_xref="taxon:44689"
/clone="SLB870"
/clone_lib="Dictyostelium d
/dev_stage="slug"
a 78 c 103 g 174 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D
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/lab_host="E. coli strain XLOLR"
                                                                                                                                                                                                                                                            /organism="Dictyostelium discoideum"
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                                                                                                                                                                                                                                                                                                195 GAAGAGTAGCGGTCCTTATGGTGTTCTAGTGTATCTTCATGGAGGCGGTTTTGTAATAGG
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                               AGTATCAGTGGACTATAGGTTAGCTCCAGAATACAAGTTTCCTTCTGCAGTTATCGATTC
                                                                                                    GGDGDSKAKGDRAWAWRAKATRAAAADATAAATAAKATAWATKTTTKKTTTTTKTTTT
                                                                                                                                                               CGATGTGGAATCTTATGACCCATTATGTAGAGCAATTACAAATGCGTGCAATTGCGTTGT
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Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billa
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN03G04 of DrossBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL098379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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a 108 c 131 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McCarter,J., Clifton,S., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Glbbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strongyloides stercoralis. Strongyloides stercoralis
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                                                                                                                                                                                                                                                                                                                                                                                                                                 The library was constructed by Dr. Thomas Nutman NIAID, NIH (tnutman@nih.gov). DNA Sequencing by: University Genome Sequencing Center St. Louis. Seq primer: -40RP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Washington Univ. Nematode EST Project, Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Lo
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Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Panagrolaimoidea;
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                 /note="Vector: Lambda Uni-ZAP XR (Stratagene); Site_1: ECORI; Site_2: XhOI; mRNA was purified from 4 x 10E5 filariform larvae which had been isolated from infected humans. CDNA was constructed and, using adaptors, was cloned unidirectionally into the vector from the ECORI site to the XhOI site. The library has an unamplified titer of 1.5 x 10E6 ptu/ml and an amplified, undiluted titer of 7 x 10E9 ptu/ml. The average insert size of the unamplified library is 975 bp (range, 500-1500)."
                                                                                                                                                                                                                                                                                                 /strain="Filariform larvae obtained f:/db_xref="taxon:6248" /clone 14-"-----
                                                                                                                                                                                                                                                                                         /clone_lib="TBN95TM-SSFH"
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Query Match Best Local S Matches 74

h 4.9%; Similarity 60.7%; 74; Conservative

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Score 45.2; DB 174; pred. No. 0.025; 0; Mismatches 48;

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RESULT 9
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                                                                                                                                                                             61 AAAGCCCCAGTAGAAGAGGTAAGAAAGATATTTAGGCAATTAGCGTCGGCAGCTCCCAAA 120
                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the 1sogenic Strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACRAC Resource Center can be found at http://bacrac.med.html.ph.
                                                                                        GTCGAAGTTGGAAAAGTAGAAGATATAAAAAATACCAGGCAGTGAAAACCGTTATAAAACGCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAATACGATCCACTAAGGGATCAAGGGAGAAGCGTATGCAAATAAACTACTACAAGCTGGA 783
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AGAGTGTATTTTCCGAAGAGTAGCGGTCCTTATGGTGTTCTAGTGTATCTTCATGGAGGC
                                             AMAAAAAAWARAAATGCTWGCGATGGWAAAAAGACMARAAAAWGAAAGTGWCAWMAWACGT 230
                                                                                                                                     AAWACGWWAGWAAAATWWTAGAGMAWATGTTTTTCTRAAAAACAWAWAAAAAAAAAAAAAAA 290
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/clone="BACR17L15"
/note="end : TET3"
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227 ATCTTCATGGAGGCGGTTTTGTAATAGGCGATGTGGAATCTTATGACCCATTATGTAGAG 286

ATGGTGGTTGTTTTGGAAGTTCCAAACAGAGGGCTTTTGACTTCCTGAATAGAT 148

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins (M., Bonaldo, M.F., Chiapelli, B., M., DuBuque, T., Favello, A., Gish, W., Hawkins (M., Bonan, M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moore (M., Bonan, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Be, Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
    82; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest park Parkway, Box 8501, St. J
Tel: 314 286 1810
Fax: 314 286 1810
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                    (Pharmacia), digested with Not I and cloned into the No and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."

1 45 c 57 g 71 t
                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="GDB:3755587"
                                                                                                                                                                                                                                                                                                                             /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                         /sex="temale"
                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares_pregnant_uterus_NbHPU
                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:469585"
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Score 43.6; DB pred. No. 0.064; 0; Mismatches
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                                                                                                              654 AGACTTTAGGTTCTCTCCAATTCTGGCGCAAGATTTCAACGGATTACCTCCAGCCTTGAT 713
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                                   714 AATAACAGCAGAATACGATCCACTAAGGGATCAAGGAGAAGCGTATGCAAATAAACTACT 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAATTACAAATGCGTGCAATTGCGTTGTAGTAGTATAGGTTAGGTTAGCTCCAGAAT 346
ACTGACCGCGGAGCTGACGTGTTGAGGGATGAAGGATTGCGCTATGGTTGCGAATTGCT
                                                                        ACAAGTTTCCTTCTGCAGTTATCGAT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCACTTTCCTGCTCAGTTTGAAGAT 234
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MR-BT041-220199-048 E
AI904070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        &t3-220199&t4-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://www.ludwig.org.br/seg/gethtml.pl?tl=MR&t2=MR-BT041-048.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia;
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                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Natl. Acad. Sci. U.S.A. 97
                                                                                                                                                                                                                                                             inote "Organ: breast; Vector: puc18; Site_1: SmaI; Site_2 SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 19), 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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1 to 299)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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Primates;
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                                                                                                                                                                     Score 43.6; DB 103; Pred. No. 0.068;
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TTCTGCAGTTATCGATTCATTTGACGCTACTAATTGGGGTTTATAACAATTTAGATAAATT 416

TTCTAATGATATCAATACTATTAAGTGCACTTTTTGTGATAATGATAAAGAATTTAATGA 290

Query Match

Local

89; Conservative

4.7%;

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Score 43.4; DB Pred. No. 0.084; 0; Mismatches

DB 174;

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                                                                                                                                                                                                                                                                                                                                                                                                                                The library was constructed by Dr. Thomas Nutman NIAID, NIH (tnutman@nih.gov). DNA Sequencing by: University Genome Sequencing Center St. Louis. Seq primer: -40RP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: McCarter JP
The Washington Univ. Nematode EST Project,
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McCarter, J., Clifton, S., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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                      167
          /note="Vector: Lambda Uni-Zap XR (Stratagene); Site_1: ECORI; Site_2: XhoI: mRNA was purified from 4 x 10E5 filariform larvae which had been isolated from infected humans. CDNA was constructed and, using adaptors, was cloned unidirectionally into the vector from the ECORI site to the XhoI site. The library has an unamplified titer of 1.5 x 10E6 pfu/ml and an amplified, undiluted titer of 7 x 10E9 pfu/ml. The average insert size of the unamplified library is 975 bp (range, 500-1500)."
                                                                                                                                                                                                                                                                                 /strain="Filariform larvae obtained
/db_xref="taxon:6248"
/clone_lib="TBN95TM-SSFH"
                                                                                                                                                                                                                                                             /lab_host="XL-1 Blue MRF'
                                                                                                                                                                                                                                                                                                                                                       organism="Strongyloides stercoralis"
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                                                                                                                                                                                                                                                          (Stratagene)"
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GCGATTGCGGGAGGATAGTGCTGGAGGAAA
                                                                                                        GTTGCGGCGATTAAGTGGTTAGGGAAGCAAGCTAATTTGGCGGAATGTAGTAGGTCAAGT 250
                                                                                                                                                                         TTTGACGCTACTAATTGGGTTTATAACAATTTAGATAAATTTGATGGAAAGATGGGAGTT 435
                                                                                                                                                                                                                                              ATTGCTGTTGGGTATAGATTGGCACCGGAGAGTATGTTTCCGGCTGCGTTTGAAGATGGG 190
                                                                                                                                                                                                                                                                                  GATACGGTTTCCAATGATGTTTTTTGTAGGAAATTGGCGAAATCTTGTGATGCTATTGTG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGTGGAATCTTATGACCCATTATGTAGAGCAATTACAAATGCGTGCAATTGCGTTGTA 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l (bases I to 503)
Alcala, Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E., Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronnning, C.M., Nierman, W., Fraser, C.M., Giovannoni, J.J., Martin, G.B. and Tankslu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clemson University Genomics Institute
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Solanum; Lycopersicon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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05; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="tomato germinating seedlings, TAMU"
/tissue_type="whole seedlings"
/dev_stage="7 days post imbibtion"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/note="Vector: pBlueScript SK(-); Site_1 = EcoR1; Site_2:
/note="Vector: pBlueScript Sk(-) = EcoR1; Site_2:
/note="Vector: pBlueScript 
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/clone="cLEI13C19"
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/cultivar="TA496"
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Pred. No. 0.15;
0; Mismatches 104;
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                                                                                                                                               383
                                                                                                                                                                                  697
 263
                                                                                                          757
                                                                                          TATGCAAATAAACTACTACAAGCTGGAGTCTCAGTTACTAGTGTGAGATTTAACAACGTT 816
                                   ATACACGGATTCCTCTCATTCTTTCCGT 844
ATTCATGGAGCTTTATCATTCATGACTT 236
                                                                                                                                              TTGCCACTAACCTATATTCTTACTTGTCAACATGATCTCTTAAGAGATGATGGACTTATG 324
                                                                                                                                                                                TTACCTCCAGCCTTGATAATAACAGCAGAATACGATCCACTAAGGGATCAAGGAGAAGCG 756
                                                                      TATGTTACAAGACTTCGAAATGTTGGAGTCCAAGTTGTTCATGAACATATTGAGGATGGA
                                                                                                                                                                                                                    | Similarity
| 82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AII30823 460 bp mRNA EST 27-OCT-1998 qc09g08.xl Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone mAGE:1709150 3' similar to gb:L32179 Human arylacetamide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further Insert Length: 1176 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 415.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                              NbHL19W."
a 92 c
                                                                                                                                                                                                                                                                                                                                                                             double-stranded CDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT/T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatina Bonaldo. This library was constructed from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         same fetus as the fetal lung library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares_fetal_heart_NbHH19W"
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/clone="IMAGE:1709150"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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                                                                                                                                                                                                                                   4.6%;
55.4%;
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VERSION
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DEFINITION
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Best Local Similarity 56.4%;
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                                                                                                                                                                                                                                                                                      350 GATACGGTTTCCAATGATGTTTTTTGTAGGAAATTGGCGAAATCTTGTGATGCTATTGTG 409
                                                                                                                                                                                                                                                                                                                                                                                79; Conservative
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: dfrisch@CI
5 prime sequence.
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: David Frisch
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lycopersicon esculentum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Budaryota; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW932320 515 bp mRNA EST 30-MAY-2000
EST338163 tomato fruit mature greėn, TAMU Lycopersicon esculentum
cDNA clone cLEF48A5 5', mRNA sequence.
AW932320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; CLEF - Fruit were tagged at the lcm stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seeds and locules were discarded pericarp" . 92 c 130 g 170 t
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/cultivar="TA496"
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/clone="cLEF48A5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="mature green (3-5 days pre-ripening)"
lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="tomato fruit mature green, TAMU"
tissue_type="fruit pericarp"
                    2001, 21:50:20
                                                                                                                                                                                                                                                                                                                                                                              Score 42.4; DB 121;
Pred. No. 0.17;
0; Mismatches 61;
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Minimum DB
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

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        GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
      ATGCCCCTAGATCCTAGAAT.....TATTTTATGATAAAATTTAA 918
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US-89-56-171C-803
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US-99-739-449-6925
US-99-735-632-1503
US-60-248-505-197
US-99-335-032-13206
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	GGGAGTTGCGATTGCGGGAGAAA 	CTACTAATTGGGTTT 	TCAGTGGACTATAGGTTAGCTC	GGAGGCGGTTTTGTAATAGGCGATGTGGAATCTTATGACCCATTATGTAGAGCAATTACA	Score 38.6; DB 6; Length Pred. No. 0.38; 0; Mismatches 114; Indels	No: 1427470CB1	RESSED IN LUNG CANCER 5/60/281,593 -04	ALIGNMENTS US/60281593			US-08-956-1/10-3/9 PCT-US01-01339-6396 PCT-US01-01339-6395 US-60-248-505-164		
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Best Local Similarity
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353
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APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: HOOVET, Kenley K.
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB248P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Michael R. Fannon TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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Gil H. Choi
GCAGG 357
                                   GGAGG 461
                                                                      AAAGAAAATAAAATGAATTTACCTATTGATTTAATCAAGTAATTATTGGCGGTGAYTCT
                                                                                                        TATAACAATTTAGATAAATTTGATGGAAAGATGGGAGTTGCGATTGCGGGAGATAGTGCT 456
                                                                                                                                                                       GCTCCAGAATACAAGTTTCCTTCTGCAGTTATCGATTCATTTGACGCTACTAATTGGGTT 396
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                                                                                                                                                                                                                                                                                                 GTTATTTTTTGGATGCACGGTGGTGGTTATATTGCGGGTGATAAGCAGTATAAAAACCCA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/956,171C FILING DATE: 20-Oct-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (301)
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Craig A. Rosen
Steven C. Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (301)
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Pred. No. 1.
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                                                                   Sequence 727, Application PC/TUS0104098A
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc:
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 2695, Application PC/TUS0104098A GENERAL INFORMATION:
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Best Local
CURRENT APPLICATION NUMBER: PCT/US01/04098A CURRENT FILING DATE: 2001-02-05 PRIOR APPLICATION NUMBER: Not Yet Assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Novel Nucleic Acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID
SOFTWARE: Custom
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PRIOR FILING DATE: 2000-02-03
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PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/598,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: Not Yet Assigned PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: 09/728,422 PRIOR FILING DATE: 2000-11-30 PRIOR APPLICATION NUMBER: 09/693,325 PRIOR APPLICATION NUMBER: 09/693,325 PRIOR FILING DATE: 2000-10-20 PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-02-05
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PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR FILING DATE: 2000-09-01
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                                                                                                                                                                                                                                                                                         1142 CTGGCTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                1202 CAGAAGTATATGGTTGATCCAGGCAGAATTTGCATTTCTGGTGACAGTGCTGGTGGAAAT 1143
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les 125; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 09/560,875 FILING DATE: 2000-04-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTGAGCAAATTCATGATGTTGTACGGGCCACAAAGTATTTCCTGAAGCCAGAAGTCTTA 1203
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Pred. No. 1
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PRIOR FILING DATE:

2001-01-30

PRIOR APPLICATION NUMBER: 09/728,422 PRIOR FILING DATE: 2000-11-30

APPLICATION NUMBER: 09/693,325

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; ORGANISM: Agrobacterium tumefaciens US-09-739-449-6925
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; LOCATION: (1)..(1698)
PCT-US01-04098A-727
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                                                                                                                                                                                         Sequence 6925, Application US/09739449

GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
                                                         NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 6925
LENGTH: 909
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SEQ ID NO 727
                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
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PRIOR FILING DATE: 2000-02-03
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SOFTWARE: Custom
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                                        TYPE: DNA
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APPLICATION NUMBER: 09/663,561
FILING DATE: 2000-09-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cagaagtatatggttgatccaggcagaatttgcatttctggtgacagtgctggtggaaat 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTGATGGAAAGATGG------GAGTTGCGATTGCGGGAGATAGTGCTGGAGGAAAT 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggctgggccttggcaagtgcaaaaatcaggtattatgatgagctgtgtacagcaatggct 876
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Pred. No. 1.6;
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Best Local Sin
Matches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT FILING DATE: 105/09/739,449
CURRENT FILING DATE: 2000-12-19
CURRENT FILING DATE: 1000-12-19
                                                                                                                                                                                            Sequence 21503, Application US/09737223
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SEQ ID NO 219
LENGTH: 542340
                                                  NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 21503
LENGTH: 473
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                                                                                                                       CURRENT APPLICATION NUMBER: US/09/737, 223
CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 09/332,782
PRIOR FILING DATE: 1999-06-04
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               TYPE: DNA
ORGANISM: Homo sapiens
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                         344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 TGTATCCTTCATGGAGGCGGTTTTGTAATAGGCGATGTGGAATCTTATGACCCATTATGTA 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tctatctgcatggcggcggccttgtcgtgggcgggctggacagccatgatgacgtctgtg 96156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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52.78;
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; OTHER INFORMATION: n = A,T,C
US-09-737-223-21503
                 RESULT 9
US-09-335-032-12206/c
Sequence 12206, Application US/09335032
GENERAL INFORMATION:
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, NAME/KEY: misc_feature

; LOCATION: (1)...(403789)

; OTHER INFORMATION: n = A,T,C or G

US-60-248-505-197
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GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: c1000918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 197
LENCTH: 403789
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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Best Local Similarity
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APPLICANT: Velculescu, Victor
                                                                                                                           139204 acatataataaaacaatgctttaacaagtcttcatgaagaatctaacttcacaaccca 139261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: (1)...(473)
                                                                                                                                                                                                                                           448
                                                                                                                                                                                                                                                                                                                   388
                                                                                                                                                                                                                                                                                                                                                                      328 TATAGGTTAGCTCCAGAATACAAGTTTCCTTCTGCAGTTATCGATTCATTTGACGCTACT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 AATGCGTGCAATTGCGTTGTAGTATCAGTGGACTATAGGTTAGCTCCAGAATACAAGTTT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239
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                                                                                                                                                     TTGAAGTATCAAATACTGGTTTACCCAGCGGTAAGTTTAGATAACGTTTCAAGATCCA 565
                                                                                                                                                                                                                                                                                                  AATTGGGTTTATAACAATTTAGATAAATTTGATGGAAAGATGGGAGTTGCGATTGCGGGA 447
                                                                                                                                                                                                                                       GATAGTGCTGGAGGAAATTTGGCAGCGGTTGTAGCTCTTCTTTCAAAGGGTAAAATTAAT 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cctgagcaaattcatgatgttgtacgggccacaaagt 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gaggaattgaatgctgtcattgtttccattgaatacaggctagttccaaaaggtttatttt 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggctgggccttggcaagtgcaaaaatcaggtattatgatgagctgtgtacagcaatggct 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAGGCGGTTTTGTAATAGGCGATGTGGAATCTTATGACCCATTATGTAGAGCAATTACA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81;
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Pred. No. 18;
0; Mismatches 127;
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Pred. No. 2;
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Best Local Similarity
Watches 73; Conserve
                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description US-09-270-849B-1126
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SEQ ID NO 1126
LENGTH: 964
TYPE: DNA
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APPLICANT: Swimmer et al.
TITLE OF INVENTION: Insect genome survey devices
                                                                                                                                                                          Query Match
Best Local Similarity
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SEQ ID NO 12206
LENCTH: 315341
TYPE: DNA
                                                                                                                                                          Matches
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CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
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CURRENT FILING DATE: 1999-06-16
PRIOR APPLICATION NUMBER: US 60/035,917
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: US 09/012,031
PRIOR FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 12219
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APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: Characterization of the Yeast
TITLE OF INVENTION: Transcriptome
FILE REFERENCE: 01107.78572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                    550 AACGTTTCAAGATCCATGATAGAGTACTCTGATGGGTTCTTCCTTA 595
                                                                                                                490 TCAAAGGGTAAAATTAATTTGAAGTATCAAATACTGGTTTACCCCAGCGGTAAGTTTAGAT 549
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                                                                          763 taaaaggaggaaacgaatccatctttataaattatgtttaatcgggcattgatgctgaat 822
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aacgtttgaaattccgtggtatacaactgaattgccttcttctta
                                                                                                                                                        61;
                                                                                                                                                        Conservative
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53.3%;
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57.5%;
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Pred. No. 19;
0; Mismatches
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                                                                                                                                                                            Score 34; I
Pred. No. 5.
                                                                                                                                                                                                                                                                          of Artificial Sequence:
                                                                                                                                                        Mismatches
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RESULT 11 US-08-956-171C-128 ; Sequence 128, App

Application US/08956171C

GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                              RESULT
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                                                                                                                                                                                                       Sequence 12205, Application US/09335032 GENERAL INFORMATION:
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Best Local
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APPLICANT: Velculescu, Victor
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: Characterization
TITLE OF INVENTION: Transcriptome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (301) 30 TELEFAX: (301) 30 TELEPHONE: (301)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 AAAAGTAGAAGATATAAAAAT 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 TCCTAGAATTAAAAAGTTACTAGAATCAGCTCTTACTATACCAATTGGTAAAGCCCCAGT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
COMPUTER: HP Vectra 486/33
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TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
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LENGTH: 6048 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 610-5790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCAGTAATTTGTGCACCAGCAATTCAATTAGATGCATTAACTACTGCAGTTAAAGAAGG 3818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Pred. No. 11;
0; Mismatches
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                                              of the Yeast
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RESULT 14
US-09-270-849B-52466/c
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US-09-737-223-11751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-12205
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11751, App. GENERAL INFORMATION
                                                                                                                         Sequence 52466, Application US/09270849B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.6%;
Best Local Similarity 55.8%;
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LENGTH: 813137
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                                                             APPLICANT: Swimmer et al.
TITLE OF INVENTION: Insect genome survey devices
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/737,223
CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 09/332,782
PRIOR FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/270,849B
CURRENT FILING.DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
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PRIOR FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 12219
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CURRENT FILING DATE: 1999-06-16
PRIOR APPLICATION NUMBER: US 60/035,917
PRIOR FILING DATE: 1997-01-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                          93 TAGGCAATTAGCGTCGGCAGCTCCCAAAGTCGAAGTTGGAAAAGTAGAAGATA 145
                                                                                                                                                                                                                                                                                                                                                                         66 agcataagctgtggccatgactactgaagtaggctctgtgtctgaagtgaagaaggactc 125
                                                                                                                                                                                                                                                tagccagttaggaacagatgcaaccaaggaaaacctaaagaagtagcagaaa 178
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Pred. No. 9.
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FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/270,849B
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9923
LENGTH: 1585
TYPE: DNA
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-849B-9923
Search completed: June 3, Job time: 28127 sec
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US-09-270-849B-9923/c
; Sequence 9923, Application US/09270849B
; GENERAL INFORMATION:
; APPLICANT: Swimmer et al.
; TITLE OF INVENTION: Insect genome survey devices
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-849B-52466
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SEQ ID NO 52466
LENGTH: 719
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.6
Best Local Similarity 47.2
Matches 100; Conservative
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Best Local Similarity 57.1%;
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                                                                                                                         531 CCCAGCGGTAAGTTTAGATAACGTTTCAAGAT 562
                                                                                                                                                                                                      471 AGCGGTTGTAGCTCTTTTCAAAGGGTAAAATTAATTTGAAGTATCAAATACTGGTTTA 530
                                                                                                                                                                                                                                                            477 AAAGTTTTCTGTACTTTTTTTTTTTTTTTTTTTTTATATATCTTAAAGCAACGTTTT 418
                                                                                                                                                                                                                                                                                                                                             214 ATACATGGGCTTGCTATTAGCTTAGAATACCTGAGTTCTTGCGGT 170
                                                                                                  357 TGTTTCGATTTCTTTTTATATATTTTCTCGAT 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.6%; Score 32.8; 47.2%; Pred. No. 14;
                   2001, 04:05:08
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Pred. No. 10;
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5989 TCCTAGTATTATTTCACACCCTTATATATCACCCCTTATCTATGGTGAGTTTCACGAACT 5930
                                                                                                                                                                                    6049 TGATGCCCCCTCCCTTACAGGAGGAGAAATGGAATTTTATACCGCATGTTACGTTTCTGA 5990
                                                                                                                                                                                                                                                 6106 TGGTCAAGCTTTAATTAGCCCTGTATTGGAT---TTTACCCGATGGAGAAATGGCGGAAA 6050
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                                                         639 CCCTGCAGATTTGCTAGACTTTAGGTTCTCTCCAATTCTGGCGCAAGATTTCAACGGATT 698
                                                                                                                                                                                                      579 TGATGGGTTCTTACCAGAGAGCATATAGAGTGGTTCGGTTCTCAATACTTACGAAG 638
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                              759 TGCAAATAAACTACTACAAGCTGGAGTCTCAGT 791
                                                                                                                                                                                                                                                                                                                                  AGGAAATTTGGCAGCGGTTGTAGCTCTTTCTTTCAAAGGGTAAAATTTAATTTGAAGTATCA 518
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Search completed: June 3, 2001, 02:13:58 Job time: 44736 sec

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RESULT 14
US-60-215-161-2527/c
Cruence 2527, Application US/60215161
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; LOCATION: (10722)..(11393)
US-60-215-161-2527
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Best Local Similarity
Matches 302; Conserv
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SEQ ID NO 2527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences FILE REFERENCE: 38-21(5184')A CURRENT APPLICATION NUMBER: US/60/215,161
CURRENT FILING DATE: 2000-06-30
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TYPE: DNA
ORGANISM: Xenorhabdus
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                                                                                                                              222 AGTGTATCTTCATGGAGGCGGTTTTGTAATAGGCGATGTGGAATCTTATGACCCCATTATG 281
                                                                                                                                                                                                                    162 TGAAACCGTTATAAACGCTAGAGTGTATTTTCCGAAGAGTAGCGGTCCTTATGGTGTTCT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              639
AGAATACAAGTTTCCTTCTGCAGTTATCGATTCATTTGACGCTACTAATTGGGTTTATAA 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAATTTAGATAAATTTGGATGGAAAG---ATGGGAGTTGCGATTGCGGGAGATAGTGCTGG 458
                                  AGCTGAAATAGCTTCAAAAAACACAAGTAAGAGTCATGGCTGTTGATTTTAGATTAGCTCC
                                                                      TAGAGCAATTACAAATGCGTGCAATTGCGTTGTAGTATCAGTGGACTATAGGTTAGCTCC 341
                                                                                                           AATTTATATTCGTGGCGGATTTGTTGTGGGCTCGTTAGATTCGCATCATAGTGTTAC 6347
                                                                                                                                                                                    TGGAAAATATTTGAAATTTCGTATTTATGAACCACTACATATAGATAATGACGGATTAAT 6407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCTACTGCTTATATAATGGGGGCAGAAAAAGATCCTTTAGTTATTGATGCTCAAGAGTA 5870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCTAGTATTATTTCACACCCTTATATATCACCCCTTATCTATGGTGAGTTTCACGAACT
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Slater, Steven C.
Spiridonov, Sergei
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                                                                                                                                                                                                                                                              Conservative
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47.7%;
                                                                                                                                                                                                                                                                            Score 81; DB 53; Length 18187; Pred. No. 1e-11;
                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                              ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9599)..(10735)
US-60-215-161-2528
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                                                                                                                                                                                                                                                                                                                                                                                         : NUMBER OF SEQ ID NOS:
SEQ ID NO 2528
: LENGTH: 18187
: TYPE: DNA
: ORGANISM: Xenorhabdus :
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Best Local Similarity
Matches 302; Conserv
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CURRENT APPLICATION NUMBER: US/60/215,161
CURRENT FILING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                            6406
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                                                                                                                                       6466 TGGAAAATATTTGAAATTTCGTATTTATGAACCACTACATATAGATAATGACGGATTAAT 6407
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459
                                                                                                                                                                           162 TGAAACCGTTATAAACGCTAGAGTGTATTTTCCGAAGAGTAGCGGTCCTTATGGTGTTCT 221
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                                                            AATTTATATTCGTGGTGGCGGATTTGTTGTGGGCTCGTTAGATTCGCATCATAGTGTTAC 6347
                                                                                              AGTGTATCTTCATGGAGGCGGTTTTGTAATAGGCGATGTGGAATCTTATGACCCATTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCTAGTATTATTTCACACCCTTATATATCACCCCTTATCTATGGTGAGTTTCACGAACT
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Hinkle, Gregory J.
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Huesing, Joseph E.
Krasomil-Osterfeld,
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                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                             8.8%; Score 81; DB 53;
47.7%; Pred. No. 1e-11;
vative 0; Mismatches 325;
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; ORGANISM: Xenorhabdus sp. FEATURE: AAME/KEY: CDS LCCATION: (16660)..(18186) US-60-215-161-2525
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US-60-215-161-2525
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CURRENT FILING DATE: 2000-06-30

NUMBER OF SEQ ID NOS: 8409

SEQ ID NO 2525

I.FNORTH: COLUMN AND ADDRESS OF THE PROPERTY OF TH
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TITLE OF INVENTION: Xenc
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12139 tgatgcccctctccttacaggaggagaaaatggaattttataccgcatgttacgtttctga 12198
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                                                                            402 CAATTTAGATAAATTTGATGGAAAG---ATGGGAGTTGCGATTGCGGGAGATAGTGCTGG
                                                                                                                                                                                                                                                                                                                                                                  282 TAGAGCAATTACAAATGCGTGCAATTGCGTTGTAGTATCAGTGGACTATAGGTTAGCTCC 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             699 ACCTCCAGCCTTGATAATAACAGCAGAATACGATCCACTAAGGGATCAAGGAGAAGCGTA
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                                                                                                                                                                                                                                        AGAATACAAGTTTCCTTCTGCAGTTATCGATTCATTTGACGCTACTAATTGGGTTTATAA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aatttatattcgtggtggcggatttgttgtgggctcgttagattcgcatcatagtgttac
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Huesing, Joseph E.
Krasomil-Osterfeld,
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; LOCATION: (14674)..(14781)
US-60-215-161-2526
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Sequence 2526, Application US/60215161;
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
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SEQ ID NO 2526
LENGTH: 18187
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Best Local Similarity
Matches 302; Conserv
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CURRENT FILING DATE: 2000-06-30
NUMBER OF SEC. 1
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                                                                                                                                                                                                     222 AGTGTATCTTCATGGAGGCGGTTTTGTAATAGGCGATGTGGAATCTTATGACCCATTATG
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                                                                              AGCTGAAATAGCTTCAAAAACACAAGTAAGATCATGCTGTTGATTTTAGATTAGCTCC
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AGAAAATCCATTTCCTCATTCTTTGGAGGATTGTTATAACGCTGTGATATATGCTCAAAA
                                     AGAATACAAGTTTCCTTCTGCAGTTATCGATTCATTTGACGCTACTAATTGGGTTTATAA 401
                                                                                                                        TAGAGCAATTACAAATGCGTGCAATTGCGTTGTAGTATCAGTGGACTATAGGTTAGCTCC 341
                                                                                                                                                                AATTTATATTCGTGGTGGCGGATTTGTTGTGGGCTCGTTAGATTCGCATCATAGTGTTAC
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Slater, Steven C.
Spiridonov, Sergei
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Huesing, Joseph E.
Krasomil-Osterfeld, Karina
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                                                                                                                                                                                                                                                                                                                                      Conservative
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47.7%;
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                                                                                                                                                                                                                                                                                                                                                   Score 81; DB 53; Length 18187; Pred. No. 1e-11;
                                                                                                                                                                                                                                                                                                                                    Mismatches 325; Indels
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; LOCATION: (12607)..(13749)
US-60-215-161-2523
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US-60-215-161-2523
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SEQ ID NO 2523
LENGTH: 18187
TYPE: DNA
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Best Local Similarity 47.7%;
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                                                                                                                                                                                                                                                                                                                                                                11782 aatttatattcgtggtggcggatttgttgtgggctcgttagattcgcatcatagtgttac 11841
                                                                                                                                                                                                                                                                                                                                                                                                                                                   11722 tggaaaatatttgaaatttcgtatttatgaaccactacatatagataatgacggattaat 11781
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                                                                                                                                                             402 CAATTTAGATAAATTTGATGGAAAG---ATGGGAGTTGCGATTGCGGGAGATAGTGCTGG 458
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AATACTGGTTTACCCAGCGGTAAGTTTAGATAACGTTTCAAGATCCATGATAGAGTACTC 578
                                    agctaatatggctgtagttattgcgatgatgtgtcgtgatagaaatggtcccaaatttgt 1208:
                                                                                                                       aaatgcatcatctctggggataaatccaaaataatataataattgctggagatagctctgg 12021
                                                                                                                                                                                                     agaaaatccatttcctcatttttggaggattgttataacgctgtgatatatgctcaaaa 11961
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                                                                            ACCTCCAGCCTTGATAATAACAGCAGAATACGATCCACTAAGGGATCAAGGAGAAGCGTA 758
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Hinkle, Gregory J.
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Huesing, Joseph E.
Krasomil-Osterfeld, Karina
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Pred. No. 1e-11;
0; Mismatches 325; Indels 6
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; LOCATION: (15211)..(16632)
US-60-215-161-2524
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CURRENT FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 2524
LENGTH: 18187
Typer: """
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Best Local Similarity 47.7%;
Matches 302; Conservative
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APPLICANT:
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ORGANISM: Xenorhabdus
                                                                  11962 aaatgcatcatctctggggataaatccaaataataataattactggaggatagctctgg 1202
                                                                                                                                                          11902 agaaaatccatttcctcattctttggaggattgttataacgctgtgatatatgctcaaaa 11961
                                                                                                                                                                                                                                                  11842 agctgaaatagcttcaaaaacacaagtaagagtcatggctgttgattttagattagctcc 11901
                                                                                                                                                                                                                                                                                                                                     11782 aatttatattcgtggtggcggatttgttgtgggctcgttagattcgcatcatagtgttac 11841
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402 CAATTTAGATAAATTTGATGGAAAG---ATGGGAGTTGCGATTGCGGGAGATAGTGCTGG 458
                                                                                                                                                                                    342 AGAATACAAGTTTCCTTCCTGCAGTTATCGATTCATTTGACGCTACTAATTGGGTTTTATAA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 TGAAACCGTTATAAACGCTAGAGTGTATTTTCCGAAGAGTAGCGGTCCTTATGGTGTTCT 221
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                                                                                                                                                                                                                                                                                                                                                                                   222 AGTGTATCTTCATGGAGGCGGTTTTGTAATAGGCGATGTGGAATCTTATGACCCATTATG 281
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Huesing, Joseph E.
Krasomil-Osterfeld, Karina
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Hinkle, Gregory J.
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Slater, Steven C.
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Pred. No. 1e-11;
0; Mismatches 325; Indels 6
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; LOCATION: (2550)..(3263)
US-60-215-161-2521
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Best Local Similarity 47.7%;
Matches 302; Conservative
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SEQ ID NO 2521
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CURRENT FILING DATE: 2000-06-20
NUMBER OF CENTRELY 2000-06-20
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TYPE: DNA
ORGANISM: Xenorhabdus
12139 tgatgcccctctccttacaggaggagaaatggaattttataccgcatgttacgtttctga 12198
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                                                                              12082 tggtcaagctttaattagccctgtattggat---tttacccgatggagaaatggcggaaa
                                                                                                                                                                                                                                                    11962
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                         TGATGGGTTCTTCCTTACCAGAGAGCATATAGAGTGGTTCGGTTCTCAATACTTACGAAG
                                                                                                                                                             {\tt agctaatatggctgtagttattgcgatgatgtgtcgtgatagaaatggtcccaaatttgt}
                                                                                                                                                                                      AGGAAATTTGGCAGCGGTTGTAGCTCTTCTTTCAAAGGGTAAAATTTAATTTTGAAGTATCA
                                                                                                                                                                                                                                             aaatgcatcatctctggggataaatccaaataataataataattgctggagatagctctgg
                                                                                                                                                                                                                                                                                        CAATTTAGATAAATTTGATGGAAAG---ATGGGAGTTGCGATTGCGGGAGATAGTGCTGG 458
                                                                                                                                                                                                                                                                                                                              agaaaatccatttcctcattctttggaggattgttataacgctgtgatatatgctcaaaa
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                                                                                                                      AATACTGGTTTACCCAGCGGTAAGTTTAGATAACGTTTCAAGATCCATGATAGAGTACTC
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Huesing, Joseph E.
Krasomil-Osterfeld, Karina
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Slater, Steven C.
Spiridonov, Sergei
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; LOCATION: (4440)..(6653)
US-60-215-161-2522
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LENGTH: 18187
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CURRENT APPLICATION NUMBER: US/60/215,161
CURRENT FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS:
1-ENORMAL SERVICE SERVICE
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Best Local Similarity 47.7%;
Matches 302; Conservative
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APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Xeno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11722 tggaaaatatttgaaatttcgtatttatgaaccactacatatagataatgacggattaat 11781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Xenorhabdus sp.
                                                                                                                                                                                                                                                                                                                              11962 aaatgcatcatctctggggataaatccaaataataataattactggtggagatagctctgg 12021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11902 agaaaatccatttcctcattctttggaggattgttataacgctgtgatatatgctcaaaa 11961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11842 agctgaaatagcttcaaaaacacaagtaagagtcatggctgttgattttagattagctcc 11901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11782 aatttatattcgtggtggcggatttgttgtgggctcgttagattcgcatcatagtgttac 11841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
12082 tggtcaagctttaattagccctgtattggat---tttacccgatggagaaatggcggaaa 12138
                                                                                  519 AATACTGGTTTACCCCAGCGGTAAGTTTAGATAACGTTTCAAGATCCATGATAGAGTACTC 578
                                                                                                                                                                                                                                                                                                                                                                                                            402 CAATTTAGATAAATTTGATGGAAAG---ATGGGAGTTGCGATTGCGGGAGATAGTGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342 AGAATACAAGTTTCCTTCTGCAGTTATCGATTCATTTGACGCTACTAATTGGGTTTATAA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 TGAAACCGTTATAAACGCTAGAGTGTATTTTCCGAAGAGTAGCGGTCCTTATGGTGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 TAGAGCAATTACAAATGCGTGCAATTGCGTTGTAGTATCAGTGGACTATAGGTTAGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 AGTGTATCTTCATGGAGGCGGTTTTGTAATAGGCGATGTGGAATCTTATGACCCCATTATG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCTGCAGATTTGCTAGACTTTAGGTTCTCTCCAATTCTGGCGCAAGATTTCAACGGATT
                                                                                                                                                                                                                                               ccctactgcttatataatgggggcagaaaaaagatcctttagttattgatgctcaagagta 12318
                                                                                                                                                                 agctaatatggctgtagttattgcgatgatgtgtcgtgatagaaatggtcccaaatttgt
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Huesing, Joseph E.
Krasomil-Osterfeld, Karina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325;
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TGCAAATAAACTACTACAAGCTGGAGTCTCAGT

791

TACAAATAAACTAAATTCAAATGGTATCGATGT 5837

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APPLICANT: Hinkle, Gregory J.

TITLE OF INVENTION: Xenorhabdus sp. Ge
FILE REFERENCE: 38-21(51847)A

CURRENT APPLICATION NUMBER: US/60/215,161

CURRENT FILING DATE: 2000-06-30

NUMBER OF SEQ ID NOS: 8409

SEQ ID NO 2519

LENGTH: 18187

TYPE: DNA

ORGANISM: Xenorhabdus sp.
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US-60-215-161-2519
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; LOCATION: (369)..(1274)
US-60-215-161-2519
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Best Local Similarity 47.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 TGAAACCGTTATAAACGCTAGAGTGTATTTTCCGAAGAGTAGCGGTCCTTATGGTGTTCT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTGTATCTTCATGGAGGCGGTTTTGTAATAGGCGATGTGGAATCTTATGACCCATTATG 281
ACCTCCAGCCTTGATAATAACAGCAGAATACGATCCACTAAGGGATCAAGGAGAAGCGTA 758
                                                                                                                                                                         TGATGGGTTCTTCCTTACCAGAGAGCATATAGAGTGGTTCGGTTCTCAATACTTACGAAG 638
                                                                                                                                                                                                                    tggtcaagctttaattagccctgtattggat---tttacccgatggagaaatggcggaaa 12138
                                                                                                                                                                                                                                                AATACTGGTTTTACCCAGCGGTAAGTTTTAGATAACGTTTTCAAGATCCATGATAGAGTACTC 578
                                                                                                                                                                                                                                                                                                         agctaatatggctgtagttattgcgatgatgtgtcgtgatagaaatggtcccaaatttgt 1208:
                                                                                                                                                                                                                                                                                                                                       AGGAAATTTGGCAGCGGTTGTAĢCTCTTTCAAAGGGTAAAATTAATTTGAAGTATCA 518
                                                                                                                                                                                                                                                                                                                                                                                                CAATTTAGATAAATTTGATGGAAAG---ATGGGAGTTGCGATTGCGGGAGATAGTGCTGG 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agaaaatccatttcctcattctttggaggattgttataacgctgtgatatatgctcaaaa 11961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAATACAAGTTTCCTTCTGCAGTTATCGATTCATTTGACGCTACTAATTGGGTTTATAA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agctgaaatagcttcaaaaacacaagtaagagtcatggctgttgattttagattagctcc 11901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aatttatattcgtggtggcggatttgttgttgggctcgttagattcgcatcatagtgttac 11841
                                         tectagtattattteaeaecettatateaeceettatetatggtgagttteaegaaet 12258
                                                                                    CCCTGCAGATTTGCTAGACTTTAGGTTCTCCCAATTCTGGCGCAAGATTTCAACGGATT 698
                                                                                                                             tgatgcccctctccttacaggaggagaaatggaattttataccgcatgttacgtttctga 12198
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Huesing, Joseph E.

Krasomil-Osterfeld, Karina C.

Malvar, Thomas M.

Slater, Steven C.

Spiridonov, Sergei
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; LOCATION: (1288)..(2337)
US-60-215-161-2520
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GENERAL INFORMATION:
APPLICANT: Corbin, David R.
APPLICANT: Goldman, Barry S.
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Best Local Similarity 47.7%;
Matches 302; Conservative
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SEQ ID NO 2520
LENGTH: 18187
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11722 tggaaaatatttgaaatttcgtatttatgaaccactacatatagataatgacggattaat 11781
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                                                                                                                                                                                                                                                                                            12082 tggtcaagctttaattagccctgtattggat---tttacccgatggagaaatggcggaaa 12138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11902 agaaaatccatttcctcattctttggaggattgttataacgctgtgatatatgctcaaaa 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11842 agctgaaatagcttcaaaaacacaagtaagagtcatggctgttgattttagattagctcc 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               402 CAATTTAGATAAATTTGATGGAAAG---ATGGGAGTTGCGATTGCGGGAGATAGTGCTGG 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 TGAAACCGTTATAAAACGCTAGAGTGTATTTTCCGAAGAGTAGCGGTCCTTATGGTGTTTCT 221
639 CCCTGCAGATTTGCCTAGACTTTAGGTTCTCTCCAATTCTGGCGCAAGATTTCAACGGATT 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              342 AGAATACAAGTTTCCTTCTGCAGTTATCGATTCATTTGACGCTACTAATTGGGTTTATAA 401
                                                                                                                                                                                                                                                                                                                                                                                   519 AATACTGGTTTACCCAGCGGTAAGTTTAGATAACGTTTCAAGATCCATGATAGAGTACTC 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 TAGAGCAATTACAAATGCGTGCAATTGCGTTGTAGTATCAGTGGACTATAGGTTAGCTCC 341
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                                                                                                                              tgatgcccctctccttacaggaggagaaatggaattttataccgcatgttacgtttctga 12198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agctaatatggctgtagttattgcgatgatgtgtcgtgatagaaatggtcccaaatttgt 12081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGAAATTTGGCAGCGGTTGTAGCTCTTCTTTCAAAGGGTAAAATTTAATTTGAAGTATCA 518
                                                                                                                                                                                                                 TGATGGGTTCTTCCTTACCAGAGAGCATATAGAGTGGTTCGGTTCTCAATACTTACGAAG
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Slater, Steven C.
Spiridonov, Sergei
Hinkle, Gregory J.
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Huesing, Joseph E.
Krasomil-Osterfeld, Karina
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: NUMBER OF SEQ ID NOS: 8252

: SEQ ID NO 817

: LENGTH: 1092

: TYPE: DNA

: ORGANISM: Acinetobacter baumannii

US-09-328-352-817
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Best Local Similarity
Matches 366; Conserv
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
EILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                  1012
1072 ttttgggataaaaatagttaa
                         898 GTATTTTATGATAAAATTTAA 918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481
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                                                                              actccgatttctagaaaagcaaaacgttatacgatcgaaattagtaaaaactttagaaag 107:
                                                                                                                                                                                        GCTGGAGTCTCAGTTACTAGTGTGAGATTTAACAACGTTATACACGGATTCCTCTCATTC
                                                                                                                                                                                                                                                                                                                        gatccaataatttcacctacctatggcaatctaaagaaaaacccgcctgcttttgtgatt
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                                                                                                                         TTTCCGTTGATGGAGCAAGGAAGATGCTATAGGTCTGATAGGGTCTGTGTTAAGACGA
                                                                                                                                                             aatggcgtgaaaatgcattatgaagaatttctggatcagacccatggctttattaacctg
                                                                                                                                                                                                                                             acagcggggcatgatgttttacatgatgaagctaaaatatatagtcataagttaagacaa
                                                                                                                                                                                                                                                                                      ACAGCAGAATACGATCCACTAAGGGATCAAGGAGAAGCGTATGCAAATAAACTACTACAA 777
                                                                                                                                                                                                                                                                                                                                                                  TTTAGGTTCTCCCAATTCTGGCGCAAGATTTCAACGGATTACCTCCAGCCTTGATAATA
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Pred. No. 1.1e-12;
0; Mismatches 429;
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CURRENT APPLICATION NUMBER: US/60/215,161
CURRENT FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 408
LENGTH: 18187
TYPE: DNA
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; NAME/KEY: CDS
; LOCATION: (8143)..(8541)
US-60-215-161-408
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Matches 302; Conserv
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Best Local :
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ORGANISM: Xenorhabdus
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                                                                                                                                                                                                                                                                                                                                                                                         CAATTTAGATAAATTTGATGGAAAG----ATGGGAGTTGCGATTGCGGGAGATAGTGCTGG
                                                                                                                                                                                                                                        AATACTGGTTTACCCAGCGGTAAGTTTAGATAACGTTTTCAAGATCCATGATAGAGTACTC
                                                                                                                                                                                                                                                                                          AGCTAATATGGCTGTAGTTATTGCGATGATGTCGTGATAGAAATGGTCCCAAATTTGT
                                                                                                                                                                                                                                                                                                                 AGGAAATTTGGCAGCGGTTGTAGCTCTTCTTCAAAGGGTAAAATTTAATTTGAAGTATCA
CCCTACTGCTTATATATGGGGGGCAGAAAAAGATCCTTTAGTTATTGATGCTCAAGAGTA
                                  ACCTCCAGCCTTGATAATAACAGCAGAATACGATCCACTAAGGGATCAAGGAGAAGCGTA 758
                                                                                                          CCCTGCAGATTTGCTAGACTTTAGGTTCTCTCCAATTCTGGCGCAAGATTTCAACGGATT
                                                                                                                                             TGATGCCCCTCTCCTTACAGGAGGAGAAATGGAATTTTATACCGCATGTTACGTTTCTGA
                                                                                                                                                                               TGATGGGTTCTTCCTTACCAGAGAGCATATAGAGTGGTTCGGTTCTCAATACTTACGAAG
                                                                                                                                                                                                                   TGGTCAAGCTTTAATTAGCCCTGTATTGGAT---TTTACCCGATGGAGAAATGGCGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAATACAAGTTTCCTTCTGCAGTTATCGATTCATTTGACGCTACTAATTGGGTTTATAA
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Slater, Steven C.
Spiridonov, Sergei
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Pred. No. 1e-11;
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Best Local
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 936 NUCLEOTIDES
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: GENOMIC DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
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 838
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hes 369;
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TOPOLOGY: LINEAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
SOFTWARE: WORD PE
                                                                                                                                                                           GATTTCAACGGATTACCTCCAGCCTTGATAATAACAGCAGAATACGATCCACTAAGGGAT 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTCTAGTGTATCTTCATGGAGGCGGTTTTGTAATAGGCGATGTGGAATCTTATGACCCA 276
TACAGAGGCGTGCTTCACGGATTCATCAATTACTATCCCGTGCTGAAGGCTGCGAGGGAT
                               TTTAACAACGTTATACACGGATTCCTCTCATTCTTTCCGTTGATGGAGCAAGGAAGAGAT 864
                                                                    GAAGGAGAAGTTTTCGGGCAGATGCTGAGAAGAGCCGGTGTTGAGGCGAGCATCGTCAGA
                                                                                                        CAAGGAGAAGCGTATGCAAATAAACTACTACAAGCTGGAGTCTCAGTTACTAGTGTGAGA
                                                                                                                                         CTTGAGAAC --- CTACCTCCTGCGCTGATCATAACCGCCGAATACGACCCGCTGAGAGAT
                                                                                                                                                                                                                  CAGTACTTCTCCAGAGAGAAGATAAGTTCAAGCCCCTCGCCTCCGTAATCTTTGCGGAC
                                                                                                                                                                                                                                                    CAATACTTACGAAGCCCTGCAGATTTGCTAGACTTTAGGTTCTCTCCAATTCTGGCGCAA 684
                                                                                                                                                                                                                                                                                       CTGGAGTTTGGAGAGGGGCTGTGGATTCTCGACCAGAAGATAATGAGTTGGTTCTCGGAG
                                                                                                                                                                                                                                                                                                           ATAAAGCATCAAATTCTAACTTACCCCGTTGTGAACTTTGTAGCCCCCACACCATCGCTT 600
                                                                                                                                                                                                                                                                                                                                                                                  TTGAAGTATCAAATACTGGTTTACCCAGCGGTAAGTTTAGATAACGTTTCAAGATCCATG 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGGAGGAAATTTGGCAGCGGTTGTAGCTCTTCTTTC-----AAAGGGTAAAATTAAT 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGAGAACCGGGAGGAGCTGAGGATTGACCCGTCAAAAATCTTCGTTGGGGGGGACAGT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATAACAATTTAGATAAATT---TGATGGAAAGATGGGAGTTGCGATTGCGGGAGATAGT 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTCCTGAGCACAAGTTTCCCCCCCCCAGTTTATCATTGCTACGATGCGACCAAGTGGGTT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTCCAGAATACAAGTTTCCTTCTGCAGTTATCGATTTCATTTTGACGCTACTAATTTGGCTT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTATGCAGGAGAAYYGCGAGACTTTCAAACTCTACCGTAGTCTCCGTGGATTACAGGCTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTATGTAGAGCAATTACAAATGCGTGCAATTGCGTTGTAGTATCAGTGGACTATAGGTTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGGGACGGAATCTTGCCCCGGCGCTTTCAATAATGGCGAGAGACAGCGGAGAAGATTTC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 54.(
69; Conservative
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WORD PERFECT 6.0
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Pred. No. 2.6e-28;
2; Mismatches 297;
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US-09-328-352-817; Sequence 817, Application US/09328352; GENERAL INFORMATION:

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CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILLING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 619
LENGTH: 999
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-619
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US-09-328-352-619
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GENERAL INFORMATION:
APPLICANT: GRAY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 287; Conserv
                                                                                                                                                                                                                                            462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282 tgtgttgtatctacatggtggtggttggatggtgggtggactcgattcacatgagtttat 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            898 GCGATAAACCAGATTGCCGCTCT
                      AGCGTATGCAAATAAACTACTACAAGCTGGAGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAACAATTTAGATAAATTTGATGGAAAGATGGGAG---TTGCGATTGCGGGAGATAGTGC 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCAGAATACAAGTTTCCTTCTGCAGTTATCGATTCATTTGACGCTAATTGGGTTTA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTAGTGTATCTTCATGGAGGCGGTTTTGTAATAGGCGATGTGGAATCTTATGACCCATT 278
                                                                                                                                                                                  ACGAAGCCCTGCAGATTTGCTAGACTTTAGGTTCTCTCCAATTTCTGGCGCAAGATTTCAA 692
                                                                                                                                                                                                                                                                                   GTACTCTGATGGGTTCTTCCTTACCAGAGAGCATATAGAGTGGTTCGGTTCTCAATACTT 632
                                                                                                                                                                                                                                                                                                                                                                GTATCAAATACTGGTTTACCCAGCGGTAAGTTTAGATAACGTTTCAAGATCCATGATAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 accagagcatcgctttccagcagcctttgaagattgtttagcagtgtatcactggcttaa 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               taccagttatttgtgtaaggacttaaatgcggttgttattggtgtggattaccgcttggc 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGTAGAGCAATTACAAATGCGTGCAATTGCGTTGTAGTATCAGTGGACTATAGGTTAGC
tctctttacccaaaaactggaacaagcaggcatccc
                                                                            agatatgcctacaagttttgtggctgttgcagaatatgaccctttaagtgatgacggtta
                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGAGGAAATTTGGCAGCGG---TTGTAGCTCTTCTTTCAAAGGGTAAAATTAATTTGAA 512
                                                                                                                      CGGATTACCTCCAGCCTTGATAATAACAGCAGAATACGATCCACTAAGGGATCAAGGAGA 752
                                                                                                                                                               tccgaactcacaagattggcaggatttacgtctagctcctttattggcgacggacttttc 761
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; LENGTH: 918 NUCLEOTI
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: GENOMIC
US-09-382-242-32
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                                                                                                                                                              Query Match
Best Local Similarity
Matches 918; Conserva
                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION UNMBER: 38,347
REFERENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-570
                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 918 NUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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 181
                    181
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                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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AGAGTGTATTTTCCGAAGAGTAGCCGGTCCTTATGGTGTTCTAGTGTATCTTCATGGAGGC
                                                                                AAAGCCCCAGTAGAAGAGGTAAGAAAGATATTTAGGCAATTAGCGTCGGCAGCTCCCAAA 120
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CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4225 EXECUTIVE SQUARE, STE 1400
                                                                                                                                                                                                                                                                                                         619-678-5099
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VENTION: ESTERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MURPHY, Den
REID, John
MAFFIA, Ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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WORD PERFECT 6.0
                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LINK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROBERTSON, Daniel E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PS/2
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                                                                                                                                                                                                                                GENOMIC DNA
                                                                                                                                                                                                                                                    SINGLE
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                                                                                                                                                                          100.0%;
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                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                     09010/010001
                                                                                                                                                                          Score 918; DB 17
Pred. No. 2e-252;
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                                                                                                                                                                                     DB 17;
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APPLICANT:
                                                                                                                                  APPLICANT:
                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     APPLICANT:
                                                                                         NUMBER OF SEQUENCES:
                                                                                                    TITLE OF INVENTION:
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                                                                                                                          APPLICANT:
                                     STREET: 4225 EX
CITY: LA JOLLA
STATE: CALIFORN
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                   ZIP:
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                                                                       ADDRESSEE:
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                                      CALIFORNIA
                                                           4225 EXECUTIVE
                                                                                                                                                              MURPHY, Den
                             USA
                                                                                                            KOSMOTKA,
                                                                                                                                                                          Dennis
                                                                                                              Anna
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Sequence 31, Application US/09382242 GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      841 CCGTTGATGGAGCAAGGAGATGCTATAAGGTCTGATAGGGTCTGTGTTAAGACGAGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 GCTCTTCTTTCAAAGGGTAAAATTAATTTGAAGTATCAAATACTGGTTTACCCCAGCGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGTTCTCCAATTCTGGCGCAAGATTTCAACGGATTACCTCCAGCCTTGATAATAACA
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                                                                                                                                                                                                                                                                                                                                    LINK, Steven
SWANSON, Ronald V.
WARREN, Patrick V.
                                                                                                                                                                                                                                                                                                                                                                                                                      MAFFIA, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROBERTSON, Daniel E.
                                                                                                                                                                                                                 FISH & RICHARDSON
                                INCH DISKETTE
                                                                                                                                                                                                                                                                                              ESTERASES
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
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1: /cgn2_6/ptodata/2/pna/VC

2: /cgn2_6/ptodata/2/pna/US

3: /cgn2_6/ptodata/2/pna/US

4: /cgn2_6/ptodata/2/pna/US

5: /cgn2_6/ptodata/2/pna/US

6: /cgn2_6/ptodata/2/pna/US

7: /cgn2_6/ptodata/2/pna/US

8: /cgn2_6/ptodata/2/pna/US
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918
1 ATGCCCCTAGATCCTAGAAT.....TATTTTATGATAAAATTTAA 918
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1275.941 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
                                                                                                         cgn2_6/ptodata/2/pna/US082_COMB.seq: *
cgn2_6/ptodata/2/pna/US083_COMB.seq: *
cgn2_6/ptodata/2/pna/US084_COMB.seq: *
cgn2_6/ptodata/2/pna/US085_COMB.seq: *
cgn2_6/ptodata/2/pna/US086_COMB.seq: *
cgn2_6/ptodata/2/pna/US086_COMB.seq: *
cgn2_6/ptodata/2/pna/US086_COMB.seq: *
cgn2_6/ptodata/2/pna/US089_COMB.seq: *
cgn2_6/ptodata/2/pna/US090_COMB.seq: *
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cgn2_6/ptodata/2/pna/US097B_COMB.seq: *
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cgn2_6/ptodata/2/pna/US000C_COMB.seq: *
cgn2_6/ptodata/2/pn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/pna/US06
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44: /cgn2_6/ptodata/2/pna/US6012_COMB.seq:*
45: /cgn2_6/ptodata/2/pna/US6013_COMB.seq:*
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59: /cgn2_6/ptodata/2/pna/US6020_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

0 0	o	0 0000	Result No.
44444 90 12 13 14 13	22222222222222422002242200024	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	NO.
442.4 42.4 41.6 41.8	44444 455555 300000000000000000000000000000000		Score 918 137 91.2 82.6
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Sequence 2343, App Sequence 430, App Sequence 954, App Sequence 2773, App Sequence 7244, Ap Sequence 6216, Ap Sequence 5961, Ap	e 9983 A e 9983 A e 767 App e 767 App e 767 App e 12043 A e 10682 A e 10682 A e 14381 A e 4341 A e 4341 A	equence 2510, equence 2521, equence 2521, equence 2524, equence 2526, equence 2527, equence 2527, equence 2527, equence 2527, equence 2529, equence 2530, equence 2531, eq	cription equence 32, App equence 31, App equence 619, Ap equence 817, Ap equence 817, Ap

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Post-processing: Minimum Match 0%
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-08-602-359A-32
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US-08-232-463-1
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US-08-928-361B-3
US-08-973-462-3
US-08-973-462-2
US-08-973-462-1
US-08-98-1-891-79-1
US-08-682-517-14
US-08-682-517-14
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Sequence 31, Appl
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Sequence 2, Appli
Sequence 3, Appli
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Sequence 3, Appli	Sequence 5, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 5, Appli	Sequence 9, Appli	Sequence 10, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Patent No. 5231168

ALIGNMENTS

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US-08-602-359A-32
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ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION: 619-678-5070
TELEPHONE: 619-678-5070
TELEPAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 NUCLEOTIDES
TYPE: NUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32, Appli
Patent No. 5942430
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,35:
FILING DATE: February 16, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
             TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: GENOMIC
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TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
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4225 EXECUTIVE SQUARE, STE 1400
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SWANSON, Ronald V.
WARREN, Patrick V.
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REID, John
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                 GENOMIC DNA
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RESULT 2 US-08-602-359A-31

Sequence 31, Application US/08602359A

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; STRANDEDNESS: SINGI
; TOPOLOGY: LINEAR
; MOLECULE TYPE: GENOM:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 936 NUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKET
COMPUTER: IBM PS.7
COPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: WARREN, Patrick V. APPLICANT: KOSMOTKA, Anna TITLE OF INVENTION: ESTERASES NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08 FILING DATE: February 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: UZIP: 92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                               GCTCCAGAATACAAGTTTCCTTCTGCAGTTATCGATTCATTTGACGCTACTAATTGGGTT
TTGAAGTATCAAATACTGGTTTACCCAGCGGTAAGTTTAGATAACGTTTCAAGATCCATG
                                                            GCTGGAGGAAATTTGGCAGCGGTTGTAGCTCTTTC----AAAGGGTAAAATTAAT
                                                                                                GCTGAGAACCGGGAGGAGCTGAGGATTGACCCGTCAAAAATCTTCGTTGGGGGGGACAGT
                                                                                                                              TATAACAATTTAGATAAATT---TGATGGAAAGATGGGAGTTGCGATTGCGGGAGATAGT
                                                                                                                                                               GCTCCTGAGCACAAGTTTCCCCCCCCCAGTTTATCATTGCTACGATGCGACCAAGTGGGTT
                                                                                                                                                                                                                           TTATGCAGGAGAAYYGCGAGACTTTCAAACTCTACCGTAGTCTCCGTGGATTACAGGCTC
                                                                                                                                                                                                                                              TTATGTAGAGCAATTACAAATGCGTGCAATTGCGTTGTAGTATCAGTGGACTATAGGTTA 336
                                GCGGGACGGAATCTTGCCCCGGCGCTTTCAATAATGGCGAGAGACAGCGGAGAAGATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4225 EXECUTIVE
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REID, John
MAFFIA, Ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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SWANSON, Ronald V.
WARREN, Patrick V.
                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENOMIC DNA
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                                                                                                                                                                                                                                                                                                                                                          Score 137; DB 2; 1
Pred. No. 1.9e-33;
2; Mismatches 297;
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E, STE 1400
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US-08-232-463-14/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                            FILING DATE:
APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                     TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                         SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          778
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
STRANDEDNESS: single
                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTAACAACGTTATACACGGATTCCTCTCATTCTTTCCGTTGATGGAGCAAGGAAGAGAT 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAGGAGAAGTTTTCGGGCAGATGCTGAGAAGAGCCGGTGTTGAGGCGAGCATCGTCAGA 837
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                   nucleic acid
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                                                                                                                             (703)683-4109
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                                                                                                                                                                                            30472/114 IMMU
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; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CLASSIFICATION:
ATTORNEY/AGENT IN
                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KEELING, PETER L. APPLICANT: KNIGHT, MARY E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1161 REFERENCE TERRETERE 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP:
                                                                                             APPLICATION NUMBER: 08/3 FILING DATE: 29-NOV-1994 CLASSIFICATION: 800
                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 15-DEC-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pilispuly Purchaser: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 AATTAAAAAGTTACTAGAATCAGCTCTTACTATACCAATTGGTAAAGCCCCCAGTAGAAGA 77
                                          FILING DATE:
                                                                                                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTGGAATCTTATGACCCATTATGTAGAGCAATTACAAATGCGTGCAATTGCGTTGTAGT 317
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                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                  CUSHMAN DARBY & CUSHMAN
Intellectual Property Group
Pillsbury Madison & Sutro Li
     INFORMATION:
                                      21-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MODIFICATION OF STARCH
SYNTHESIS IN PLANTS
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                                                                                                                                  08/346,602
                                                                                                                                                                                                          us/08/572,951
                                                          08/263,921
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                                                                                                                                                                                                                                               Version #1.25
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; TYPE: DNA ; ORGANISM: Cryptosporidium parvum US-08-700-651-1
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Best Local Similarity 27.3
    Matches 126;
                                           Query Match
                                                                                                                                                                                              SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08700651B Patent No. 6015882
                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                           TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPTOSPORIDIUM PARVUM TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILLING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILLING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202) 822-9944
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2380 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: PETERSEN, CAROLYN
                                                                                                                                                                        ENGTH: 5163
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REFERENCE/DOCKET NUMBER: 2021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1496 AYTAYACNAAYTAYACNTTYGARACNYTNG 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1376 ARGGNGGNTGGGGNYTNCAYGAYATHATHAAYCARAAYGAYTGGAARYTNCARGGNATHG 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1316 ARACNGCNGAYMGNGTNGTNACNGTNWSNAAYGGNTAYATGTGGGARYTNAARACNWSNG 1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1196 ARGGNMGNGGNCCNGTNGAYGAYTTYGTNAAYTTYGAYYTNCCNGARCAYTAYATHGAYC 1255
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TOPOLOGY: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNAAYGGNATHGAYATGWSNGARTGGAAYCCNGCNGTNGAYGTNCAYYTNCAYWSNGAYG 1495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGATTGCGGGAGATAGTGCTGGAGGAAATTTGGCAGCGGTTGTAGCTCTTCTTTCAAAGG 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGACGCTACTAATTGGGTTTATAACAATTTAGATAAATTTGATGGAAAGATGGGAGTTG 436
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    Conservative
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                     3.9%;
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27.3%; Pred. No. 0.052;
tive 54; Mismatches 186;
    0;
                        Score 36; DB 3
Pred. No. 0.18;
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  Mismatches 150;
                                           DB 3; Length 5163;
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                                                     TELEFAX: 650-324 ... 4:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE S163 base pairs
FRIGHT: 5163 base pairs
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                              REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                   CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 60/026,062
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: FLOPPY disk
COMPUTER: BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                           FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Peters
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 385 Sher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94306-1840
                                    STRANDEDNESS:
                                                                                                                                                                                                     NAME: Verny, Hana
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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5 Sherman Avenue, Suite 6
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                                      double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES INFECTIONS
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Query Match Best Local Similarity

3.98;

Score 36; DB 3; Pred. No. 0.18; 0; Mismatches 15

Length 5163; 0; Indels

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Best Local Similarity
Matches 126; Conserv
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LENGTH: 5318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CTYPTOSPORTIGIUM PARVUM TITLE OF INVENTION: INFECTIONS FILE REPERENCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: NELSON, RICHARD, C.
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                                   GCTGGAGGAAATTTGGCAGCGGTTGTAGCTCTTCTT 489
                                                                                                                                             TTAGCTCCAGAATACAAGTTTCCTTCTGCAGTTATCGATTCATTTGACGCTACTAATTGG 393
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GTTGTGGTTGTAGTTGTTGTGTTGTTGTTGTT 853
                                                                     GTTGTTGTTGTTAGTTGTTGTTGGTTCTTGGTAGTTGTGGTTGTGGTTGTGGTT
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                                                                                                                                                                                                                                                                                                                                             Matches 126;
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: VETTY, Hand
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
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TITLE OF INVENTION:
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TITLE OF INVENTION:
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APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Relaction CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                     NUMBER OF SEQUENCES:
                 454 GCTGGAGGAAATTTTGGCAGCGGTTGTAGCTCTTCTT
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                                                                                                  394 GTTTATAACAATTTAGATAAATTTGATGGAAAGATGGGAGTTGCGATTGCGGGAGATAGT 453
                                                                                                                                                                      334 TTAGCTCCAGAATACAAGTTTCCTTCTGCAGTTATCGATTTGACGCTACTAATTGG 393
                                                                                                                                                                                                                                       274 CCATTATGTAGAGCAATTACAAATGCGTGCAATTGCGTTGTAGTATCAGTGGACTATAGG
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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385 Sherman Avenue, Suite 6
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Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                           Mismatches 150; Indels
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; LOCATION: (2)..(1891)
US-08-973-462-3
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Best Local Similarity 48.5%;
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Patent No.
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CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER FILING DATE: 1996-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: FR 95/07007 EARLIER FILING DATE: 1995-06-13 NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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ORGANISM: P. falciparum
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                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/505,377
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                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                             APPLICANT: SUGIMOTO, TOSh1yuk1
TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME WHICH
TITLE OF INVENTION: RELEASES TREHALOSE FROM NON-REDUCING SACCHARIDE
                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                       STREET: 419 Seven
CITY: Washington
STATE: D.C.
                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                    COUNTRY: U
ZIP: 20004
CLASSIFICATION:
                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                     ADDRESSEE:
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o. 5856146
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5, 6191270
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                                                                                                                                                                                                                                                                419 Seventh Street N.W. Ste. 300
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                                                                                                                                                                                                     U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   MITSUZUMI, Hitoshi
                                                                               PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                       Browdy and Neimark
                                                                                                                                         Floppy disk
                   21-JUL-1995
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Best Local Similarity 51.2%;
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Applic Patent No. 5856146
                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                    SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1099 AAATTTGTAGTCTTCATACAAAATCACGATCAAGTAGGAA 1138
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TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP NOT YET RECEIVED FILING DATE: 04-JUL-1995
ATTORNEY/AGENT INFORMATION:
                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME WHICH TITLE OF INVENTION: RELEASES TREHALOSE FROM NON-REDUCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                  APPLICATION NUMBER: FILING DATE: 21-JU
                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Browdy, Roger L
REGISTRATION NUMBER: 25
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 21-JUI
                                 CLASSIFICATION:
                                                                                                                                                                                                COUNTRY: UZIP: 20004
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APPLICATION NUMBER:
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                                                  21-JUL-1995
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11-APR-1995
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JP 190180/1994
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 11-AP

11-APR-1995

JP 109128/1995

PRIOR APPLICATION DATA:

21-JUL-1994

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Browdy, Roger L
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: MI'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/505,377
FILING DATE: 21-JUL-1995
                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/798,269
FILING DATE:
                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KUBOTA, Michio
APPLICANT: SUGIMOTO, Toshiyuki
TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME WHICH
TITLE OF INVENTION: RELEASES TREHALOSE FROM NON-REDUCING SACCHARIDE
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LENGTH: 1668 base pairs
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ATTORNEY/AGENT INFORMATION:
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TELEFAX: 249688
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                                                                                                                                                                                                                                                                                                                  CITY: Washington
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                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                 COUNTRY:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                               U.S.A.
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51.2%;
JP 190180/1994
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US-08-798-269-5
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APPLICANT: MITSUZI
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TELEX: 249688
INFORMATION FOR SEQ ID NO:
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ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: MITS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEPHONE: (202) 737-3528
                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/505,377
FILING DATE: 21-JUL-1995
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LENGTH: 1668 base pairs
                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SUGIMOTO, TOShiyuki
TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME WHICH
TITLE OF INVENTION: RELEASES TREHALOSE FROM NON-REDUCING
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                                                                                                                                                                                                                                                     ZIP:
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CITY: Washington
STATE: D.C.
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                                                                                                                                                    SOFTWARE:
                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                           APPLICATION NUMBER:
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                     COUNTRY:
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419 Seventh Street N.W. Ste.
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JP 190180/1994
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                                                                                                                                                      Version #1.30
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APPLICATION NUMBER: FILING DATE: 11-APR-PRIOR APPLICATION DATA:

11-APR-1995

JP 109128/1995

YET RECEIVED

FILING DATE: 21-JUL-1994
PRIOR APPLICATION DATA:

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; NAME/KEY: CDS
; LOCATION: (1)..(5361)
US-08-973-462-2
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Best Local S
Matches 82
                    Query Match 3.8%;
Best Local Similarity 48.1%;
    Matches
                                                                                                                                                                                                                 SEQ ID NO 2
LENGTH: 5361
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APPLICANT: DRUILHE, PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08973462B Patent No. 6191270
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DRUILHE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 0660-01.25-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1998-02-06
                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: FR 95/07007
EARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: PCT/FR96/00894 EARLIER FILING DATE: 1996-06-12
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REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: MITS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEPAX: (202) 737-3528
                                                                                                                                                                             TYPE: DNA
ORGANISM: P. falciparum
                                                                                                                                                              FEATURE:
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Local Similarity 51.2%;
hes 82; Conservative
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    Conservative
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Score 34.8; DB 4;
Pred. No. 0.43;
0; Mismatches 107;
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    107;
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                                    Length 5361;
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; TYPE: DNA
; ORGANISM: P. falciparum
US-08-973-462-1
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US-08-973-462-1
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Best Local Similarity
Matches 99; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: PCT-9FR96/00894
EARLIER FILING DATE: 1996-06-12
EARLIER APPLICATION NUMBER: FR 95/07007
EARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC FILE REFERENCE: 0660-0125-0 PCT
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Result
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     918
145.8
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Copyright (c) 1993 - 2000 Compugen Ltd
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Potato multicystat	Polynucleotide seq	Generic human cycl	Human gene express	Human secreted pro	Streptococcus pneu	Human T gene DNA.	Human secreted pro	Arabidopsis thalia	Human secreted pro	Arabidopsis thalia	Arabidopsis thalia		Arabidopsis thalia	Arabidopsis thalia	Human gene signatu	Borrelia burgdorfe	Sequence encoding	Methanococcus jann	P. falciparum live	P. falciparum live	DNA encoding Sulfo	Trehalose-releasin	Arabidopsis thalia	Arabidopsis thalia	alc	DNA encoding a por		ORF encoding a por	Cryptosporidium pa	Staphylococcus aur	Soluble starch syn	Zea mays soluble s	Human pancreatic c

ALIGNMENTS

RESULT

T79330;

T79330 standard; DNA; 918 BP

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Callen W, Kosmotka A, Link S, Maffia AM, M Reid J, Robertson DE, Swanson RV, Warren PV;
                                                                                                                                                                                                                                                                          Esterase; thermostable enzyme; ester; chiral compound; cheese; pulp; paper; lignin removal; sugar; lignocellulose; disease resistance; feedstuff; ss.
Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in cheese
                                       WPI; 1997-425035/39.
P-PSDB; W23077.
                                                                                                                                                                                                                                                                                                                              DNA encoding Sulfolobus solfataricus esterase P1-8LC
                                                                                                                                                                                                                                                                                                                                                        16-FEB-1998 (first entry)
                                                                                                                                            16-FEB-1996;
                                                                                                                                                                      11-FEB-1997;
                                                                                                                                                                                                                          W09730160-A1
                                                                                                                                                                                                                                                  Sulfolobus solfataricus strain Pl
                                                                                                                    (RECO-) RECOMBINANT BIOCATALYSIS INC.
                                                                                                                                                                                               21-AUG-1997
                                                                                                                                              96US-0602359.
                                                                                                                                                                      97WO-US02039
                                                                                          Murphy
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or P

paper manufacture, and to study plant resistance to disease

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from genomic gene libraries. They can be used for recombinant production of the enzymes in host cells, and as probes to identify related sequences. The esterases are stable at high temperature and in organic solvents, making them superior for use in production of pure chiral compounds used in pharmaceutical, agricultural and other chemical industries. A method is claimed for transferring an amino group from an amino acid to an alpha-keto acid using a claimed esterase. The enzymes may also be useful as ripening starters in cheese making, in lignin removal in paper and pulp manufacture, in carbohydrate derivative synthesis, in fermentable sugar production from lignocellulosic waste, in the study of plant wall structure, plant resistance to disease and organic matter decomposition and to select plants bred for production of highly coderated in the study of plant select plants bred for production of highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Sim
Matches 918;
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                                                                                                   AGTTTAGATAACGTTTCAAGATCCATGATAGAGTACTCTGATGGGTTCTTCCTTACCAGA
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                                                                        agtttagataacgtttcaagatccatgatagagtactctgatgggttcttccttaccaga
                                                                                                                                                                           gctcttctttcaaagggtaaaattaatttgaagtatcaaatactggtttacccagcggta
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.3e-256;
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          temperature and in organic solvents, making them superior for use in production of pure chiral compounds used in pharmaceutical, agricultural and other chemical industries. A method is claimed for transferring an amino group from an amino acid to an alpha-keto acid using a claimed esterase. The enzymes may also be useful as ripening starters in cheese making, in lignin removal in paper and
                                                                                  This DNA sequence codes for esterase 23mc1 (W23080) of Metallosphaera prunae. Newly identified polynucleotides (T79321-40) encoding esterases (W23069-88), some polynucleotides (Talimed, can be used for recombinant production of the enzymes in host cells, and as probes to identify related sequences. The esterases are stable at high temperature and in organic solvents, making them superior for use in
                                                                                                                                                                                                                  Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in cheese paper manufacture, and to study plant resistance to disease
                                                                                                                                                                                                                                                                                                                          Reid
                                                                                                                                                                                          Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                               11-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Esterase; thermostable enzyme; ester; chiral compound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding Metallosphaera prunae esterase
                                                                                                                                                                                                                                                                                                                                                                   (RECO-) RECOMBINANT BIOCATALYSIS INC.
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obertson DE,
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Best Local
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             16-FEB-1998
                                            T79329;
                                                                          T79329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 905 BP; 207 A; 254 C; 241 G; 203 T; 0 other;
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                                                                                                                                                    ataactgccggtaaactagccattcaccacattgctggggttctgagatctgtccttta
                                                                                                                                                                                  ATGGAGCAAGGAAGAGATGCTATAGGTCTGATAGGGTCTGTTTAAGACGAGTATTTTA 905
                                                                                                                                                                                                                  gtatcaaccttggttagatatcaaggaatgattcacggcttcctgtccttctacgagtgg
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             (first entry)
                                                                          DNA;
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217 GTTCTAGTGTATCTTCATGGAGGCGGTTTTGTAATAGGCGATGTGGAATCTTATGACCCA 276

Query Match Best Local Matches

Local Similarity 369;

14.9%;

Conservative

2;

Score 137; DB 18; Pred. No. 4.8e-30; 2; Mismatches 297;

Length 936; Indels

15;

Gaps

4;

Sequence

936 BP;

235 A;

220 C;

265 G; 214 T; 2 other;

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(W33076) of Archaeoglobus fulgidus VC16, an isolate that grows complimally at 85 deg C and pH 7.0. It can be amplified from a C pBluescript vector by PCR (see T79317-18). Claimed, newly identified polynucleotides (T79321-30) encoding esterases (W23069-77, W23088) were recovered from genomic gene libraries. They can be used for recombinant production of the enzymes in host cells, and as probes to identify related sequences. The esterases are stable at high temperature and in organic solvents, making them superior for use in production of pure chiral compounds used in pharmaceutical, agricultural and other chemical industries. A method is claimed for transferring an amino group from an amino acid to an alpha-keto acid using a claimed esterase. The enzymes may also be useful as ripening starters in cheese making, in lignin removal in paper and pulp manufacture, in carbohydrate derivative synthesis, in fermentable sugar production from lignocellulosic waste, in the study of plant wall structure, plant resistance to disease and organic matter decomposition and to select plants bred for production of highly degradable animal feeds.
                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in cheese paper manufacture, and to study plant resistance to disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Reid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                               This DNA sequence codes for thermostable esterase VC16-16MC
                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-425035/39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (RECO-) RECOMBINANT BIOCATALYSIS INC
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resistance; feedstuff;
                                                                                                                                                                                                                                                                                                        Page 50-51; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Robertson DE,
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f; ss.
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V, Warren I
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, aa:Ile)
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RESULT T79336 ID T7 XX T7 XX T7 XX T7 XX DT 16 XX DE DN XX Es KW Pu Wh XX KW AU XX KW Pu Wh XX KW AU XX KW Pu Wh XX KW AU X
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disease resistance;
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                        21-AUG-1997
                                                                                                                                                                                      unsure
                                                                                                                                                                                                                                                                 Whale mat sample 11.801
                                                                                                                                                                                                                                                                                                                                                                           Esterase; thermostable enzyme; ester; chiral compound; cheese;
                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding whale mat sample 11.801 esterase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                    Location/Qualifiers 331..333
                                                                                                                                  /note= "encodes
                                                                                                                                                                                                                                                                                                                      removal; s
feedstuff;
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f; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 276; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This DNA sequence codes for whale mat sample 11.801 esterase es2 (W23083). Newly identified polynucleotides (T79321-40) encoding esterases (W23069-88), some of which are claimed, can be used for recombinant production of the enzymes in host cells, and as probes to identify related sequences. The esterases are stable at high temperature and in organic solvents, making them superior for use in production of pure chiral compounds used in pharmaceutical, agricultural and other chemical industries. A method is claimed for transferring an amino group from an amino acid to an alpha keto acid using a claimed esterase. The enzymes may also be useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ripening starters in cheese making, in ilgnin removal in paper and pulp manufacture, in carbohydrate derivative synthesis, in fermentable sugar production from lignocellulosic waste, in the study of plant wall structure, plant resistance to disease and organic matter decomposition and to select plants bred for production of highly degradable animal feeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 69; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 914 BP; 211 A; 243 C; 262 G; 195 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        paper manufacture, and to study plant resistance to disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in cheese
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                                                                                                                                                                                                                                                                                                                                                                                          CTCCAGAATACAAGTTTCCTCTCTGCAGTTATCGATTCATTTGACGCTACTAATTGGGTTT
ACTTACGAAGCCCTGCAGATTTGCTAGACTTTAGGTTCTCTCCAATTCTGGCGCAAGATT
                                                      aggaattgcgtgatgcctacatcttgccgaaatccagaatggagtatttcctcggcctat
                                                                                                                                                        TGAAGTATCAAATACTGGTTTTACCCAGGGGTAAGTTTAGATAACGTTTCAAGATCCATGA
                                                                                                                                                                                                                                                                                                               ATAACAATTTAGATAAATTTGATGGAAAGATGG----GAGTTGCGATTGCGGGAGATAGTG
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                                                                                            TAGAGTACTCTGATGGGTTCTTCCTTACCAGAGAGCATATAGAGTGGTTCGGTTCTCAAT
                                                                                                                                  cagatctgcaagtcctgatctatccggcgctggatgcacgcatgatctcgacctcgatgg
                                                                                                                                                                                                             cagggggcaatcttgccgccgttgtctgccaacaaccgccatgaacggcgagcgcacac
                                                                                                                                                                                                                                                     CTGGAGGAAATTTGGCAGCGGTTGTAGCTCTTCTTTCA-----AAGGGTAAAATTAATT
                                                                                                                                                                                                                                                                                         gcgccaacgcaacaaccttggcggcgatcctgaacgtatcggcgttggcggcgatagcg
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Swanson RV, Warren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 103.6; DB 1
Pred. No. 2.3e-20;
1; Mismatches 240
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Best Local Sin
Matches 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Esterase; optically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotide C66279 encodes an esterase protein B35739. The esterase hydrolyses oleyl benzoate and p-nitrophenyl benzoate. The invention includes a vector containing the esterase gene, and a method for preparing the esterase protein. The esterase is useful for the preparation of optically active substances necessary for the intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C66279;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1189 BP; 391 A; 219 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 6-8; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New esterase for hydolyzing oleyl bezoate and p-nitrophenol and for preparing optically active substances necessary for intermediate materials for drugs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NAGS ) NAGASE SANGYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Esterase gene sequence
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                                 AGTTATCGATTCACTTAGACGCTACTAATTGGGTTTATAACAATTTAGATAAATTTGATGG
                                                                                                       aaaagtgcaagtcctcagtatcgattatcctcttgcgcctgaggtttcacctcaacattt
                                                                                                                                                                                                                  gtttgttgtaggtggtttagatactcatgatgaggtttgtcgtatattggcaaaatatgc
                                                                                                                                                                                                                                              TTTTGTAATAGGCGATGTGGAATCTTATGACCCATTATGTAGAGCAATTACAAATGCGTG
                                                                                                                                                                                                                                                                                                                       AGTGTATTTTCCGAAGAGTAGCGGTCCTTATGGTGTTCTAGTGTATCTTCATGGAGGCGG 242
                                                                                                                                                             CAATTGCGTTGTAGTATCAGTGGACTATAGGTTAGCTCCAGAATACAAGTTTCCTTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                               cgatattgattcagtagaagatattcgtttacctctccaaagcggaactgtttttgcgag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 65.4; DB 21
Pred. No. 2.9e-09;
0; Mismatches 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346;
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                                             This invention describes a novel esteras of 1,4-diacetoxy-cis-2,3-epoxybutane to (2S,3R)-4-acetoxy-2,3-epoxybutan-1-ol, &
        p-nitropalmitic acid as the substrate and no esterase Tween 20 as the substrate. The new enzyme can be used of an insect pheromone of high biological activity.
                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                 Disclosure;
                                                                                                                                     New esterase used to prepare insect pheromone of 1,4-di:acetoxy-cis-2,3-epoxybutane to (2s,
                                                                                                                                                                             WPI; 1999-257698/22.
P-PSDB; W93498.
                                                                                                                                                                                                                   (NITL )
                                                                                                                                                                                                                                                        04-SEP-1997;
                                                                                                                                                                                                                                                                                  04-SEP-1997;
                                                                                                                                                                                                                                                                                                                                   JP11075850-A.
                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Esterase; hydrolysis; 1,4-diacetoxy-ci
(2S,3R)-4-acetoxy-2,3-epoxybutan-1-ol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacterial esterase genomic DNA
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                                                                                                                           3R)-4-acetoxy-2,3-epoxy-butan-1-ol
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                                                                         invention describes a novel esterase which catalyses the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tactgctgggcatgatgtattacatgatgaagggaaaatctatagctataa
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                                                                                                                                                                                                                   ) NITTO D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                Page 11-13; 16pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                        97JP-0240066
                                                                                                                                                                                                                                                                                  97JP-0240066.
                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 104..1263
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                                                                                                                                                                                                                                                                                                                                                             "esterase"
                                              and has no lipase activity using
                                                                                                                                                                                                                                                                                                                                                                                                                                                  pheromone;
                                                                                                                                                    catalyses
                     activity using for the synthesis
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Best Local Similarity
Matches 151; Conserv
   25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

29-MAR-1999

01-APR-1999

06-APR-1999

16-APR-1999

16-APR-1999

21-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

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23-APR-1999

23-APR-1999

23-APR-1999

24-MAY-1999

06-MAY-1999

06-MAY-1999

06-MAY-1999

07-MAY-1999

07-MAY-1999

07-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                     Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C39057 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                25-FEB-2000;
                                                                                                                                                                                                                                                                                                        06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana DNA fragment SEQ ID NO: 23208
                                                                                                                                                                                                                                                                                                                                                                                                                                           17-OCT-2000 (first entry)
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   990S-012380

990S-012380

990S-0125788

990S-0126785

990S-0126785

990S-01287462

990S-0128714

990S-0128714

990S-0130077

990S-013047

990S-013047

990S-013047

990S-013048

990S-0132485

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990S-0132485
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Pred. No. 8e-09;
0; Mismatches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123; Indels
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                                                                                                                                                                                                                                                                       Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                       Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags -
                    Claim 87; Page 1773; 3161pp; English.
                                                                                    WPI; 2000-594572/56
                                                                                                          Berka RM,
                                                                                                                                                                                     22-MAR-2000; 2000WO-US07781.
                                                                                                                                                                                                                                WO200056762-A2.
                                                                                                                                                                                                                                                     Aspergillus niger.
                                                                                                                                                                                                                                                                                                                                           Aspergillus niger EST SEQ ID NO:4009.
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                                                                                                                              (NOVO ) NOVO
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                                                                                                          Rey MW,
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                                                                                                                               NORDISK BIOTECH INC. NORDISK AS.
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99US-0161404.
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99US-0161359.
99US-0161361.
99US-0161361.
99US-01619920.
99US-0161993.
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Pred. No. 0.00066;
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                                                                                                          Clausen
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The present invention describes a method for monitoring differential

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
New esterase structural gene -
                                                 P-PSDB;
                                                                            WPI; 1999-257707/22
                                                                                                                                                                                                                               16-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Esterase; structural gene; aromatic vinegar; high grade sake flavour;
                                                                                                                                                                             16-SEP-1997;
                                                                                                                                                                                                                                                                                   23-MAR-1999
                                                                                                                                                                                                                                                                                                                                JP11075860-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA enncoding an esterase protein.
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                                                                                                                           (NAKA-) NAKANO SUMISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X35306 standard; DNA; 954 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               715 ATAACAGCAGAATACGATCCACTAAGGGATCAAGGAGAAGCGTATGCAAATAAACT 770
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                                                    Y01820
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Pred. No. 0.0012;
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useful for preparation of vinegar
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                   Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F12065;
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                                                                                                                                                                                                                                                                                                                            22-MAR-1999;
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                                                                                                                                                                                                                                          (NOVO ) NOVO
                                                                                                                                                                                                                                                                                                                                                                               22-MAR-2000; 2000WO-US07781.
                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 aaatgccaaaagctggccagtgatctaggatttcagattttttcagttgattatcgtctg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 TTATGTAGAGCAATTACAAATGCGTGCAATTGCGTTGTAGTATCAGTGGACTATAGGTTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATAACAATTTAGATAAATTTGATGGAAAGATGGGA---GTTGCGATTGCGGGAGATAGT
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                                                                                                                                                                                       RM,
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                                                                                                                                                                                       Shuster JR,
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                                                                                                                                                                                    Kauppinen S,
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                                                                                                                                                                                                                                                                                                                                                                                                   expressed sequence tag; Fusarium venenatum; Aspergillus Aspergillus Oryzae; Trichoderma reesei; identification; Culture condition; environmental stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F08431 standard; cDNA; 606
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expression
                                22-MAR-1999;
                                                                                           22-MAR-2000; 2000WO-US07781
                                                                                                                                                                                                                                                                                                               Fusarium venenatum
                                                                                                                                                                                                                                                                                                                                                                                        metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusarium venenatum EST SEQ ID NO:954.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTATGTAGAGCAATTACAAATGCGTGCAATTGCGTTGTAGTATCAGTGGACTATAGGTTA 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           esent invention describes a method for monitoring differential sion of genes in a first filamentous fungal (FF) cell relative to sion of the same genes in one or more second filamentous fungal The method uses fluorescence-labeled nucleic acids isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                99US-0273623
                                                                                                                                                                                                                                                                                                                                                                             environmental stress; spore morphogenesis;
engineering; catabolic pathway engineering; ss
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Pred. No. 0.0048;
0; Mismatches 85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           niger;
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                                                                                                                                                                                                                                                                                                                                                                                                                           same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from Fr cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how Fr cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monitoring differential expression of genes in filamentous uses fluorescence-labeled nucleic acids isolated from the c substrate of expressed sequence tags .
                                                                                                                                                                                                Sequence 606 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 86; Page 747; 3161pp; English
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115 acctccacggtggtggctatgtatttggaaacattccttcagaagacgctatttgtaccg
                                            227 ATCTTCATGGAGGCGGTTTTGTAATAGGCGATGTGGAATCTTATGACCCATTATGTAGAG 286
                                                                                       Local Similarity
nes 101; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RM,
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                                                                                         Conservative
                                                                                                                                                                                                                                          claimed in
                                                                                                                                                                                                147 A; 181 C; 131 G; 138 T; 9 other;
                                                                                                           4.6%;
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                                                                                                                                                                                                                                        present invention.
                                                                                                           Score 42.2; DB Pred. No. 0.012;
                                                                                       Mismatches
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                                                                                                                             DB 21;
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                                                        09-MAR-2001
 Human; pancreas;
                           Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:72.
                                                                                                              C98844 standard; cDNA; 1875
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                                                                                                                                                                                                                                      ttgccttcccaacagcgtgggacgacaccgaagacactttccactgggttcacgacaaca
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                                                                                                                                                                                                                                                                   ACAAGTTTCCTTCTGCAGTTATCGATTCATTTGACGCTACTAATTGGGTTTATAACAATT 406
                                                                                                                                                                                                                                                                                            ccattgctcttggagccaacgttaccgtcgtgaacctgaactaccgccatgcgccggact
                                                       (first entry)
pancreatic cancer; pancreatic
 cancer antigen;
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Best Local S
Matches 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and antiinflammatory activities, and can be used in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to detect, treat
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linkage analysis; tissue identification; tissue typing; forensic
neural; immune system; muscular; reproductive; gastrointestinal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C98773 to C99231 encode the human pancreatic cancer associated proteins called pancreatic cancer antigens, given in B54008 to B54466. The human pancreatic cancer antigens have cytostatic, neuroprotective, nootropic, antiques and the control of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 546-547; 1379pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1875 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAR-2000; 2000WO-US05989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pulmonary; cardiovascular; renal; proliferative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nootropic;
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          409
                                                                                                                                                                                                             756
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                                                                                                                                                                                                                                                                                                                                                                                                                 235 GGAGGCGGTTTTGTAATAGGCGATGTGGAATCTTATGACCCATTATGTAGAGCAATTACA 294
GATAAATTTGATGGAAA---GATGGGAGTTGCGATTGCGGGAGATAGTGCTGGAGGAAAT
                                                                                                                                                                                                          gacagacttgatgctgtcgtcgtatcaaccaactacagattagcacctaagtatcatttc
                                                                   ccaattcaatttgaagatgtatataatgccttaaggtggttcttacgtaaaaaagttctt
                                                                                                              CCTTCTGCAGTTATCGATTCATTTGACGCTACTAATTGGGT-----TTATAACAATTTA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-579444/54
                                                                                                                                                                                                                                                                             AATGCGTGCAATTGCGTTGTAGTATCAGTGGACTATAGGTTAGCTCCAGAATACAAGTTT 354
                                                                                                                                                                                                                                                                                                                                          ggctggtgcgtggaagtgctgctctaagtggttatgacttgctgtcaagatggacagca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B54079.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunomodulatory; relaxant; contraceptive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0124270.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38.6;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T; 5 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                      The present sequence represents an isolated nucleic acid molecule which has been isolated and comprises a nucleotide sequence encoding a polypeptide having soluble starch synthase (SSS) activity, where the polypeptide is encoded by a maize gene. The isolated nucleic acid molecule can be used to produce transgenic plants with altered starch production. The transgenic plants produced using the nucleic acid molecule have an enhanced ability to produce structurally-altered starch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1995;
21-JUN-1994;
29-NOV-1994;
                        1316 aracngcngaymgngtngtnacngtnwsnaayggntayatgtgggarytnaaracnwsng
                                                                                                                                                                                                                                                               Sequence 2380 BP; 333 A;
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Column 31-33; 29pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid molecule, used to produce transgenic plants comprises nucleotide sequence encoding polypeptide having soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5824790-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays soluble starch synthase gene SSS56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-OCT-1998
                                                                                                                                                                 197 AGAGTAGCGGTCCTTATGGTGTTCTAGTGTATCTTCATGGAGGCGGTTTTGTAATAGGCG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1995;
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; glycogen
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TTGACGCTACTAATTGGGTTTATAACAATTTAGATAAATTTGATGGAAAGATGGGAGTTG
                                                       TATCAGTGGACTATAGGTTAGCTCCAGAATACAAGTTTCCTTCTGCAGTTATCGATTCAT
                                                                               ayttyaarytntaygayaayathggnggngaycaywsnaaygtnttygcngcnggnytna 1315
                                                                                                          ATGTGGAATCTTATGACCCATTATGTAGAGCAATTACAAATGCGTGCAATTGCGTTGTAG
                                                                                                                                   arggnmgnggnccngtngaygayttygtnaayttygayytnccngarcaytayathgayc 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGGCAGCGGTTGTAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gcaaaatatggtgtgaaccctgagagaatcggtatttctggagatagtgcaggagggaat
                                                                                                                                                                                                                                                                                                                                                                                                                            synthase activity, where polypeptide
                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yellow-dent corn line; blosynthetic pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0572951.
94US-0263921.
94US-0346602.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA; 2380
                                                                                                                                                                                                          4.18;
27.38;
                                                                                                                                                                                                                                                               266 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathway; branching enzyme;
                                                                                                                                                                                                                       Score 37.2;
                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             518
                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              maize; soluble starch synthase;
                                                                                                                                                                                                                                                               272 T;
                                                                                                                                                                                                           . 58
                                                                                                                                                                                                                       DB 19;
                                                                                                                                                                                            186;
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maize gene
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   1256
                                                                                                                                                                                                                                                   produce plants with an increased capacity for producing starch, or a capacity to produce starch with an altered fine structure. They can also be used to isolate the corresponding genomic sequences from crop plants, to determine the contribution of the SSS gene to the net regulation of starch biosynthesis, and to modify the levels of starch produced by the plant. Transgenic plants (esp. maize) can be used to produce hybid plants which have higher rates of
                                                                                                                                                                                                                                                                                                                                                                 soluble starch synthase (SSS). They were isolated from a maize inbred line W64A library by screening with a probe (T67288) based on pea SSS, rice SSS and maize GBSS. The cDNAs can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding soluble starch synthase - used to produce transgenic plants with increased capacity for producing and storing starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T67287;
                                                                                                                                                                                                      Sequence 2478 BP; 347 A; 276 C; 533 G; 289 T; 1033 other;
                                                                                                                                                                                                                                     starch synthesis at temperatures above the normal optimum.
                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA clones SSS10.52,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 23-26; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keeling PL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ZENE ) ZENECA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soluble starch synthase; SSS56; transgenic plant; cereal; maize;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soluble starch synthase cDNA clone SSS56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T67287 standard;
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                               257
                                                                                                                                            Local Similarity
                                                                             AGAGTAGCGGTCCTTATGGTGTTCTAGTGTATCTTCATGGAGGCGGTTTTGTAATAGGCG 256
ayttyaarytntaygayaayathggnggngaycaywsnaaygtnttygcngcnggnytna 1315
                             ATGTGGAATCTTATGACCCATTATGTAGAGCAATTACAAATGCGTGCAATTGCGTTGTAG 316
                                                           arggnmgnggnccngtngaygayttygtnaayttygayytnccngarcaytayathgayc 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aytayacnaaytayacnttygaracnytng 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTAAAATTAATTTGAAGTATCAAATACTGG 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tnaayggnathgayatgwsngartggaayccngcngtngaygtncayytncaywsngayg 1495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGATTGCGGGAGATAGTGCTGGAGGAAATTTGGCAGCGGTTGTAGCTCTTCTTTCAAAGG
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                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Knight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                          4.18;
27.38;
                                                                                                                                                                                                                                                                                                                                                                                                              SSS6.31 and SSS56 (T67285-87) code for maize
                                                                                                                          54;
                                                                                                                                          Score 37.2; DB Pred.,No. 0.59;
                                                                                                                            Mismatches
                                                                                                                                                         DB 18;
                                                                                                                            186;
                                                                                                                                                        Length 2478;
                                                                                                                            Indels
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                                                                                                                        Gaps
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RESULT 15
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                                                                                                                                                    the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The
                                                                                                                                                                                                                                                This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
                                                                                          be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis,
                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide(s) and proteins derived stored on computer readable medium and anti-S.aureus vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
  for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
                                                          skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used
                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 1677; 3271pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-374922/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barash SC,
Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V75114;
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homologues of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGATTGCGGGAGATAGTGCTGGAGGAAATTTGGCAGCGGTTGTAGCTCTTCTTTCAAAAGG 496
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used
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                                                                                                                                                                                                                                                                 Sequence 989 BP; 376 A; 152 C; 156 G; 302 T; 3 other;
                                        457 GGAGG 461
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353 gcagg 357
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                               June 2, 2001, 21:11:19 ; Search time 10284.9 Seconds (without alignments) 1316.347 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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10 11	876	ω 4. τυ	21	Result No.
82.6 81.2	105.8 105.8 99.6	150.6 149.2 112.2	721.2 215.8	Score
8.00		16.4 16.3 12.2	78.6 23.5	Query Match
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AF294430 AF034088 AP001516	ACESTAA ACESRTA BAAMYLA	AE000985 AP000993 AP001514	SSOLP2N16 SSOLP2N16	ID
AF294430 Bacillus AF034088 Pseudomon AP001516 Bacillus	X71598 A.calcoacet X74839 A.calcoacet X62835 B.acidocald	AE000985 Archaeogl AP000993 Thermopla AP001514 Bacillus	AL512977 Sulfolobu AL512977 Sulfolobu	Description

/GUNTY="TEANON: 20110/GUNTY SOLITIONS SOLITION	AL512977.1 GI:12313146 Sulfolobus solfataricus. M Sulfolobus solfataricus Archaea; Crenarchaeota; Sulfolo 1 (bases I to 81844) Sensen, C.W. Direct Submission Submitted (17-JAN-2001) Sensen Submitted (17-JAN-2001) Sensen Blosciences, 1411 Oxford St. Ha Blosciences, 181844 Occapion/Qualifiers 1. 81844	16 1 10N	42.4 4.6 105184 42.4 4.6 145129 42.4 4.6 177633 42.4 4.6 177633 42.2 4.6 1013 41.4 4.5 1623 41.4 4.5 19305 40.8 4.3 10405 39.8 4.3 104785 39.8 4.3 110000 39.8 4.3 110000	5.2 2134 2 MSLIP2 5.2 35346 6 CET09B9 5.1 100269 13 ATF18022 5.1 100269 13 ATF18022 5.1 1020 9 AX065883 5.0 346510 2 AP003011 5.0 1080 1 AB012140 4.9 39150 3 MTCY21B4 4.8 9830 2 AF736BD 4.7 16440 1 AE001993 4.7 1645 94 AF182426 4.6 27893 14 SPAC1039	71.6 7.8 10266 1 AE004380 60.2 6.6 33837 5 CEF27C8 56.2 6.1 16768 1 AF150928 53.2 5.8 11203 14 SPAPBIAN1 51.2 5.6 43523 3 MTCY349 50.6 5.4 954 1 AB023896 49 5.3 870 9 AX066921
gene .	CDS	gene	gene	gene	gene CDS

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complement(3092...3454)
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                                                                                                                                                                                                                                                                                                                                                                                                    complement(5569. .6582)
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complement(7350
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AGGTTCTCTCCAATTCTGGCGCAAGATTTCAACGGATTACCTCCAGCCTTGATAATAACA
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                                                                                                                                      GAGCATATAGAGTGGTTCGGTTCTCAATACTTACGAAGCCCTGCAGATTTGCTAGACTTT
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                                                                                                                                                                                                                                                                                                                                                      GCTCTTCTTTCAAAGGGTAAAATTAATTTGAAGTATCAAATACTGGTTTACCCCAGCGGTA 540
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0; Mismatches
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2.2e-153;
ches 123;
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<pre>gene</pre>	TAAAGTPSGFLETGKEFTTYNGIPAVEFLDYNNYTYISLQYMIPLKSYYSINIDASN LTYSATAITKGDLNFTTGPYNLYNVSFNYVYGNYTVHLFLLVASSNAEINLLNYSNH VALNITGLKFISLLVPITTFHDLLGVSKFIVNGSFNIILTTSTGSTGSAYYYNTSVPI IGSYIPGTNYYMISIPYSGNIVIFGNYYSNYVNGSINIKNNDVGHGFSLLYALSAVI VAVVITATYMLRKF Complement(47215503) /gene="sucD" /gene="sucD" /EC_number="6.2.1.5" /CCodon_start=1 /transl_table=11 /product="Succinyl-CoA synthetase, alpha subunit" /protein_id="CAC24279.1" /protein_id="CAC24279.1" /db_xref="GI:12313151" /translation="MLKYGTKLVAGVTPGKGGTQVNSVPVYDTVKDANKEHEADASII FVPARYAVDAIYEAVDAGIKLIVTITEHIPVLDMARAIKYARARGARIIGPNCPGIIA PESSLVGILPARAFKKGKIGIVSRGGTLYFUSELLKNSGMGGSTVIGGGDFIIGTS TLEVAKMFDODDETEKTVVTGETGGTWERETA, AFAYKGETIKVDITAVTAGMTDREKE	/codon_start=1 /transl_table=11 /protein_id="CAC24277.1" /db_xref="GI:12313149" /translation="MKKKAIGSDDGYYVIFFISESEIGYKKTQINEMYYVSFIIVLL VFILYVIFRYILVLTLFIIPILVYLFTIAISLHLYKPEIYEKITRVEIKDKIIKIHTS NKTFIHRGKIIGFTDQI" 3686. 4735 /gene="ORF-bac03_014" /codon_start=1 /transl_table=11 /product="Hypothetical protein" /product=""Hypothetical protein" /protein_id="GC24278.1" /db_xref="GI:12313150" /translation="MKRYLILELYLTSIIFIPITYSSNOFSFLNIGNTISYNIYETSS RIGTYLTFNISMALVWAGTYFYNIGKSYNKYPPAINWNNLTTENISGSYPYPISYWIN

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gene

CDS

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/gene="ogt"
10033. 100
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LKGKVGIESQDRLITKGRAIGIISNYAKVYELHMÖDGKIDPTIYRNQNVTTESFDP
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HNANIVLNDTQIPNNPNISADGKILLYVGDSPSNFANNGILSGQTAVGILDNISAGYY
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TISSTTSSVETTSTSFTLTSTSTTISTSSTSTSSTTTTSSSTTSSTTITTQSVTLPP
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ffhKLDLyfegkpinlrepinlktypfrlsvfkevmkipmgkvmtykqiadslgtspr
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/protein_id="CAC24285.
/db_xref="GI:12313157"
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/product="Methylated-DNA-protein-cysteine"
/protein_id="CAC24284.1"
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/protein_id="CAC24283.1"
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LASILREELKRNVSFY REYIVHELVHLLEPK K" Complement(736. Genee "AF1708" Complement(736. /genee "AF1708" /note-"similar t identity: 38.95; putative" /codon_start=1 /trans1_table=11 /product="type I subunit" /protein_id="AAB	10	Woose, C. R. and Venderst Submission Submitted (15-DEC Medical Center Dr In order to show origin of this ve- of the original version. On Dec 16, 1997 t. Location	Non-Sendand Sendand Se	Archaea; Euryarchaeot Archaeoglobus. 1 (bases 1 to 13104) Klenk, H.P., Clayton, R Ketchum, K.A., Dodson, Kichardson, D.L., Kerl Fleischmann, R.D., Quade
LASILREELKRNVSFYSRLLGINYGRIFIKMOKTKWASCSSKGNLSFNLASLALPEKL REYIVVHELVHLLEPKHSRLFWETVGFYYPEYEAERELKKYWIFVERNEVWRMLRAL K" Complement(7363609) gene="AF1708" Complement(7363609) /gene="AF1708" Complement(7363609) /gene="AF1708" /gene="Similar to GB:L77117 Sp:Q57588 PID:159264 percent /dentify: 38.95; identified by sequence similarity; putative" /codon_start=1 /product="type I restriction-modification enzyme, R subunit" /product="type I restriction-modification enzyme, R subunit" /product="AAB8956.1" /db_xref="GI:364840" /translation="MKKEROSEDYLSEILKSFGWEERKLSPDILDLTEFKAALKRIN DVDDEDIKEVLNYLETRSFDVEGSMQILDAIKKGVTIKDSEGILKTIKLIDYANPEAN	113104 /organism="Archaeoglobus fulgidus" /organism="Archaeoglobus fulgidus" /db_xref="taxon:2234" complement(80739) /gene="AF1707" complement(80739) /gene="AF1707" /note="hypothetical protein; identified by GeneMark; /putative" /codon_start=1 /transl_table=11 /product="A. fulgidus predicted coding region AF1707" /product="A. fulgidus predicted coding region AF1707" /protein_id="AAB89540.1" /brotein_id="AAB89540.1" /translation="MNVVVERKNVRNVRIQVLADGKVRVVAPPDEDVDSFISKHADWIKKRABIESLAEEIKGKERMLLLNGKFYHLVMDSGFEIKEGEEVGVVKYYSLRNLKRN LASILREELKRNVSFYSRLLGINYGRIFIKMQKTKWASCSSKGNLSFNLASLALPEKL	Woese,C.R. and Venter,J.C. Direct Submission Submitted (15-DEC-1997) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA In order to show the genes in ascending order on the genome, the origin of this version has been moved by TIGR to position 2093570 of the original version and the opposite strand is shown from the original version. On Dec 16, 1997 this sequence version replaced gi:2648834.	Peterson, S., Reich, C.I., McNeil, L.K., Badger, J.H., Glodek, A., Zhou, L., Overbeek, R., Gocayne, J. D., Weldman, J.F., McDonald, L., Utterback, T., Cotton, M.D., Spriggs, T., Artiach, P., Kaine, B.P., Sykes, S.M., Sadow, P.W., D'Andrea, K.P., Bowman, C., Fujil, C., Garland, S.A., Mason, T.M., Olsen, G.J., Fraser, C.M., Smith, H.O., Woese, C.R. and Venter, J.C. Woese, C.R. and Venter, J.C. The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus Nature 390 (6658), 364-370 (1997) 98049343 2 (bases 1 to 13104) Klenk, H.P., Clayton, R.A., Tomb, J., White, O., Nelson, K.E., Ketchum, K.A., Dodson, R.J., Gwinn, M., Hickey, E.K., Peterson, J.D., Kirkness, E.F., Dougherty, B.A., McKenney, K., Adams, M.D., Loftus, B., Peterson, S., Reich, C.I., McNeil, L.K., Badger, J.H., Glodek, A., Zhou, L., Overbeek, R., Gocayne, J.D., Weidman, J.F., McDonald, L., Utterback, T., Cotton, M.D., Spriggs, T., Artiach, P., Kaine, B.P., Sykes, S.M., Mason, T.M., Olsen, K.J., Fraser, C.M., Smith, H.O., Garland, S.A., Mason, T.M., Olsen, G.J., Fraser, C.M., Smith, H.O.,	Euryarchaeota; Archaeoglobales; Archaeoglobaceae; obus. 1 to 13104) 1 Clayton,R.A., Tomb,J., White,O., Nelson,K.E., 1 Lo., Dodson,R.J., Gwinn,M., Hickey,E.K., Peterson,J.D., 1 Clayton,C., Gwinn,M., Hickey,E.K., Peterson,J.D., 1 Clayton,C., Gwinn,M., Bickey,E.K., Peterson,J.D., 1 Clayton,C., Gwinn,M., Bickey,E.K., Kams,M.D., Loftus,B., 2 Dougherty,B.A., McKenney,K., Adams,M.D., Loftus,B., 3 Dougherty,B.A., McKenney,K., Adams,M.D., Loftus,B.,

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VVAVSRHACLYYKQALDKFLNENETEIPWTFQQNDSKEILDYLEKLRKKYGKSELKEI
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TTGAAGTATCAAATACTGGTTTACCCAGCGGTAAGTTTAGATAACGTTTCAAGATCCATG 567
                                      GCGGGAGGGAATCTTGCCGCGGCGGTTTCAATAATGGCGAGAGACAGCGGAGAAGATTTC
                                                                            GCTGGAGGAAATTTGGCAGCGGTTGTAGCTCTTCTTTC----AAAGGGTAAAATTAAT
                                                                                                                GCTGAGAACGCCGAGGAGCTGAGGATTGACCCCGTCAAAAATCTTCGTTGGGGGGGACAGT
                                                                                                                                                      TATAACAATTTAGATAAATT---TGATGGAAAGATGGGAGTTGCGATTGCGGGAGATAGT
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complement(8990. .9062)
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                                                                                                                                                                                   Submitted (20-DEC-1999) Masashi Suzuki, National Institute of Bioscience and Human-Technology, Centre of Structural Biology;
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Thermoplasma volcanium genomic DNA, complete sequence,
                                                                                                                                                                                                                         Suzuki, M.
Direct Submission
                                                                                                                                                                                                                                                                                               sequence of Thermoplasma volcanium Proc. Natl. Acad. Sci. U.S.A. 97 (26),
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Kawashima-Ohya,Y., Watanabe,K., Yamazaki,M.,
                                                                                                               Fax:81-298-54-6041)
                                                                                                                               URL:http://www.aist.go.jp/RIODB/archaic/,
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Takami, H.,
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An improved physical and genetic map
Bacillus sp. C-125
Extramock:
           Takami, H. and Takaki, Y. Direct Submission
Direct Submission
Submitted (22-mAR-2000) Hideto Takami, Japan Marine
Technology Center, Deep-sea Microorganisms Research
Natsushima, Yokosuka, Kanagawa 237-0061, Japan
(E-mail:takamih@jamstec.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Replication origin region of the Bacillus halodurans C-125
                                                                                                                            Extremophiles 4 (4), 209-214 (2000) 20426005
                                                                                                                                                          Nakasone,K., Masui,N., Takaki,Y., Sasak
Hirama,C., Fuji,F. and Takami,H.
Characterization and comparative study
alkaliphilic Bacillus halodurans C-125
                                                                                                                                                                                                                                                     Takami, H. and Horikoshi, K. Analysis of the genome of an industrial point of view Extremophiles 4 (2), 99-108 (
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9 (sites)
                                                                                                                                                                                                                                                                                                                                   Complete genome sequence of the alkaliphilic bacterium halodurans and genomic sequence comparison with Bacillu Nucleic Acids Res. 28, 4317-4331 (2000)
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8 (sites)
Takami, H., Nakasone.
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Takami, H., Takaki, Y., Nakasone, K.,
Sasaki, R., Hirama, C., Fuji, F. and M
Genetic analysis of the chromosome
halodurans C-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takami,H. and Horikoshi,K.
Reidentification of facultatively alkaliphilic
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URL:http://www.jamstec.go.jp/jamstec-e/bio/DEEPSTAR/FResearch.html.
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2011-1790
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                                                                                                                                                                                                                                                                                 unknown conserved protein
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/gene="BH1999"
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Pred. No. 1.1e-15;
0; Mismatches 358;
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299850; 18;

Gaps

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X71598
X71598.1 GI:431
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                                                                                                                                                                                                                                                                                                                                   Submitted (20-APR-1993) K.J. Hellingwerf, E.C. Slater Institute, Biocentrum Amsterdam, Dept of Microbiology, Nieuwe Achtergracht 127, 1018 WS Amsterdam, NETHERLANDS
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Acinetobacter calcoaceticus
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Direct Submission
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                                                                                                                                                                                                                    /clone="paka24 and 360. .396
/codon_start=1
/transl_table=11
/product="carboxylesterase"
/protein_id="CAA50601.1"
                                                                                                                                                                                                                                                                   /organism="Acinetobacter calcoaceticus'
/strain="BD413"
                                                                 /gene="estA"
/EC_number="3.1.1.1"
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  GAGCAAGGAAGATGCTATAGGTCTGAT 878
                                                                              GTTACTAGTGTGAGATTTAACAACGTTATACACGGATTCCTCTCATTCTTTCCGTTGATG
                                                                                                                    GATGTATTACATGAAGGCGAAATCTATAGCCATAAGCTACGTCAAGCAGGGGTTAAA
                                                                                                                                                        GATCCACTAAGGGATCAAGGAGAAGCGTATGCAAATAAACTACTACAAGCTGGAGTCTCA
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/translation="MTAFVQTTQEVLEKGHGPAARALDKLPSFVQESIAKVLGYPYQY
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LAPEVSFQRLIQSCEDALAWVYQNKRHFKILKNQIAVAGDSAGGNISTVVAQRAIGKV
YAQDAQFLIYPVVDFKSRHPSFYAYKDGLVLTGNDVDYVTDYYATKHAVHLDDPIISP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01-SEP-1993) K.J. Hellingwerf, E.C. Slater Institute, Biocentrum Amsterdam, Dept of Microbiology, 1018 WS Amsterdam,
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1 (bases 1 to 2458)
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              /translation="MLKRVAIVLGGLLISAHALANTMVEMKTNLGNIEIELYNNKAPI
SAKNFESYVKNNFYNGTIFHRVIPNFMIQGGGFETNMKEKATAAPIKNEASNGLANTR
GTLAMARTSNPDSATSQFFINVADNNFLNASRTDAGYAVFGKVIKGMDVVDKIANVPT
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STYGMHQNVPKQPVKIISVQIKSINTAK"
                                                                                                                                                                                                                                      /rpt_type=INVERTED
/rpt_unit=1731. .1;
1830. .1833
                                                               /product="peptidy1 proly1-cis-trans-isomerase,
/protein_id="CAA52834.1"
/db_xref="SWISS-PROT:P42693"
/db_xref="SWISS-PROT:P42693"
                                                                                                                                    /codon_start=1
/transl_table=11
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/gene="rotA"
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/protein_id="CAA52833.1"
/db_xref="GI:602781"
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/rpt_unit=360. .375
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amy gene; amylase.
Alicyclobacillus acidocaldarius.
Alicyclobacillus acidocaldarius
Bacteria; Firmicutes; Bacillus/Clostridium group;
Alicyclobacillus group; Alicyclobacillus.
1 (bases 1 to 7872)
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B.acidocaldarius
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KOIVula, T.T., Hemila, H., Pakkanen, R., Sibakov, M. and Palva, I.
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                                                                                       Similarity
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                                                            Conservative
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HAKGFHIILDGVFEDTGSDSVYFNKFGNFHSNGAWQAYLKNQPSLSPYYSWYWTGNT
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YQGAILVTPSDAPMAYLQEEDSQNEIAWTPVQGAIGYRVWRQNPNGQWVPFGPVLPAT
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TQKGIYVGADGTESLGPIQFHENWDSPPYDPNIPPLSDPKIASLRGNGQWNIDFFGGD
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INNNFPLPVGTVTLSTLQANPGDTVTVSDPVGDFAGSQDQPNHTVIRFVNSSGETAAT
VNGTNASWNSYQFTVPQSLPNGLYRVEIDTVAKDADGVVNVELDRSAELIVGPLPAWM
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/transl_table=11
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/strain-"ATCC 27009"
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Bacillus pumilus
Bacillus/Clostridium
Bacteria; Firmicutes; Bacillus/Clostridium
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                   Submitted (08-AUG-2000) Microbiology, University of Stellenbosch, Biology Building, De Beer Street, Stellenbosch 7600, South Africa
                                                                                                                                                                                                                               Pieterse, A., Cordero Otero, R.R. and van Zyl, W.H. Cloning and characterization of a novel Bacillus esterase (estA) gene in Escherichia coli
                                                                                                                                                           Direct Submission
                                                                                                                                                                          Pieterse, A.,
                                                                                                                                                                                                             Unpublished
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                               /organism="Bacillus pumilus"
/db_xref="taxon:1408"
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/gene="estA"
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                                                      ACCESSION
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Best Local
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                                                                                                                                                                                     TTTAAA
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                                                                                                                                                                                                                                                                                  TCAAGGAGAAGCGTATGCAAATAAACTACTACAAGCTGGAGTCTCAGTTACTAGTGTGAG
                                                                                                                                                                                                                                                                                                                                  ATCCTTAGCACAAATGCCTCCAGCTCTCGTCATCACAGCTGAAAGAGATTCGCTAGCTCA
                                                                                                                                                                                                                                                                                                                                                         AGATTTCAACGGATTACCTCCAGCCTTGATAATAACAGCAGAATACGATCCACTAAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAATACTTACGAAGCCCTGCAGATTTGCTAGACTTTAGGTTCTCTCCAATTCTGGCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAGCCAGCGTTTGAAGAAGCGATCCCAGTTGAATTGGCGAGGCTCTTTAATTCCTTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATGATAGAGTACTCTGATGGGTTCTTCCTTACCAGAGAGCATATAGAGTGGTTCGGTTC 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCAATTGCCTATCAAGTGCTTGATTATCCGCCGCTTGATCTAGCCACTGATCCAGCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCAGGAGGAAATTTGGCAACGGCTGCTTGTCTATTGAATATTCAAAGAGGAAATACACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGTGTCCAGTCATTGCAGACCGGGCGCAATGTATCGTCGTCAATGTCGAGTATCAGCT 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTATGTAGAGCAATTACAAATGCGTGCAATTGCGTTGTAGTATCAGTGGACTATAGGTT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTTTTTGTGAATTTACATGGCGGCGGATTTATCATGGCCAGTGCTGAAATGGATAATCC 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTTCTAGTGTATCTTCATGGAGGCGGTTTTGTAATAGGCGATGTGGAATCTTATGACCC 275
                                                                                                                                                                                                                                                               AGAAGCCGACCAATATGCGAAGAAGTTAAAAGAAGCAGGGGTAGATGTCACGTACAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                            TCTGCAAGGCCAAGATCCGCACAATCCGCTCGTTTCTCCGGTTTTTGCAGATCGTTC---
                                                      Pseudomonas
AF034088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MMLEEQIKIAASLRQPSEGSLASQSELKPVNPPEVNKMEYDIPT SAGETKVWVFKPVNTQKQLLPVVNLHEGGFINGSAEMDNPGCYDLADRAQCIVNVE YQLAPEHPFPAALHECYDVLKWLYEHPEELQIDIRNALAIGHSAGGNLATAACLLNU QROTTPIAYAHLEADRAQKPAFEEAIPVELARLFNSFYLQGQDPHNPLVSPROTTPIAYQVLDYPPLDLATDPAQKPAFEEAIPVELARLFNSFYLQGQDPHNPLVSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="carboxyl esterase
/protein_id="AAG09918.1"
/db_xref="GI:9964294"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transl_table=11/
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sp. B11-1
                                    GI:2853611
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                                                                     B11-1 lipase (lipP) gene,
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Pred. No. 2.4e-10;
0; Mismatches 279
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Best Local Sin
Matches 312;
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MEDLINE
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TITLE
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TGCAGGATACCGGGCAGGGCGATGATCCCTTGGCCTCACCTTTGCGGGCCGAGACGCTGG
                                  TACGAAGCCCTGCAGATTTGCTAGACTTTAGGTTCTCCCAATTCTGGCGCAAGATTTCA
                                                                                                                                              GTTATCAGTGTCTGTTTTACCCGGGTCACCGATGCTCGCTGCGACAGTCAATCCTATGAGG
                                                                                                                                                                                                                       GGGGCAATCTGGCGCTCGCGGTCAGTCGCCTCGCCGCGCCAACGCCCAAGGTCCGAAGATCA
                                                                                                                                                                                                                                                           AGCACGCTGCCGAACTCGGCGTCGATGGCCGTCGCCTGGCCCTGGCCGGAGACAGCGCCG
                                                                                                                                                                                                                                                                                                                                ATAACAATTTAGATAAATTTGATGGAAAGATGGGAGTTGCGATTGCGGGAGATAGTGCTG
                                                                                                                                                                                                                                                                                                                                                                       CGGAAAAACCATTTCCCGGCCGCCGCCGCTGGATTGCTATGCGGCCACTTGCTGGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCGCTCCCTTGCCAGTCAAACGGAGGCGGTGGTTGCTCTGTCGCCTTATCGACTGGCGC
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                                                                     AGTTTGCCGAGGGCTACTTCCTCACTGGCGCGATGATGTATTGGTTCTGGCAGCAGTATT
                                                                                                           AGTACTCTGATGGGTTCTTCCTTACCAGAGAGCATATAGAGTGGTTCGGTTCTCAATACT
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98125658
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Choo,D.W., Kurihara,T., Suzuki,T., Soda,K. and Esaki,N.
A cold-adapted lipase of an Alaskan psychrotroph, Pseud
strain B11-1: gene cloning and enzyme purification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas sp. B11-1
Bacteria; Proteobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 9.0%;
Similarity 47.6%;
12; Conservative
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/transl_table=11
/product="lipase"
/protein_id="AAC38151.1"
/protein_id="AAC38151.1"
/db_rref="g1:2853612"
/db_rref="g1:2853612"
/translation="MPLIDKQIAAVLQQFSELPAPDFSQLDAAQYRQFCDNLLPAIPGD
/translation="MPLIDKQIAAVLQLTVEHAAELGVDGRRLATHALLAGDSAGGNL
/translation="MPLIDKQIAAVLQLTVEHAAELGVDGRRLATHALLAGDSAGGNL
/translation="MPLIDKQIAAVLQLTVEHAAELGVDGRRLATHALLAGDSAGGNL
QTEAVVVSVAYRLAPENHFPAAPLDCYAATCWLVEHAAELGVDGRRLATAGLAGSAGGNL
ALAVSRLAAQROGPKISYCCLFYPVTDARCDSGSYEEFAEGYPLTGAMNYWFWQQYLQ
DTGQGDDDLASPLRAETLADLPPTTLITAEFDPLRDEGEAFALRLQQAGVSVRVQRCE
GMINGFISMAPFVERAAHLISDAAADLRRALN"
151 a 283 c 297 g 196 t
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Pred. No. 9.5e-09;
0; Mismatches 334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence analysis of a 32-kb region including the major ribosomal protein gene clusters from alkaliphilic Bacillus sp. strain C-125 Biosci. Biotechnol. Biochem. 63 (2), 452-455 (1999)
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Takami,H., Takaki,Y., Nakasone,K., Hirama,C.,
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                                 Biosci. Biotechnol.
                                                                             Takami, H. and Horikoshi, K.
                                                                                                                                                                              Genome analysis of facultatively alkalihilic Bacillus
                                                                                                                                                                                                                                                             Genetic analysis of halodurans C-125
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Sasaki,R., Hirama,C., Fuji,F. and Masui,N.
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                                                              Reidentification of facultatively alkaliphilic Bacillus
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 Nakasone, K.,
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Takaki,Y., Maeno,G., Sasaki,R.,
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Hirama, C., Fuji, F. and Takami, H.
Characterization and comparative study
alkaliphilic Bacillus halodurans C-125
Extremophiles 4 (4), 209-214 (2000)
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Technology Center, Deep-sea Microorganisms Research
Natsushima, Yokosuka, Kanagawa 237-0061, Japan
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Tel:81-468-67-3895, Fax:81-468-66-6364)
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Epaktonviltldsnigtaldowmtoveeeykperiiaivadpktoggilamsnrptf
NPNEYEOITNYMNYAVSDRYEPGSTMKVFTLAAALEEGVLNVNEQYQSGTYAIRNDTN
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/translation="MHYSNUTVRRRLIFVLLVGLATFLIIMLRLGYVOFALGDWLTGQ
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RLTIDSRVQTIIERELDIAEATYSPDGAIAIAMNPNTGEILGMSSRPHYNPENREVR
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/protein_id="BAB06291 1"
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KGGIGGSTFLEVVENSCNPGFVVLGERLGKDRLFDYIEAFGFGGOTTGIDLGGEAKGII
FNRDRIGPLEGATTAFGGGUSVFTPLOQVAAVSAAVNGGYLYEPVVAKOMVDPYTGEVV
ESSAPKMKRQIISEETSKEVRYALESVVARGTGQGAFVDGYRVGGKTGTAQKAKDGRY
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PPIRDHNQGRGWGTISYLEAMQRSSNVGFSKIALEKLGPEKLYEYLDEFGFGEPTGIC
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                                                                                                                                                                                                      /protein_id="BAB06296.1"
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/db_xref="GI:10175198"
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RKIASEAGLNRETLAKWLATVFRSLDETEHTLPLYERVKTLAGRSWYYTDFFAELLL
YLFRDEGLVVPDSGDDSFRTIEKSCFEMLIQKTKNVQGAFAQVKKLEDAGVGRFBIL
TETNAHLFYVEEGSRYRIDYTGENYELNGKNQTFSREELLEHLTLHPERFSNNVVTRP
VMQDALFPVLAFVAGFGEISYWATLKRVFHECGMKNSPVVPRISATCVPSAVQKWFAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVRNPDGPGYLNGHGKNIFSFIGMAPKDDPSVIVYVAVDRPSLNTNQVGSEPVAKIFN
TIMNHSLQYLNISPSVEELKDEEEEGYELADFIGESARSAREELEQAGMKVYVLGEGD
TVEGQQPYSGHKLLEGERVILRTESESYTLPSMIGWSLRDVLKVANVLDVNVNLFGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mfmgeyrhnvdekgrmiipakfreelgetfvytrgldrclfvyp
Qvewkkleeslknlpftkkdaraftrfffsgateceldkogrvniasplrefaqlkke
CVVIGVSNRVEIWSKELWEEYFAESEESFSEIAENIVDFDL"
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/gene="BH2574"
                                                                                                                                    QLLNIVGDDFIPRLISMNINKMGVHYLVKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(6487. .8103)
/gene="BH2577"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (5901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSSPQLDEDERGFSYHRDAPLDMRMNRSQSLSAYEVVNQWDFIELMKIISRYGEERFA
KQIARKIEQSREKKPIRTTGELVDIIKEAIPAPARRTGGHPAKRTFQAIRIAVNDELG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mfehvTvLknesvIGLNIKpDGIYvDCTLGGAGHSQEIVKQLTGGGHLYAFDQQYALSHAKETLSPYRGSFTLIESNFRYMREKLEELGVHHVDGVLFDLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(4939.
/gene="BH2575"
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AKSLGMKLEDENVKVVQN"
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                                                                                                        complement(8180.
                                                                                                                                                            GKLANKNWSIIESQLRFMERRMKRHVRERFEHELSKFDEAERWLKPNGLLQERHDHVI
                                                                                                                                                                                        KQYSYEEAIAHGLEKEKEGWLEEQTPWPIDQVVEEAITQIRHSHKPIKDLAEQIGETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAB06295.1"
/db_xref="GI:10175197"
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  8.8%;
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  Score 81.2; DB 2; Pred. No. 1.1e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAGCGTATGCAAATAAACTACTACAAGCTGGAGTCTCAGTTAC 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTACGAAGCCCTGCAGATTTGCTAGACTTTAGGTTCTCTCCAATTCTGGCGCAAGATTTC 690
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2 (bases
                                                       disses 1 to 10266)

Heidelberg, J. F., Elsen, J.A., Nelson, W.C., Clayton, R.A., Gwinn, J. Dodson, R.J., Haft, D.H., Hickey, E.K., Peterson, J.D., Umayam, L.A. Gill, S.R., Nelson, K.E., Read, T.D., Tettelin, H., Richardson, D., Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I., Ermolaeva, M.D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I.,
Sellers, P., McDonald, L., Utterback, T., Fleishmann, R.T., Nierman, W.C., White, O., Salzberg, S.L., Smith, H.O., Colwell, R.R., Mekalanos, J.J., Venter, J.C. and Fraser, C.M.
                                                                                                                                                                                                                                          Sellers,P., McDonald,L., Utterback,T., Fleishmann,R.D., Nierman,W.C. and White,O.
DNA sequence of both chromosomes of the cholera pathoge
                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.

1 (bases 1 to 10266)

Heidelberg, J. F., Eisen, J. A., Nelson, W. C., Clayton, R. A., Gwinn, M. L., Dodson, R. J., Haft, D.H., Hickey, E.K., Peterson, J. D., Umayam, L., Gill, S. R., Nelson, K. E., Read, T. D., Tettelin, H., Richardson, D., Gill, S. R., Nelson, K. E., Read, T. D., Tettelin, H., Richardson, D., Ermolaeva, M. D., Vamathevan, J., Bass, S., Qin, H., Dragoi, I.,
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                           /gene="VCA0484"
1949 .2236
/gene="VCA0484"
                                                                                                                 /gene="VCA0485"
2377. 2748
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                     95". .2748
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2377. .2748
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similarity; putative"
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Query Match
Best Local :
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GCAAATAAACTACTACAAGCTGGAGTCTCAGTTACTAGTGTGAGATTTAACAACGTTATA
                                                                                                                                                                                                                                                                                                                                                 CATGGCGGTTGTTTCATTAGCGGTGGTTTTGAAACACATGAAGCACAACTAAGGCAGTTA 5049
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                                                                                  CCTCCAACCTTGATTATCACTGCTGAGTATGACCCACTGCGAGATGAAGGAGGAGTTG
                                                                                                                                                                                                    GAGCGGTTGGCCAGTGAAAAAGAACTGAATCTATTGGCACGAAAGGATCTTCAAGGTTTA
                                                                                                                                                                                                                                                         CTGCAGATTTGCTAGACTTTAGGTTCTCTCCAATTCTGGCGCAA-GATTTCAACGGATTA
                                                                                                                                                                                                                                                                                                                 GATTTCATTATTACTGCACAAATGTTGTTGTCCGGTTTCCAGCTTTATGCGGGTGAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                             CTAATATATCCCATGGTTGACCCCTTGGGGGTGTCTGATAGTTATCAGAAAAACGGTACA 5349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGTTTACCCAGCGGTAAGTTTAGATAACGTTTCAAGATCCATGATAGAGTACTCTGAT 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTCTTGCTACAGCACTTCGTTTGAAAAATAAAAAGCTGTGGCTACCTGAGAAAACAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAGCGGTTGTAGCTCTTTCCAAAGGGTAAAATTAATTTG-----AAGTATCAAATA 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAATATGGCGGCGATACTGAACATGTATTCTTTGTCGGTGATAGTGCAGGTGCACAATTA 5229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACCCATCAGCTCATGATGATGTATTTCAGGCCGCATTAGGTATCAAAGAACATGGTCAT 5169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTCCTTCTGCAGTTATCGATTCATTTGACGCTACTAATTGGGTTTATAACAATTTAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTCATTTATCAGAGACTATAGTAGTTTGCATTAAGTACCGCTTAGCACCAGAGCATGCA 5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACAAATGCGTGCAATTGCGTTGTAGTATCAGTGGACTATAGGTTAGCTCCAGAATACAAG
                                                                                                                                          CCTCCAGCCTTGATAATAACAGCAGAATACGATCCACTAAGGGATCAAGGAGAAGCGTAT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAATTTGATGGAAAGATGGGA.---GTTGCGATTGCGGGAGATAGTGCTGGAGGAAATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="VCA0491"
5743. .6216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="This region contains an authentic point mutation,
causing a premature stop, and is not the result of a
sequencing artifact; identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mlclslvvmrcQplrralnaQvnsldlrmnrniefrtkklhski
vlsmvasyvvftlvenwftbTefQLmsflvGvtTmvviylflalflfkkahlsvtGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to PID:1054866 sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VFLHGLKAELIAKRGIFGTQYIQITSNTEKGYHRLKVTKDQIALADWNLLLGKCI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
/protein_id="AAF96395.1"
/db_xref="GI:9657895"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITAEYDPLRDEGEQLYRLLLSQGVDAYCERYLGVIHGFYQLSGVSESARRCIRNIANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="VCA0493"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="VCA0493"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="VCA0491"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 71.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 2.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PID:2271024; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 10266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
CEF27C8/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                                                                                                                      FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                              gene
                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                              source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACGGATTCCTCTCTTTCCGTTGATGGAGCAAGGAAGAGATGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACAGGTTGCTTCTTTCCCAAGGTGTTGACGCTTATTGTGAACGTTACCTAGGTGTAATA 5589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

EXCEPTION: This sequence is not the entire insert of clone F27C8. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (13-DEC-1995) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, England and Department of Genetics, Washington University, St. Louis, Mo 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                        For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence Z68221.

The true left end of clone W09C2 is at 33731 in this sequence. The true right end of clone T05A1 is at 2250 in this sequence. The true right end of clone T05A1 is at 2250 in this sequence. The start of this sequence (1. .104) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neighbouring submissions.
The true left end of clone F27C8 is at 1 in this sequence.
right end of clone F27C8 is at 4860 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The C.elegans Sequencing Consortium.

Erratum: [[published errata appear in Science 1999 Jan 1,288(5398):35 and 1999 Mar 26;283(5410):2103 and 1999 3;285(5433):1493]]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans. Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans cosmid F27C8, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; E16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence Z68221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The end of this sequence (33731. .33837) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     available information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 33837)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases
                                                                                     complement(join(11628. 12948. .13133))
                                                       12948. .13133))
/gene="F27C8.6"
                                                                                                                                                                       complement(join(11628. 12948. .13133))
  /note="similar to esterase
cDNA EST yk105e10.5 comes
                                                                                                                                                                                                                                                                                 /organism="Caenorhabditis
/db_xref="taxon:6239"
                                                                                                                                          /gene="F27C8.6"
                                                                                                                                                                                                                            /clone="F27C8"
                                                                                                                                                                                                                                                         /chromosome="IV"
                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Esterase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to 33837)
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                                                                                                               .11768,11871.
                                                                                                                                                                                                 .11768,11871.
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  this
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                                                                                                                                                                                                 .12110,12162.
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HSVVELPPNQYYRTRSEISAIDKMPDPFVRNLPRTQSASSMIARPRSSGGFPQYFTRS
EVEDLQQMTDPFSKSERGMTPTRGPPMGFSSVQCTVEX PGWSKDVMETWKEMYKQCKM
NGRYLLSEAQTESNAPVFLRPAVGGKKVSSSRALSNLSNSBONKKYCRGVTOSFSGHS
LNUNDPMFKEHDPKVQPSVLISCLSLPTTSPVSVVKPKMTGVKKTDSEIMEINALPSS
FNSNSFYTAKTSNTSGHSNDGSAKSEKSQRSQKSEKSQKLKKPIPQSQYLYPN*
JOHN(18086. .18107,18174. .18278,18335. .18507,18622. .18707
JGHNE**E72C8.4*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MGKKLAANAENLFSGGMMFLKTFLNISKENIYIFFILKYLYLKY
LYFSKRENKTFIVFRNSLHANAAPOHFERLAKILQAKRRAGDFSTCDVKIQLKTGFDM
VHSVVICAHSDVESETFDNQRAFYQPFNMTDDFDQNKRFADDMYSGEIDIPETTIAD
VLAVASYLRVTMLQRQIEQXILNHNGSPIMALNIASARAFSVMDHTMNDLVHGFTEKM
TGLGIDEVAKLTANSMIAVMAAVLPMKKKVPLVNMFISMIVCKQPERETINTIIQSLY
TSDITYDTLYAIRYSLKQYLTNSEIASKSQLTISFSGTIEIKIVPKKESMVSEKSSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-"contains similarity to pfam domain: pF00651 (BTB/POZ domain), Scorse-88.0, E-value-6e-23, N=1 cDNA EST yk377d4.3 comes from this gene cDNA EST yk377d4.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YENGPHAMLNEHSELDEASKSVDDIEQWTLNAINNA"

Complement (Join (14231 . 14526, 14574 . 114848, 14895 . . 14972,

15025 . . 15147, 15257 . . 15577, 1577 . . 15943, 15987 . . 16082,

16127 . . . 16282, 16592 . . 16766, 16980 . . 17074, 17211 . . . 17291))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mlkakkesnytkgivpvlitifillitgyalykplpegftiskwd
RAVWHVVEPALRVAYYYPSRWFTKPSNWVQWTRGALNTLSKTLGLLVNTHGQVDIKWH
KWNETPVKVYRPTNNKTSTDGAVLFIHGGGFALGNVDWYDSLVKRWAYEMKTLFISIE
     join(21507.
22583. .227
                                                                                                                                                                                                                                                complement(join(19337. .19428,19533.
/gene="F27C8.3"
                                                                                                                                                                                                                                                                                                   complement(join(19337. .19428,19533.
/gene="r27C8.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(14231. .14526,14574. .14848,14895.
15025. .15147,15257. .15577,15777. .15943,15987. .1
16127. .16282,16592. .16766,16980. .17074,17211. .1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YRLSPETVFPGGILDCEAAIDHFFDFGAVQFGVNTSKVVIMGDSAGGNLATVIAQRRA
ARNSFPKLAGQVLIYPLLQMADMQTVSYRYFHSRLRGYALVDPESVAYYYMFYAGIDM
DEKAYLVPSVISNGHVANHLQSEASEIMSYKSVIEMKHNYKNHSITERWEVSQSYEAQ
                                                                                 /db_xref-"SPTREMBL:Q19836"
/translation-"MQGIHGLVDIPKMDTGLSYHGEETKNGERSIDLLKNKPSHDKFE
VQKLSITEILKNVAPPEKGLITHSTDHGKELCHRRETNLKILPYMSRIRRAMNSHLLD
                                                                                                                                                                                                                                                                                                                                                                              /db_xref="SPTREMBL:Q19837"
/translation="MKTSALAFLALVCASSAFVVPQNADQCGAVDITKMAKRYVPSQN
SDATCEICLDLVLLAETYABEDEAIVQHHMDAYCVEHYKNHASQALCKLLIDDIAHAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLMEPFLTNPDFSPLMRKDLSNLPPTMVITCEFDILRDEGLIYGERLKVSGVPTTTIH
                                                                                                                                                                  /protein_id="CAA92461.1"
/db_xref="GI:3876347"
                                                                                                                                                                                                                                                                                                                                                        [EDTDQNPTGVCQKVIHKTCPYNN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAA92462.1"
/db_xref="GI:3876348"
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/gene="F27C8.5"
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/db_xref="GI:3876350"
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507. .21707,21760. .21880,21932. .22123,22335. .22462.
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yk444d6.5 comes
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                                                                                                                                                                                                                                                                                                                                           12666 TCTTGGAAACGTCGACATGTATGACTCGCTCGTCAAGAGGATGGCATATGAGATGAAAAAC 12607
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424 -AAGATGGGAGTTGCGGGAGAGATAGTGCTGGAGGAAATTTGGCAGCGGTTGTAGC
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                                                                                                                                                                                                                                                                                                                                                                                                       249 AATAGGCGATGTGGAATCTTATGACCCATTATGTAGAGCAATTACAAATGCGTGCAATTG 308
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                                                                                              CGATTGTGAAGCCGCTATTGATCACTTCTTCGATTTTTGGAGCCGTGCAATTCGGAGTGAA 12487
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/TGRYTKNGYWFKLSWGGNEEWREMANEMWYRNEFLVDSSSFLLYQRLFENNDGKLKLL
TAKNIRGEVLGLYLLSESSYRESTIGPIFVODEFRHIGIGSTLMEETLKNTDNIVFN
ASKSYYITHSENNTEDOWERIREFERECTMERKNAFSEKSDENQQIVAAFDENTGS
CVGISILREIQNEDGHIPDLLLAPLHAKSTAIAEILLQKSLKKHYNPEDDYDDVDHL
AIYRRSYNFFIFSNCESLMFPLKKLTGNDGSNLPAINHDMIFASDPTVFLC"
complement(join(23793. 23854,23920. 24061. 24232,
24361. 24751,24986. 25139,25187. 25312,25399. 25704,
25876. 26053))
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SAVPVYGIFIGWKNKPKWFNEFIDSSTVFIQKLFMVVDEDKED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation-"MTAEKĒPIKSREGDEAPQNETEGKGKGLEKSLTIFNGVSŃIVGC
IIGSGLFVSPHGVQEGAGSVGLSLIVWLISGITTALGAYCYĀELGTLIKKSGGDYAIYL
MEAFGPFVAFIRMIEAIVVRRCTWIVALFFAIYGLRFFPDCAPPDVAELLAILL
IVLMTAINCISVRLATIVQDWFTIAKVVALCIIILTGLGLLFFGESQYKDSFENIFEN
TSQDFFXVSLAFYSGLFAYSGWHFLWFIVEELGNBKRNLPLATAISITSGTVIYVLTN
VALYTAISPDEMLESPAYAVLFANKLYGKFAFIMPLCVAGSTIGSANGVIFTSARLFY
SGAREGQMPAVLTMINKKTKTPIPAVILTGALSIAYLLASKDVYQLINYIQISYWLAI
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/db_xref="GI:3876345"
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/gene="F27C8.2
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(SW:E16_HUMAN), contains similarity to Pfam
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Pred. No. 0:00077;
0; Mismatches 178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               areCBA is an operon in acinetobacter sp. Strain ADP1 and controlled by AreR, a sigma(54)-dependent regulator J. Bacteriol. 183 (1), 405-409 (2001)
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Jones, R.M., Pagmantidis, V. and Williams, P.A.
sal genes determining the catabolism of salicy
of a supraoperonic cluster of catabolic genes
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                                                                                                                                                                                                                                                   Sequence update by submitter
On Oct 27, 1999 this sequence version replaced gi:4929528
                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (12-MAY-1999) Microbiology, University of Georgia, Biological Sciences Bldg., Athens, GA 30602, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strain ADP1
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J. Bacteriol. 181 (15), 4568-4575 (1999)
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                                                                                                                                                                                                                                                                                                                   Submitted (27-OCT-1999) Biological Sciences, University of Wales Bangor, Bangor, Gwynedd, Wales LL57 2UW, United Kingdom
                                                                                                                                                                                                                                                                                                                                                                                  Williams, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 (bases 1 to 7253)
Collier, L.S., Neidle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 16768)
                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1
                                                                                                 Genbank Accession Number opposite direction"
                                     complement(38. .1183)
                                                                            complement(38. .1183)
                                                                                                                      /note="this position is contiguous
Genbank Accession Number AF009224,
                                                                                                                                                                                                     /organism="Acinetobacter
/strain="ADP1"
                                                            /gene="benP"
                                                                                                                                                                              /db_xref="taxon:62977"
note="putative
                    'gene="benP"
                                                                                                                                                                                                                                                                                                                                                                                                       to 16768)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neidle, E.L., Jones, R.M. and Williams, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2018-2025 (2000)
                                                                                                                                                                                                                      sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             salicylate esters are part genes in Acinetobacter sp.
                                                                                                                        but extends
                                                                                                                                         with first
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                                                                                                                                       position
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "gene
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RVEALVQAAVEHGATLEIGGKANGPFFEPSVLSQVQADNPIFSEEIFGPVAVLIPPAS
DEQALELANMGDYGLSAGIISSNVGRAMQLGAQLNVGLLHINDQTVNDETINPFGGFG
ASGNATRIGGPANPDEFTQWQWMTIQAEAPHYPF"
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SPTTPVPASTQQPLTTDDIRLSETVFPILKDIWALFKHQNICTFFLNTQFKIIAEYQN
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FNGQGKILGALDITSYREQLASMLHHLLYQGYVENEILIKKNMPAQHKLLYFQHSED
LLKTAYTGMIELDATGQIQKANQMALTLLNTSIDQLLYKFISNYFSSISTLASLEQQT
QFIRSQDEALFYARLYTPQMTKKTSHLFSTSTDDFKDIAKLSKILHSDVPILITGATG
SGKDHLARQIHEFATKDQAFISINCAAIPEHLLESELFGYEAGAFTGASAKGKRGLIE
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ADTILÞFDÞVSQKQARDYLKYGGTLKLKYDQTELRVGELWÞDLÞVTAVDRSRQLLTSY
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PNLKLKYFNASEDNKNYNIDSQNFGILETLKYRNHTVGLGYQQIVGDAYPLÞDGFLÞE
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/translation="
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/db_xref="GI:4929530"
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IDNHDFRSDLYYRICGYQIELPQLKDRPDKIDIFKTLLANAKIYSWSVNVQEQFEHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="areCBA operon"
/note="putative"
3520. .4974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'function="benzyl alcohol dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="areB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function="benzaldehyde dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .6117
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                                                                                                                                           Query Match
Best Local
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                                      6358 TTGAACTTCAAGACGTAGAAGATTTATGGATACAAGTAGACGATGGTAGCTTACGCTTAA 6417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
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                                                                            122 TCGAAGTTGGAAAAGTAGAAGATATAAAAATACCAGGCAGTGAAACCGTTATAAACGCTA 181
  182 GAGTGTA----
                                                                                                                                           Local Similarity
                                                                                                                        198;
                                                                                                                          Conservative
                                                                                                                                                                                                                          NPLFERTQYGVEATKLSHELYPVFKESILKIEIAVDEALNFNPLTSNKTFRIGLSDIG
EICLLPTLIEYLRAHAPKIKIEVEEIKIDQVEKWLIEGFIDVAVFNSTHLEFKHLEYE
TLFLERYVALVNMNHPRIRSTLSFDAYLNESHVAIKSSTGHTQVDHVLKLMGHQRKIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MFPHKLSLVLIACMPLSSYAFNGVYNTGSGOVSSGMGGVSLAQG
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SLDLGIQOFRAKGVLAGVDGOGTPIFLESHGNQWAYGVGASIGSTWEFQPNWWLGASY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPHYAGQFIELQDVEDLWIQVDDGSLRLRLYKTQRQHSESCETLIYFHGGGWCIGSIE
THDLLCRHLVWDLDVRVISVDYRLAFEYFYSQAAHDALHATQWIFEHASALGIHPDHL
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PLSAEQMSKMIQIYLKNEDFAYQWLASPLLAQSHQHLPSTLIITAEFDPLHDQGCVYF
                                                                                                                                                                                                     LEVPHFGVLQGVLDKTDLMVTLPSRAAQQYLNQSHVRVLELPFQMSEFYVGLHWFAQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(9320. .10210)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="salk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEPCQPFHDRLDLKKFYTLNIPKSYLNCTEDQALPAGFWHPKMSNRLGEFKLVEMGGS
HEAMFTRPQELATKIIEASHD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNYTHAQCSQSIADYIVKHDLSEIVLLGHSYGGTIISKVAEAIPERIQRLIYWNAFVL
QDGENMFDNMPEAYYELFTSLAAASGDNTVLLPYEVWRHAFINDADDQMAEETYKMLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8569. .9288
/gene="salE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STEMKFSKLDDYKNDLLARSEGRINLPERYGIGIKHKINQKLTLAADIVRFNWQDADG
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/protein_id="AAF04310.1"
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/gene="salD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKLKSSLVNTEYHEIKGVVHGFFEMYGVLNKTKETINIIRAWLKNNTKSK"
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                                                                                                                                                                                                                                                                                                                                                  /product="Salk"
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                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="AreA"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                              'function="regulator protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         function="alkyl salicylate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MLQSLDPQLASFFAMLENQGAPAFDIGTLNDPNINEMRNWYLNF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5201. .7181
′gene="areA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       function="putative
-TTTTCCGAAGAGTAGCGGTCCTTATGGTGTTCTAGTGTATCTTCATG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     function-"benzyl
                                                                                                                                           6.1%;
50.1%;
                                                                                                                        0
                                                                                                                                                              Score 56.2;
                                                                                                                                           Pred. No. 0.0066
                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .10210)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         facilitator
                                                                                                                                                            DB 1;
                                                                                                                        188;
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                                                                                                                                                            Length 16768;
                                                                                                                      9;
                                                                                                                      Gaps
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ACCESSION
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JOURNAL
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GAGGCGGTTTTGTAATAGGCGATGTGGAATCTTATGACCCCATTATGTAGAGCAATTACAA
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                                                                                                                                                                                                          number of introns/exons or we may not have chosen the correct splice donor/acceptor sites. CDS are numbered using the following system eg spBC25H2.01c. SP (S. pombe), B (chromosome 2), C25H2 (cosmid name), .01 (first CDS), c (complementary strand). The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

IMPORTANT: This sequence MAY NOT be the entire insert of the complementary strands.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   During 1995 to 1996 about 66% of S. pombe chromosome 1 was sequenced by the Sanger Centre. The sequencing of the S. pombe genome is now being continued with funding from The European Commission. Fourteen European sequencing laboratories, including the Sanger Centre, are participating in the project. Protein coding regions (CDS) have been predicted with the help of computer analysis using the Genefinder program in PomBase (an ACEDB database) with additional predictions for the branch-acceptor sites supplied by the program Sp3splice. CAUTION: It is possible that for any individual CDS we may have underestimated or overestimated the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Direct Submission
Submitted (03-JAN-2001) European Schizosaccharomyces genome
sequencing project, Sanger Centre, The Wellcome Trust Genome
sequencing project, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPAPB1A11
S.pombe cl
AL512486
                                                              sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. BAC pBIA11 is overlapped at the 3 end by cosmid c31G5, EMBL entry SPAC31G5,
                                          accession number 298979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fluconazole resistance esterase-lipase; FMN dependent dehydrogenase; fungal Zn(2)-Cys(6) blnuclear cluster; lactate dehydrogenase; membrane transporter; RNA binding; spliceosome associated protein 49; transcriptional regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
During 1995 to 1996 about 66% of S. pombe chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harris, D., Wood, V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Details of yeast sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fission yeast
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Location/Qualifiers
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/note="gtgagt, splice donor sequence"
1951. .1962
/note="ctaaccttgcag, splice branch and
6119. .7342
6254. .7330
/gene="SPAPB1A11.03"
/note="match to pr01070 FMN_dh, FMN-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     albicans fluconazole resistance protein"
/protein_id="CAC19726.1"
/db_xref="GI:12038980"
/translation="ILISLIVCTVYGILYLLFTAFAEVWISOYHFTSGLSGLTVISLS
                                                                                                                                                                                                        IALAPVGVQKIFNPEGESGSCAAATREHIPYIISTASATSFEDIEKASGPGERWYQLY
WPSNHDQDITISLLNRAKKTGCRVLIVTLDTETLGWRESDMDWGDFFLNPDSIGVEH
GFSDPVFRKOFKEKHGVEVEENMLEAAKEFAGIVFPGISHDWEDLKFLRKHWDGPIVL
KGIMNVPDAKKAVEYCHQGIVYSNHGCRQQDGGVASLTWLPKIVDAVGDKLDVLEDSG
VRSGADIAKALALGAKNVLIGRPYVYGLALEGSSGVSHVIRCLLGDLELTLHLSGIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative FMN dependent dehydrogenase; similar to lactate dehydrogenase" lactate dehydrogenase" /protein_id="CaC19728.1" /db_xref="c1:12038982" /translation="MFRNYNWFDAKEPISYESEIYAKGLKFQRPQITVDGRHWEQLAV /translation="MFRNYNWFDAKEPISYESEIYAKGLKFQRPQLTVTGGKYPFP /translation="MFRNYNWFDAKEPISYESEIYAKGLKFQRPQLTVFGQKYPFP /translation="MFRNYNWFDAKEPISYESEIYAKGLKFQRPQLTVTGGKYPFF /translation="MFRNYNWFDAKEPISYESEIYAKGLKFQRPQLTVTGGKYPFP /translation="MFRNYNWFDAKEPISYESEI" /translation="MF
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join(1806. .1865,1963. .2922)
/gene="SPAPB1A11.02"
join(1806. .1865,1963. .2922)
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/note="SPAPBIA11.01, SIMILARITY:Schizosaccharomyces pombe, O9p375, putative membrane transporter., (485 aa), fasta scores: opt: 805, E():0, (51.7% identity in 209 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSYKETIHAPVITPKIMDIFFENYQPTPKSPLVNPLYYPTGHKDLPPSFFQCCGWDPL
RDEGIAYEKALKAAGNETRLIVYEGVPHCFWVYYPMLSLRKKYFEDAIDGFTWLLSHV
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CRKQLAETILPLPDDVSVTDILIPTROGTEIDGRVFTPVSVPADYSLAVFYHSSGWC
MRCVRDDDSLKKILTPKFGCVCVSVDJYRLAPESKFPVAHDAIDSFKWPASNIEKLGA
NPKRGFFLGGASAGGNFVSVLSHIARDEKIKPELTGLWHMVPTLIHPADLDEETMAQF
                                                                                                                                                                   VKPKDLNRDVLYKEE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="SPAPBIA11.03, len:408, SIMILARITY:Mycobacterium
smegmatis., LA2M_MYCSM, lactate 2-monooxygenase, (393 aa),
fasta scores: opt: 950, E():0, (40.0% identity in 403 aa)"
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/protein_id="CAC19727.1"
/db_xref="GI:12038981"
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/note="SPAPB1A11.02, len:340,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVFWFVPLIGTTLVGAGFVMTFNPMNMFIVDNYGRYAASAMAAIAIPRNIFGACFPLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Schizosaccharomyces pombe"
/strain="972h-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/label=SPAPB1A11.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start='
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SPAPB1A11.03"
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    TGTTCTAGTGTATCTTCATGGAGGCGGTTTTGTAATAGGCGATGTGGAATCTTATGACCC 275
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                                                                                           Conservative
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1"
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10885. .10897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="spliceosome associated protein 49; RNA binding" /protein_id="CAC19730.1" /dp.xref="GI:12038984" /db_xref="GI:18038984" /translation="MSIREDRWQDATIYLGNLDEKVTDSILFELCLQAGPVVNIHIPR DRVRNSHNGFGFCEFLHEQDVEYACQILNQVKLFGKPIRVNRASQDRGVNTLIGANLF VGNLDPLVDERVLYDTFSALGQLVKAPQVARDENGRS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FVERILISTGYMAPSKLRSLSLQKTSJQLPCPEPNFLFNQPILITELFDGSLPENTQS
DTTSMAPYQRSLQLERWTGSLIRLSNLMSEISRALCGGYTKDLTPPWLNQSQFIRSF
ELLKAMHENLPPRAYWSYTNYSAYSSPGESAGACYTFWLLYHTTLTYLLRNULDLFB
EKSRQKSKLFSSVSQRFGQQPPTVWMDMILDQVITSADFITKLSKDPLNYIMSPFVGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="ctaattcatacag, splice branch and
11104...11203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="SPAPBIA11.05, SIMILARITY:Homo sapiens, SP49_HUMAN,
spliceosome associated protein 49, (424 aa), fasta scores
opt: 556, E():8.5e-33, (57.8% identity in 135 aa)"
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NFYRFQYLEEQSLYNFKIPGFPLCILEYGIVEDQSMKSNPDLNSFSKELFSRGTNELL
NNGDDTQSGNSTPANGVSEIRTDTILDEEVPVDPLITSILDDGRWWEEMFGSERKAGF
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VLCICAHAARFSQEEVNRFKSSTAASDYYANQAFSLLPCRFQDISLTNITCLLLLCLI
ELGSCRGAKAWLLLGMALRMYDSLDLGNEINDNPLTMGSNTYSWTEAEQKRRVYWACF
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/gene="SPAPBIA11.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (a.k.a. RRM, 1084)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(10765. .10840,10898. .11037)
/gene="sap49"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="sap49"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Match to PF00076 rrm, RNA recognition motif.
(a.k.a. RRM, RBD, or RNP domain) Score 44.29"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SPAPB1A11.04c"
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|oin(10729. .10840,10898. .11203)
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                                                                                                                                                                 Length 11203;
                                                                                                                                                                                                                                                                                                                                                                                                                              pombe chromosome
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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em_estro4

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  141 BE920651
143 BF050574
167 BE462514
166 BE353325
118 AW642884
167 BE462510
143 BF050518
118 AW625913
116 BE353489
115 AW442537
118 AW649491
173 BG096621
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BE050574 EST332732
BE462514 EST324780
BE353325 EST333606
AW648648 EST327302
BE462510 EST344766
BF050518 EST344766
AW625913 EST319808
BE353499 EST333686
AW442537 EST307467
AW649491 EST327945
BG096621 EST461140
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AW932710 EST338553
AW929945 EST358553
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9b_est59:
9b_est60:
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REFERENCE
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EST424420
CSTB10G23
                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Cathy Ronning
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                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                 potato.
Solanum tuberosum
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                                                                                                                                                                                                         clone request: please contact Research Genetics, ision tel 1-800-711-6195, email cdna@resgen.com.
          131
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20 potato leaves a
3 5' sequence
         /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in liquid nitrogen."

152 c. 128 g 157 t
                                                                                                                                     /db_xref="taxon:4113"
/clone="cSTB10G23"
                                                                                                                                                            /organism~"Solanum tuberosum"
/cultivar="Kennebec"
                                                                                         /clone_lib="potato leaves and petiol
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
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AI582719 tn16g07.x

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AV42043 AV42043

AV422039 AV42043

AV422039 AV42043
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AV675219 AV675219
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                                                                                                                                                                                                                                                                                                                                                                                                                         Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 431)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E.,
Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M.,
Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
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                                                                                                                                                                                                                                                                                                                                                 dfrisch@CLEMSON.EDU
            /note="Vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: Xhol; Fruit were tagged at 5 dpa (0.5 cm) and harvested at 7 day intervals through 35 dpa. Equal masse of tissue from each stage were combined (including seeds and locules) prior to mRNA isolation."
                                                                                                                                     /clone_lib="tomato developing/immature green fruit"
/tlssue_type="fruit"
/dev_stage="immature green (5-35 days post-anthesis/lab_host="SOLR"
                                                                                                                                                                                                                     /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEM18J23"
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Query Match
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Conservative

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Score 57.8; Pred. No. 2

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DB 143; Length 431;

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                                                                                                                                              TGGTTTACTATCACGGTGGTGGATTTGTGATTTGCAGC-----ATGGAGTCGCACGACG 298
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CCGTTTGCCGTCGTTTCGCGAGGAAAACCCCCGGCTGTTGTTGTCTCTGTTAATTATCGGC
                                                     CCTTATGCAGGAGAAYYGCGAGACTTTCAAACTCTACCGTAGTCTCCGTGGATTACAGGC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTG 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST324780 tomato flower Lycopersicon esculentum BE462514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@CLEMSON.EDU
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100 Jordan Hall, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fr. Hansen,T., Craven,M.B., Bo
Fraser,C.M., Martin,G.B., Giova
Generation of ESTs from tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 524)
van der Hoeven, R.S., Bezzeredes, J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
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                                                                                                                                                                                                                                                                                                                                                                                                        117
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="flower"
/dev_Etage="0-3mm buds"
/dev_Etage="0-3mm buds"
/dev_Etage="0-3mm buds"
/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
EcoR1; EcoR1; Site_2: EcoR1;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Lycopersicon
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cTOA13E6"
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Pred. No. 2.1e-06;
2; Mismatches 64
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B., Bowman, C.L., Ronning, C.M., Nierman,
Giovannoni, J.J. and Tanksley, S.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Clemson University
100 Jordan Hall, Clemson,
Tel: 864 656 4366
Fax: 864 656 4293
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EST353606 tomato flower
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                                                                                                           /clone_lib="tomato flower buds 0-3 mm, Cornell Universit
/tissue_type="flower"
/dev_stage="0-3mm buds"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                       /db_xref="taxon:4081"
/clone="cTOA18A9"
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Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S, Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronnning,C.M., Nierman,W., Fraser,C.M., Giovannoni,J.J., Martin,G.B. and Tanksley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generation of ESTs from
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sper
Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
I; Solanales; Solanaceae; Solanum; Lycopersicon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="tomato germinating seedlings, TAMU"
/tissue_type="whole seedlings"
/dev_stage="7 days post imbibtion"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/note="Yestor: pBlueScript SK(-); Site_1 = EcoR1; Site_2:
/note="Vector: pBlu
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/clone="cLEI6I1"
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/cultivar="TA496"
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Pred. No. 2.1e-06;
2; Mismatches 64
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5/4 bp ......
EST435676 tomato developing/immature esculentum cDNA clone cLEM18K24 5' so
Lycopersicon esculentum
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Clemson University
100 Jordan Hall, Clemson, SC 29634, US
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Lycopersicon viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
I; Solanales; Solanaceae; Solanum; Lycopersicon.
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BE462510
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                                                        BF050518.1
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Fax: 864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: dfrisch@CLEMSON.EDU
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/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
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/cultivar="TA496"
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/tissue_type="flower"
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/clone="cTOA13C20"
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                                                                                                                                                                                                                        AW025913 590 bp mRNA EST 28-MAR-2000 EST319808 tomato radicle, 5 d post-imbibition, Cornell Universi Lycopersicon esculentum cDNA clone cLEZ17D13 5', mRNA sequence. AW625913
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Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
                               van
                                                                 Lycopersicon esculentum
Eukaryota; Viridiplanter, Embryophyta; Tracheophyta;
Eukaryota; Viridiplanter, Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledona; core eudicots; Asteric
I; Solanales; Solanaceae; Solanum; Lycopersicon.
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Clemson University
100 Jordan Hall, Clemson, SC 29634, US
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Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
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                                                                                                                                                           tomato
                                                                                                                                                                                                      AW625913.1
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                        (bases 1 to 590) der Hoeven, R.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: Xhol; Fruit were tagged at 5 dpa (0.5 cm) and harvested at 7 day intervals through 35 dpa. Equal masse of tissue from each stage were combined (including seeds and locules) prior to mRNA isolation."

144 c 141 g 159 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="tomato developing/immature green fruit"
/tissue_type="fruit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4081"
/clone="cLEM18K24"
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/cultivar="TA496"
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/lab_host="SOLR"
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    Craven, M.B.,
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                        Garvin, D,,
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Pred. No. 2.1e-06;
2; Mismatches 64;
    Bowman, C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tomato fruit tissue, immature green
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Asteridae; euasterids
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                                                         van der Hoeven,R.S., Bezzeredes,J.L., Matern,A.L., Holt,I.E., Liang,F., Hansen,T., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D. Generation of ESTs from tomato flower tissue, 0-3 mm buds Unpublished (1999)
Contact: David Frisch
                                                                                                                                                                                                                                                                                          EST353686 tomato flower
Lycopersicon esculentum
BE353489
           Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, U.
                                                                                                                                                                                          Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; Asterio
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Fax: 864 656 4293
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/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Si
Xho1; supplier: Tanksley; Tissue supplied by Dave
(USDA-ARS, Ithaca, NY 14850)."
161 c 137 g 163 t
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/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEZ17D13"
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                                                                                                                                                               1 to 611)
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60.7%;
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dae; euasterids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290 TCGTCTTCCTCCACGGTGGCGGATTTGTGTATCTCAGCCCGGATACGAAGGCGTACGACG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTTATGCAGGAGAAYYGCGAGACTTTCAAACTCTACCGTAGTCTCCGTGGATTACAGGC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGCTCCGGAACACAAGTATCCTGCGCAGTATGACGATGGCTTTGATGTGCTCAAGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGTTTGCCGTCGTTTCGCGAGGAAAACCCCGGCTGTTGTTGTCTCTCTGTTAATTATCGGC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111;
                                                                                                                                                                                                                          D'Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Hansen,T.S., Ronning,C.M., Craven,M.B., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D., Giovannoni,J.J. and Martin,G.B. Generation of ESTs from tomato callus (mixed elicitor)
                                                                                                                                                                                                                                                                                                                                          Lycopersicon esculentum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sper
Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
I; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST307467 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA clone cLET41E18 5', mRNA sequence.
                                                                                                                                                                        Clemson University Genomics Institute
                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                              Contact: David Frisch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW442537.1 GI:6984719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW442537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 864 656 4293
                                                                                                Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                              tomato
                                                                                                                                    100 Jordan Hall, Clemson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                472
                                                          prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prime sequence.
                                                                                                                                                        emson University
                                                                                                                                                                                                                                                                                                                              (bases 1 to 616)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dfrisch@CLEMSON.EDU
                                                                              dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="flower"
/dev_stage="0-3mm buds"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/Note: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
/organism="Lycopersicon esculentum"
                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:4081"
/clone="cTOA18B19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Lycopersicon esculentum"
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="tomato flower buds 0-3 mm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 57.8; DB 16
Pred. No. 2.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
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REFERENCE
AUTHORS
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AW649491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 111; Conserv
                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 CCGTTTGCCGTCGTTTCGCGAGGAAAACCCCGGCTGTTGTTGTCTCTGTTAATTATCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 TTGCTCCGGAACACAAGTATCCTGCGCAGTATGACGATGGCTTTGATGTGCTCAAGTTCC 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359 TCGCTCCTGAGCACAAGTTTCCCCCCCCCAGTTTATCATTGCTACGATGCGACCAAGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 TTG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 TCGTCTTCCTCCACGGTGGCGGATTTGTGTATCTCAGCCCGGATACGAAGGCGTACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTTATGCAGGAGAAYYGCGAGACTTTCAAACTCTACCGTAGTCTCCGTGGATTACAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGTTTACTATCACGGTGGTGGATTTGTGATTTGCAGC-----ATCGAGTCGCACGACG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW649491 673 bp mRNA EST3737945 tomato germinating seedlings, TAMU Lycoesculentum cDNA clone cLEIBK20 5', mRNA sequence
                                                                                                                                                                                    Tel: 864 656 4366
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                  l (bases 1 to 673)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S, Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronnning,C.M., Nierman,W., Fraser,C.M., Giovannoni,J.J., Martin,G.B. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                                                                                          Contact: David Frisch
                                                                                                                                                                                                                                                                                                           Unpublished (2000)
                                                                                                                                                                                                                                                                                                                            Generation of ESTs from germinating tomato seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lycopersicon esculentum
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                                                                                                                                                                                                                                                                   Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tomato.
                                                                                                                                                                                                                          Clemson University
                                                                                                                                                                                                                                                                                                                                                     S.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     I; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                              prime sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                   dfrisch@CLEMSON.EDU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; CLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2.6 dichloroisonicottinic acid, BTH, jasmonic acid, ethylene, fenthion, EIX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."
                         /db_xref="taxon:4081"
/clone="cLEI8K20"
                                                               /organism="Lycopersicon
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="tomato mixed elicitor,
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cultivar="Rio Grande PtoR"
/db_xref="taxon:4081"
'clone_lib="tomato germinating seedlings, TAMU"
                                                                                                                         ocation/Qualifiers
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60.7%;
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Pred. No. 2.2e-06;
2; Mismatches 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAMU Lycopersicon
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ORIGIN
                                   BASE COUNT
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ORIGIN
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Best Local S
Matches 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cathy Ronning
Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 466)

1 (bases 1 to 500)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
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                                   0
                   /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; Tissue was supplied by Dr. Fry (Cornell University). Leaflets and petioles were isolated from 8 week old greenhouse grown plants. The plants were watered and fertilized freely. The tissue was immediately frozen in liquid nitrogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="7" days post imbibtion"
//dev_stage="7" days post imbibtion"
//note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; 7 days post imbibtion on water-agar. Mixed stage
whole germinating seedlings from seed coat emergence up
to two centimeters in seeds not showing obvious signs of
germination were discarded."
a 174 c 161 g 186 t
                                                                                                                                                                                                                                                                                             /clone_lib="potato leaves and petioles"
/tlssue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone-"cSTB44I21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:4113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cultivar="Kennebec"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Solanum tuberosum"
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Pred. No. 2.2e-06;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 TACAGGCTCGCTCCTGAGCACAAGTTTCCCCCCCCAGTTTATCATTGCTACGATGCGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 TACGACGCCGTATGCCGACGTTTCGCGAGGAAAACCCCCGGCTGTTGTTGTCTCTGATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 CACGACGCCTTATGCAGGAGAAYYGCGAGACTTTCAAACTCTACCGTAGTCTCCGTGGAT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 CCGATCATCGTCTTCTCACGGTGGCGGATTTGTGTATCTCAGCCCGGATACGAAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGTTCCTTG 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA472246 495 bp mrwa vh09h08.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:875007 5' similar to gb:L11706_cds1 HORMONE SENSITIVE LIPASE
                                                                                                                                                                                                                                                                                                                                                                         Email; mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:514487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kuchba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-HHMI Mouse EST Project
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                                      /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                        /tissue_type="mammary gland"
/dev_stage="4 weeks"
                                                                                                                                                                           /sex="male"
                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="IMAGE:875007"
                                                                                                                                                                                               /clone_lib="Soares_mammary_gland_NbMMG"
                                                                                                                                                                                                                                                           /strain="C57BL/6J"
                                                                                                                                                                                                                                                                               /organism="Mus musculus
                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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59.5%;
double-stranded cDNA was ligated to Eco RI
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Pred. No. 4e
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4e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST358553 tomato fruit mature green, TA CDNA clone CLEF49L11 5', mRNA sequence. AW932710
                                                                                                                                                                                                                                                 Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                    Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                                                                     Contact: David Frisch
                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                             Clemson University
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/db_xref="taxon:4081"
/clone="cLEF49L11"
/clone_1b="tomato fruit mature
/tlssue_type="fruit pericarp"
                                                                     /organism="Lycopersicon
/cultivar="TA496"
                                                                                                                          Location/Qualifiers
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EST354215 tomato flower
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Fax: 864 656 4293
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a 129 c
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; supplier: Tanksley; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."

152 c 110 g 175 t
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                                                                                                                                                                                                                                          Cornell University"
/tissue_type="flower"
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                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4081"
/clone="cTOC8M8"
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Lycopersicon
/cultivar="TA496"
                                                                                                                                                                                                          /dev_stage="buds 8mm-to-preanthesis"
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/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                 'clone_lib="tomato flower buds
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Pred. No. 6.4e-05
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BASE COUNT

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Database :
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
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Pending_Patents_NA_Main:*

1: /cgn2_6/ptodata/2/pna/US

3: /cgn2_6/ptodata/2/pna/US

4: /cgn2_6/ptodata/2/pna/US

5: /cgn2_6/ptodata/2/pna/US

5: /cgn2_6/ptodata/2/pna/US

6: /cgn2_6/ptodata/2/pna/US

7: /cgn2_6/ptodata/2/pna/US

8: /cgn2_6/ptodata/2/pna/US

10: /cgn2_6/ptodata/2/pna/US

11: /cgn2_6/ptodata/2/pna/US

10: /cgn2_6/ptodata/2/pna/UI

11: /cgn2_6/ptodata/2/pna/UI

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40: /cgn2_6/ptodata/2/pna/UI

41: /cgn2_6/ptodata/2/pna/UI

42: /cgn2_6/ptodata/2/pna/UI

43: /cgn2_6/ptoda
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Gapop 10.0 , Gapext 1.0
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936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGCTTGATATGCCAATCGA.....CTCTTCTTGTGTTCGACTAG
                                                              cgn2_6/ptodata/2/pna/US082_COMB.seq:
cgn2_6/ptodata/2/pna/US082_COMB.seq:
cgn2_6/ptodata/2/pna/US084_COMB.seq:
cgn2_6/ptodata/2/pna/US086_COMB.seq:
cgn2_6/ptodata/2/pna/US086_COMB.seq:
cgn2_6/ptodata/2/pna/US086_COMB.seq:
cgn2_6/ptodata/2/pna/US086_COMB.seq:
cgn2_6/ptodata/2/pna/US086_COMB.seq:
cgn2_6/ptodata/2/pna/US089_COMB.seq:
cgn2_6/ptodata/2/pna/US089_COMB.seq:
cgn2_6/ptodata/2/pna/US099_COMB.seq:
cgn2_6/ptodata/2/pna/US099_COMB.seq:
cgn2_6/ptodata/2/pna/US099_COMB.seq:
cgn2_6/ptodata/2/pna/US099_COMB.seq:
cgn2_6/ptodata/2/pna/US099_COMB.seq:
cgn2_6/ptodata/2/pna/US099A_COMB.seq:
cgn2_6/ptodata/2/pna/US095A_COMB.seq:
cgn2_6/ptodata/2/pna/US095A_COMB.seq:
cgn2_6/ptodata/2/pna/US095A_COMB.seq:
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cgn2_6/ptodata/2/pna/US096C_COMB.seq:
cgn2_6/ptodata/2/pna/US096C_COMB.seq:
cgn2_6/ptodata/2/pna/US096C_COMB.seq:
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cgn2_6/ptodata/2/pna/US090B_COMB.seq:
cgn2_6/ptodata/2/pna/US000B_COMB.seq:
cgn2_6/pt
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/2/pna/US06_COMB.seq:*
/cqn2_6/ptodata/2/pna/US07_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/2/pna/US080_COMB.seq:*
/cgn2_6/ptodata/2/pna/US081_COMB.seq:*
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56: /cgn2_6/ptodata/2/pna/US6023_COMB.seq:*
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59: /cgn2_6/ptodata/2/pna/US6027_COMB.seq:*
59: /cgn2_6/ptodata/2/pna/US6027_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ouery Score Match Length DB ID 935.2 99.9 936 17 'US-09-382-242-31 Sequence 31,

Result No.

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5.77777	, , , , , , , , , , , , , , , , , , ,	77888888444444444444444444444444444444		5.86.6
	207 287 287 606 804 807 673 187 187 187	810 663 4041 999 954 954 954 968 968 968 968		936 918 918 1529
	555550	118 116 117 117 118 128 128 128 128 128	115 115 115 116	17 17 15 28
US-60-215-161-2523 US-60-215-161-2523 US-60-215-161-2525 US-60-215-161-2525 US-60-215-161-2527 US-60-215-161-2528 US-60-215-161-2529 US-60-215-161-2529 US-60-215-161-2529	-09-684-016 -09-684-016 -09-533-559 -69-211-7507 -60-215-161 -60-215-161 -60-215-161	-60-138-103-4145 -09-404-520-3305 -09-252-991A-580 -60-082-302-377 -09-328-352-691-4341 -09-252-691-4341 -09-252-691-4341 -09-716-475-2550 -09-354-899-2783 -09-702-134-20449 -09-702-134-20449	\$\frac{1}{5} \cdot	82-242-31 82-242-32 803-840A-1
Sequence 2523, Ap Sequence 2524, Ap Sequence 2525, Ap Sequence 2525, Ap Sequence 2527, Ap Sequence 2528, Ap Sequence 2529, Ap Sequence 2529, Ap	equence 31246 equence 954, <i>t</i> equence 18563 equence 75800, equence 408, <i>t</i> equence 2519, equence 2520, equence 2521,	equence 4145, equence 3305, A equence 580, A equence 619, A equence 4341, equence 2550, equence 2783, equence 2783, equence 20449, equence 20449, equence 20449, equence 20449, equence 37433, equence 20449, equence 20	equence 9983 equence 9983 equence 767, equence 767, equence 767, equence 5085 equence 505, equence 5267 equence 2167	8

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; MOLECULE TYPE: US-09-382-242-31
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US-09-382-242-31
                                                                                                                                                                                                                                        Query Match
Best Local Sim
Matches 936;
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                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 936 NUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION UNMEER: 38,347
REFERENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 619-678-5070
TELEPAX: 619-678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF
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                181
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CITY: LA
STATE: C
COUNTRY:
                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                               TYPE: NUCLEIC ACID
STRANDEDNESS: SINGI
                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
SOFTWARE: WORD PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: FISH & KICHANDER STE 1400
STREET: 4225 EXECUTIVE SQUARE, STE 1400
                                                                                                                                                                               CCGAAGTTCGACCAGTTTTCCTCGGCCAGAGAGTACAGGGAGGCGATAAATCGAATATAC 120
             ATTAAGGGAAGGAACGGAGACATCAGAGTCAGAGTTTACCAGCAGAAGCCCGATTCCCCG
                                                                   GAGGAGAGAAACCGGCAGCTGAGCCAGCATGAGAGGGTTGAAAGAGTTGAGGACAGGACG 180
                                                                                                                                                                                                                                                   h 99.9%; Score 935.2; DB 17;
Similarity 100.0%; Pred. No. 6.4e-273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LA JOLLA
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09382242
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REID, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM: MS-DOS
WORD PERFECT 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KOSMOTKA, Anna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WARREN, Patrick V.
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAFFIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROBERTSON, Daniel E.
                                                                                                                                                                                                                                                                                                                                        LINEAR
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                                                                                                                                                                                                                                                                                                                           GENOMIC DNA
                                                                                                                                                                                                                                                                                                                                                     SINGLE
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                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                  DB 17; Length 936;
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                                                                                                                                                                                                                                                                                                           US-09-382-242-32
                                                                                                                                                                                                                                                                              Sequence 32, Applicat GENERAL INFORMATION:
                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
           COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INC
                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RI
                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    721
                                                                 STREET: 4225 EXECUCITY: LA JOLLA STATE: CALIFORNIA
                                        COUNTRY: UZIP: 92037
COMPUTER:
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                                                                                                                                                                                                                                                                                            Application US/09382242
                                                                                              4225 EXECUTIVE SQUARE,
                                                                                                                                       WARNATION: ESTERASES
                                                      USA
                                                                                                                                                                                                                                     MURPHY, Den
REID, John
                                                                                                                                                                               SWANSON, Ronald V. WARREN, Patrick V.
                                                                                                                                                                                                             MAFFIA, Anthony LINK, Steven
                                                                                                                                                                                                                                                                   ROBERTSON, Daniel E.
 IBM PS/2
                                                                                                            FISH & RICHARDSON P.C
                                                                                                                                                                                                         Steven
             INCH DISKETTE
                                                                                                                                                                                                                                                   Dennis
                                                                                              STE 1400
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US-09-382-242-32
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INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
SEQUENCE: 918 NUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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APPLICATION NUMBER: US/09/382,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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    805
                                                              838 TACAGAGGCGTGCTTCACGGATTCATTCATTACTATCCCGTGCTGAAGGCTGCGAGGGAT
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                                                                                                                                                                     745 CAAGGAGAAGCGTATGCAAATAAACTACTACAAGCTGGAGTCTCAGTTACTAGTGTGAGA
                                                                                                                                                                                                                                                                                                                                           685 GATTTCAACGGATTACCTCCAGCCTTGATAATAACAGCAGAATACGATCCACTAAGGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watch 14.6%; Local Similarity 54.0%; res 369; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: NUCLEIC ACID
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REGISTRATION NUMBER: 38
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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TOPOLOGY: LIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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                                                                                                                                                                                                                                                      GAAGGAGAAGTTTTCGGGCAGATGCTGAGAAGAGCCGGTGTTGAGGCGAGCATCGTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                 CTTGAGAAC ---CTACCTGCGCTGATAACCGCCGAATACGACCCGCTGAGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGAGTTTGGAGAGGGGCTGTGGATTCTCGACCAGAAGATAATGAGTTGGTTCTCGGAG
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TTTAACAACGTTATACACGGATTCCTCTCATTCTTTCCGTTGATGGAGCAAGGAAGAGAT
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GENERAL

APPLICANT: WHITE,

APPLICANT: WHITE,

APPLICANT: VENTER, John C.

APPLICANT: VENTER, John C.

TITLE OF INVENTION: DNA SEQUENCES FOR THE CONTROL TUBERCULOSIS

TOP INVENTION: TUBERCUL
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; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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Best Local Similarity 48.4%;
Matches 331; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1576190 TGCCGTCGTTGGCCGAGAATGCCGACGCAC---CGATCCTCGACGTCAAGGCAATTGCCG 1576134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1576250 GCGGCCCGCCCATTGTGTTTCAGCTGTTGTGGTATCCCTCCACTCTGTGGGACCAATCGC 1576191
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                                                                                                                                                                                                                                                                                                                                                              1576133 CGTTCTCCCGTTGGTACGCAGGCGAAATCGACTTGCACAACCCGCCAGCGCCAATGGCGC 1576074
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TYPE: DNA
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                                                                               764 ACCCGCTGAGAGATGAAGGAGAAGTTTTCGGGGCAGATGCTGAGAAGAGCCGGTGTTGAGG 823
                                                                                                                                                                                                                                              704 CCGTAATCTTTGCGGACCTTGAGAACCTACCTCCTGCGCTGATCATAACCGCCGAATACG 763
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Pred. No. 2.2e-12;
1; Mismatches 343;
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US-09-703-708-9983
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SEQ ID NO 9983
LENGTH: 1041
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GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/703,708
CURRENT FILING DATE: 2000-11-02
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                                                                                                                                                      658 GAGCAGTACTTCTCCAGAGAGGAAGATAAGTTCAAGCCCCTCGCCTCCGTAAT-----
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              CTGAGAGATGAAGGAGAAGTTTTCGGGCAGATGCTGAGAAGAGCCGGTGTTGAGGCGAGC
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                                                agcgtggagcaactcaagggcttgccgccgaccttgatccagaccgccgaactggatgtc
                                                                                  --CTTTGCGGACCTTGAGAACCTACCTCCTGCGCTGATCATAACCGCCGAATACGACCCG
                                                                                                                    gacagctacaccaccgacccggcgcagcgcgcgagatctacgcctcgccattgcaggcc
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Pred. No. 5.1e-13;
1; Mismatches 318;
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APPLICANT: Bower, Stanley G.
APPLICANT: Hinkle, Gregory J.

TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and FILE REFERENCE: 38-10(15804)A

CURRENT APPLICATION NUMBER: US/60/164,320

CURRENT FILING DATE: 1999-11-10
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Best Local Similarity
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SEQ ID NO 9983
LENGTH: 1041
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SEQ ID NO 9983
LENGTH: 1041
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Best Local Similarity 47.7%;
Matches 302; Conservative
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APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: xanthemonas campestris
FILE REFERENCE: 38-10(15804)B
CURRENT APPLICATION NUMBER: US/60/183,791
CURRENT FILING DATE: 2000-02-22
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Pred. No. 5.1e-13;
1; Mismatches 318;
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, NAME/KEY: unsure
; LOCATION: (1)..(46151)
; OTHER INFORMATION: unsure at all n
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CURRENT FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/164,
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION TOMBER: 1999-11-12
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TITLE OF INVENTION: xant
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ORGANISM: Xanthomonas
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                     ATCGTCAGATACAGAGGCGTGCTTCACGGATTC
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RESULT 8 US-60-164-320-767

Sequence

767, Application US/60164320

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RESULT 9
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                      Sequence 767, Application US/60183791
GENERAL INFORMATION:
APPLICANT: Bower, Stanley G.
APPLICANT: Hinkle, Gregory J.
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APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Xanthomonas campestris Genome
FILE REFERENCE: 38-10(15804)A
CURRENT APPLICATION NUMBER: US/60/164,320
CURRENT FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 18992
SEQ ID NO 767
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       TITLE
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TYPE: DNA
ORGANISM: Xanthomonas campestris
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                                                                                                                 Sequence 5085, Application US/09489039A GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
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Best Local Similarity 47.7
Matches 302; Conservative
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CURRENT APPLICATION NUMBER: US/60/183,791
CURRENT FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 18992
SEQ ID NO 767
LENGTH: 46151
APPLICANT: Gary Breton et. al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747
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OTHER INFORMATION:
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ORGANISM: Xanthomonas campestris
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                                                                                                                                                                                                                                                                                               ATCGTCAGATACAGAGGCGTGCTTCACGGATTC
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Pred. No. 2.2e-12;
1; Mismatches 318;
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US-09-663-779-521/c
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NUMBER OF SEQ ID NOS:
SEQ ID NO 5085
LENGTH: 951
TYPE: DNA
                                                                                                                    Sequence 521, Application US/09663779 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Corbin, David R.
APPLICANT: Malvar, Thomas M.
APPLICANT: Shukla, Hridayabhiranjan
APPLICANT: Shukla, Hridayabhiranjan
TITLE OF INVENTION: BACILLUS THURINGIENSIS CHROMOSOMAL GENOME SEQUENCES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 38-21(51376)B
CURRENT APPLICATION NUMBER: US/09/663,779
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                                                                                                                                                                                                                  cgggatatcgcctggcgtgtgg 934
                                                                                                                                                                                                                                                                                     ggggtgatccacggcttctttcagctggtaggcatcagcaacgccgcgcgtgatgccatg
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Pred. No. 1
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1.6e-11;
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; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-09-663-779-521
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1:
PRIOR FILING DATE: 1:
NUMBER OF SEQ ID NOS:
SEQ ID NO 521
LENGTH: 1127
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 605, Application US/09252991A
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
SEQ ID NO 605
LENGTH: 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                    Query Match
Best Local Similarity
Matches 285; Conserv
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                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                               TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                      238
   517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               813 CATGGTGGAGGTTATATCTTAGGGTCTATAGATGATAACGATGATACTTGTATGAGGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           633 TCATTAAACATTGATTCGAATCGAATTGGGGTTGCAGGAGTAAGCGCTGGCGGTGGACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436 GAGCTGAGGATTGACCCGTCAAAATCTTCGTTGGGGGGGACAGTGCGGGACGGAATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   693 TACCCAGCACCAATTGAGGATTGTTATTCAGCTTTAAAATGGATTGCTGATAATGCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376 TTTCCCCCCCCAGTTTATCATTGCTACGATGCGACCAAGTGGGTTGCTGAGAACCGGGAG
                    CCGGGTCTGGTTTACTATCACGGTGGTGGATTTGTGATTTGCAGCATCGAGTCGCACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAAAAGAAGCTAGCTGTGTGGTCGTGTCTGTAGACTACCGCTTAGCACCTGAACACCCT
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ccggcgctgctctacctgcacggtggcggctggatgctcggcggcctcgattcacacgat 576
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Pred. No. 1.7e-11;
2; Mismatches 179;
                                                                      1;
                                                                    Score 70.4; DB 16;
Pred. No. 3.9e-10;
1; Mismatches 337;
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Sequence 2167, Applic
GENERAL INFORMATION:
              APPLICATION NUMBER: 60/ 01
FILING DATE: May 14, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/05:
FILING DATE: July 2, 1997
                                                                        FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 60/ 085598
                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                        SOFTWARE:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1054
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
ATTORNEY/AGENT
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                                                                                                                                                                                                                                                                                            CITY: Waltham
STATE: Massachusetts
                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                               ZIP: 02354
                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                      Lynn A Doucette-Stamm and David Bush
VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
VENTION: ENTEROCOCCUS FAECIUM FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09107532
                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                   GENOME THERAPEUTICS CORPORATION
INFORMATION:
                                60/051571
                                                                                                                                      US/09/107,532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        461
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878 TTACACAAGTACGCTTCCAAGGAATCATCCATGATTTTGTCA 919
                                     824 CGAGCATCGTCAGATACAGAGGCGTGCTTCACGGATTCATCA 865
                                                                                                                                                             758 GAGCAAATATAAATGAACTAAATGATCTTCCTTCAGCAATGATTTTAACGGGAGAAGCGG
                                                                                                                                                                                                                                                                                                                           641 ATTCCTATCATGAATTCGGAGA----AAACTATTTTTGACAAGAGAAGGAATGATGTGGT
                                                                                                                                                                                                                                                                                                                                                                 593 CATCGCTTCTGGAGTTTGGAGAGGGGCTGTGGATTCTCGACCAGAAGATAATGAGTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                           581 GCCTCCCAATATCCAAGCAATTGCTGTATTATCCAGTCACAAACGCTGATTTTGATACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        521 GAGATTCAGTAGGTGGTAACATGGCTACAGTCATGACGATCTTAACAAAAGAACGAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                              533 AAGATTTCATAAAGCATCAAATTCTAACTTACCCCGTTGTGAACTTTGTAGCCCCCACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 46.1 es 296; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 40,489
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                                                                                                                                                                                                                                                                    TCTCGGAGCAGTACTTCTCCAGAGAGGAGGAAGATAAGTTCAAGCCCCTCGCCTCC-----
                                                                                                                                                                                    --GTAATCTTTGCGGACCTTGAGAACCTACCTCCTGCGCTGATAACCGCCGAATACG
                                                                                                                   ACCCGCTGAGAGATGAAGGAGAAGTTTTCGGGCAGATGCTGAGAAGAGCCGGTGTTGAGG
                                                                                                                                                                                                                                           TTTGGGACCAATATACGACGAATGAAGAAGAGCGTGCTGAAATCACAGCTTCGCCTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGACAGTGCGGGACGGAATCTTGCCCCCGGCGCTTTCAATAATGGCGAGAGACAGCGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATTACCAGTTATTTTTATATTCATGGAGCAGGCTGGGTTTTTGGCAGTGCTCAAACCC
                                                                             ATGTATTAAGAGATGAAGGTGAGGCTTATGCGCGCAAACTTCGTGATGCAGGGGTTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATAGTCGATCACCAGAAGCAAAATATCCAACAGCAATTGAACAAATTATGCTGTGTTGC
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46.18;
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Pred. No. 7.7e-09;
2; Mismatches 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 999
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Gaps

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757

705

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697 652 640 592 532

580

472 460 400

340 292

877 823 817

US-09-404-520-17970

GENERAL INFORMATION:

Sequence 17970, Application US/09404520

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; SEQ ID NO 17970
; LENGTH: 703
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-09-404-520-17970
δõ
                                                                                                                                                                                                                         ; NUMBER OF SEQ ID NOS: 28006
; SEQ ID NO 4145
; LENGTH: 810
; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-60-138-103-4145
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Sequence 4145, Application US/60138103
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Best Local Similarity 52.3%;
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Best Local Similarity
Matches 145; Conserv
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cao, Yongwei
APPLICANT: Timberlake, William E.
APPLICANT: Timberlake, William E.
TITLE OF INVENTION: ASSERGILLUS NIDULANS GENOME SEQUENCE AND USES THEREOF
FILE REFERENCE: 38-10(15485)D
CURRENT APPLICATION NUMBER: US/60/138,103
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cao, Yongwei
APPLICANT: Ghodssi, Azita
APPLICANT: Hinkle, Gregory J.
APPLICANT: McIninch, James
APPLICANT: Timberlake, William E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/404,520 CURRENT FILING DATE: 1999-09-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Yu, Jaehyuk
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52.3%;
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Pred. No. 8.2e-09;
0; Mismatches 132;
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Search completed: June 3, 2001, 02:12:50 Job time: 44668 sec

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Result
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

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5 US-09-103-840A-2
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US-09-737-223-21503
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                                                                  Sequence 1, Appli Sequence 2695, Appli Sequence 277, App Sequence 277, App Sequence 219, Appli Sequence 219, Appli Sequence 219, App Sequence 243, App Sequence 243, App Sequence 243, App Sequence 21503, A Sequence 2606, Ap Sequence 3028, Appli Sequence 15206, Ap Sequence 178398, Sequence 178399, Sequence 178400, Sequence 178403, Sequence 178404, Sequence 178407, Sequence 178408, Sequence 178408
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3.4 989 4 3.4 302 5 3.4 7033 5 3.4 15164 6 3.3 15164 6 3.3 9289 1 3.3 37865 1 3.3 388191 5 3.2 14416 1 3.2 14416 1 3.2 14416 1 3.2 14416 5 3.2 14416 5 3.2 14416 5 3.2 14416 5 3.2 14416 5 3.2 14416 5 3.2 14416 5 3.2 14416 5 3.2 14416 5 3.2 14416 5 3.2 14416 5 3.2 14416 5 3.2 14416 5
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US-09-543-679A-1924 US-09-543-679A-1920 US-09-543-679A-1920 US-09-543-679A-2411 US-60-248-505-37 US-09-543-679A-1923 PCT-US01-01351-472 PCT-US01-01351-472 PCT-US01-01351-472 PCT-US01-01351-472 PCT-US01-01351-472 PCT-US01-01351-472 US-09-79-79-3 US-09-70-849B-178401 PCT-US01-01339-8179

ALIGNMENTS

RESULT 1 US-09-103-840A-1/c

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; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION UNDERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
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Best Local Similarity 48.4%;
Matches 331; Conservative
1576250 GCGGCCCGCCCATTGTGTTTCAGCTGTTGTGGTATCCCTCCACTCTGTGGGACCAATCGC 1576191
                                                                                                                         1576310 CCGGAGATTCCGCCGGCGGCACCATCGCCGCGGTGATCGCGCAGCGAGCCCGCGATATGG 1576251
                                                                                                                                                                                                                                                                                      410 CCAAGTGGGTTGCTGAGAACCGGGAGGAGCTGAGGATTGACCCGTCAAAAATCTTCGTTG 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 CCGATTCCCCGGGTCTGGTTTACTATCACGGTGGTGGATTTTGTGATTTGCAGCATCGAGT 289
                                                                                                                                                         470 GGGGGGACAGTGCGGGAATCTTGCCCCGGCGCTTTCAATAATGGCGAGAGACAGCG 529
                                                                                                                                                                                                                                                                                                                                                                                                            350 ATTACAGGCTCCTGAGCACAAGTTTCCCCCCCCAGTTTATCATTGCTACGATGCGA 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 CGCACGACGCCTTATGCAGGAGAAYYGCGAGACTTTCAAACTCTACCGTAGTCTCCCGTGG 349
                                                       530 GAGAAGATTTCATAAAGCATCAAATTCTAACTTACCCCGTTGTGAACTTTGTAGCCCCCA 589
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Pred. No. 1.9e-14;
1; Mismatches 343;
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LENGTH: 4396
; TYPE: DNA
; ORGANISM: Human
US-09-821-736-1
RESULT 3
PCT-US01-04098A-2695/c
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US-09-821-736-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 1576013 ACCCTTTGCGCGACGACGGGATTCGGTACGGCGAGCTGCTGGCCGCCGGCGGTGTTCCCG 1575954
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GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PR
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001216
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: TELLING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 5
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Best Local Similarity 50.6%;
Matches 137; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          704
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                                                                                                                                                                                                                                                                                                        864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 CCGGGTCTGGTTTACTATCACGGTGGTGGATTTGTGATTTTGCAGCATCGAGTCGCACGAC 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 744 cctggcatcgtgtactaccacggtggcggggggcgtcatgggggggtttgaaaaccccaccat 803
                                                                                                       agtttcggagggcaatagccgcagtggttt 1014
                                                                                                                                                  AGTGCGGGACGGAATCTTGCCCCGGCGCTTT
                                                                                                                                                                                                  ttcctgaagtccctggatgcatatggagtggatccagcccgggttgtgggtctgcggtgac
                                                                                                                                                                                                                                   aagttacctaagcataagtttccagtgccagtaagagactgcttggtggccaccatccac 923
                                                                                                                                                                                                                                                                                                                            CTCGCTCCTGAGCACAAGTTTCCCCCCCCAGTTTATCATTGCTACGATGCGACCAAGTGG 417
                                                                                                                                                                                                                                                                                                                                                                                                ggcatatgctctcgtttgtgcaaggagagtgactccgtggttctggcagttggttaccgc 863
                                                                                                                                                                                                                                                                                                                                                                                                                               GCCTTATGCAGGAGAAYYGCGAGACTTTCAAACTCTACCGTAGTCTCCGTGGATTACAGG 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 57.8; DB 5;
Pred. No. 8.3e-08;
1; Mismatches 133;
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; SEQ ID NO 2695
; LENGTH: 1862
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-USO1-04098A-2695
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Best Local Similarity 47.5%;
Matches 201; Conservative
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TITLE OF INVENTION: NOVEL Nucleic Acids and
TITLE REFERENCE: 21272-029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/663,561
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR FILING DATE: 2000-09-01
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PRIOR FILING DATE: 2000-02-03
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PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
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                                                                                                     1022 CAAAATGTGAACACCCCAATCCTGCCCCGCTATGTCATGGTGAAGTATTGGGTGGACTAC
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962 TTC 960
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                                                                                                                                                    TTTGGAGAGGGGCTGTGGATTCTCGACCAGAAGATAATGAGTTGGTTCTCGGAGCAGTAC
                                                                                                                                                                                                                                                                                                            CTGGCTGCTGCCCTTGGACAACAGTTTACTCAAGATGCCAGCCTAAAAAATAAGCTCAAA
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Pred. No. 0.00098;
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RESULT 4 PCT-US01-04098A-727

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GENERAL INFORMATION:

Application

PC/TUS0104098A

TITLE OF INVENTION: NOVel FILE REFERENCE: 21272-029

Novel Nucleic Acids and Polypeptides

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; NAME/KEY: CDS
; LOCATION: (1)..(1698)
PCT-US01-04098A-727
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CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: NOT YET ASSIGNED
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 09/693,325
PRIOR APPLICATION NUMBER: 09/693,325
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-00-05
PRIOR PPLICATION NUMBER: 09/663,561
PRIOR PRIOR DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR APPLICATION NUMBER: 09/654,936
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SEQ ID NO 727
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
mes 201; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/620,325 FILING DATE: 2000-07-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 09/560,875
FILING DATE: 2000-04-27
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                                         TTC 669
                                                                                                                                                                                   CATCAAATTCTAACTTACCCCGTTGTGAACTTTGTAGCCCCCACACCATCGCTTCTGGAG
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ttc 1239
                                                                             caaaaatgtgaacaccccaatcctgccccgctatgtcatggtgaagtattgggtggactac
                                                                                                                  TTTGGAGAGGGGCTGTGGATTCTCGACCAGAAGATAATGAGTTGGTTCTCGGAGCAGTAC
                                                                                                                                                        ctacaagctttaatttatccagttcttcaagctttagattttaacacaccatcttatcag
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Pred. No. 0.001;
Pred. No. 209;
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SOFTWARE: PatentIn Ver.
SEQ ID NO 2
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Best Local Similarity 48.4%;
Matches 331; Conservative
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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TITLE OF INVENTION: DNA SEQUENCES
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                1575971 CGTTCTCCCGTTGGTACGCAGGCGAAATCGACTTGCACAACCCGCCAGCGCCAATGGCGC 1575912
                                                                                                                                                                                                                                                                                                                                                                                     1576028 TGCCGTCGTTGGCCGAGAATGCCGACGCAC---CGATCCTCGACGTCAAGGCAATTGCCG 1575972
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OTHER INFORMATION: "n" bases at
OTHER INFORMATION: represent a,
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824 CGAGCATCGTCAGATACAGAGGCGTGCTTCACGGATTCATCAATTACTATCCCGTGCTGA 883
                                                                                                                                                                                                            704 CCGTAATCTTTGCGGACCTTGAGAACCTACCTCCTGCGCTGATCATAACCGCCGAATACG 763
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                                                                                                                                                                                                                                                                                                                                650 GGTTCTCGGAGCAGTACTTCTCCAGAGAGAAGATAAGTTCAAGCCC-----CTCGCCT 703
                                                                                                                                                                                                                                                                                                                                                                                                                                  590 CACCATCGCTTCTGGAGTTTGGAGAGGGGGCTGTGGATTCTCGACCAGAAGATAATGAGTT 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 CCGATTCCCCGGGTCTGGTTTACTATCACGGTGGTTGGATTTGTGATTTGCAGCATCGAGT 289
                                                                                                                            764 ACCCGCTGAGAGGAGGAGGAAGTTTTCGGGCAGATGCTGAGAAGAGCCGGTGTTGAGG
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                                                                          ACCCTTTGCGCGACGACGGGATTCGGTACGGCGAGCTGCTGGCCGCCGCCGGTGTTCCCG
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Pred. No. 0.24;
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SEQ ID NOS: 13351; SEQ ID NOS: 13351; LENGTH: 542340; TYPE: DNA ORGANITATION ORGANITATION
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SEQ ID NO 6925
LENGTH: 909
TYPE: DNA
                                                                                                                             Query Match 4.0
Best Local Similarity 52.3
Matches 82; Conservative
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Best Local Similarity 52.2%;
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APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
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APPLICANT: Slatter, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
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                                     96517 taaaggctccggatctttcagacctcgcgcctgcttttgtcgttacagcggatgtggacc
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CGCTGAGAGATGAAGGAGAAGTTTTCGGGCAGATGCTGAGAAGAGCCGGTGTTGAGGCGA 826
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PCT-US01-01339-9257
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CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 6965
LENGTH: 1083
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Seguences and Uses Thereof FILE REFERENCE: 38-10(1549))C
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                                                                                                                                                                                                           Matches 112;
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Best Local Similarity
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Best Local Similarity
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SOFTWARE: PatentIn Ver. 2.
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                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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180 GATTAAGGGGAAGGAGACATCAGAGTCAGAGTTTACCAGCAGAAGCCCGATTCCCCC
                                                  537 gcacaagcgcatcggtgtcacaaccgtttatgtgacgcatgatcaggttgaggcgatgac
                                                                                           120 CGAGGAGAAAACCGGCAGCTGAGCCAGCATGAGAGGGTTGAAAGAGTTGAGGACAGGAC 179
                                                                                                                                                            60 GCCGAAGTTCGACCAGTTTTCCTCGGCCCAGAGAGTACAGGGAGGCGATAAATCGAATATA 119
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56.78;
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                                                                                                                                                                                                                          Score 36.4; DB Pred. No. 0.21;
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                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                            DB 5;
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                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-849B-74010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 74010, Applicatio GENERAL INFORMATION:
APPLICANT: Swimmer et al.
TITLE OF INVENTION: Insec
                                                                                                                Query Match 3.6%;
Best Local Similarity 51.0%;
Matches 79; Conservative
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Best Local
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                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/270,849B
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                                                                                                                                                                                                               LENGTH: 684
TYPE: DNA
ORGANISM: Artificial Sequence
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TYPE: DNA
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                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6543 aagggcggtggtgatggagaagaaggaaggagacttaggcaaacgcaagaag 6594
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                                                         144 CCAGCATGAGAGGGTTGAAAGAGTTGAGGGACAGGACGATTAAGGGGAGGAACGGAGACAT 203
                                                                                                                                                                                                                                                                                                                          ID NO 74010
 204 CAGAGTCAGAGTTTACCAGCAGAAGCCCGATTCCCCGGGTCTGGTTTACTATCACGGTGG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            657 cgagcttttcaacaatccggccaatcttttcgttgccggtttcatcggctcgcccggc 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 AGAGAGTACAGGGAGGCGATAAATCGAATATACGAGGAGAAACCGGCAGCTGAGCCAG 147
                                   ccggtagtcaacgattggtagagttgagggcagctcgttttcggggggcggaaacagtcag 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGTCTGGTTTACTATCACGGTGGTGGATTTGTGATTTGCAGCATCGAGTCGCACGAC 297
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Similarity 56.2%;
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RECEPTORS, NUCLEIC ACID MOLECULES ENCODING
PROTEINS, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                     Insect genome survey devices
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                                                                                                              Score 33.4; DB 5;
Pred. No. 1.5;
0; Mismatches 76;
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Pred. No. 9.1;
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RESULT 13
US-09-739-449-2606/c
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; LCCATION: (1)...(473)
; OTHER INFORMATION: n = A,T,C
US-09-737-223-21503
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                                                                                    PRIOR FILING DATE: 2000-02-
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 2606
LENGTH: 954
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Best Local Similarity
Matches 115; Conserv
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CURRENT APPLICATION NUMBER: US/09/737,223
CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 09/332,782
PRIOR APPLICATION NUMBER: 09/332,782
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
                                                                                                                                                                                                                                      APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens
FILE REFERENCE: 38-10(15490)C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                         ORGANISM: Agrobacterium tumefaciens
                                                                    TYPE: DNA
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NAME/KEY: unsure
                         FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 gaggaattgaatgctgtcattgtttccattgaatacaggctagttccaaaggtttatttt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ggctgggccttggcaagtgcaaaaatcaggtattatgatgagctgtgtacagcaatggct 298
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CURRENT APPLICATION UMBER: US/09/737,223
CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 09/332,782
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FRANCSEQ for Windows Version 3.0
SEQ ID NO 9028
LENGTH: 485
TYPE: DNA
                                                                               US-09-820-007-3/c

Sequence 3, Application US/09820007

SERIBAL INFORMATION:

APPLICANT: YAN, Chunhua et al

TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: MUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CL001205
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; OTHER INFORMATION: unsure at all n locations
US-09-739-449-2606
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(485)
OTHER INFORMATION: n = A,T,C or
US-09-737-223-9028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.4%;
Best Local Similarity 52.6%;
Matches 70; Conservative
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Best Local Similarity 55.8
Matches 63; Conservative
SOFTWARE: FastSEQ for Windows Version 4.0
                  CURRENT APPLICATION NUMBER: US/09/820,007
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HYSEG, INC.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 AGAGAGTACAGGGAGGCGATAAATCGAATATACGAGGAGAGAAACCGGCAGCTGAGCCAG 147
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Matches 52; Conservative
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47779 ATGAGCACAAGAAGGCCCTTTCCCC 47755
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Search completed: June 3, 2001, 03:54:06
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ALIGNMENTS

ВP

21-AUG-1997 Archaeoglobus fulgidus strain VC16 pulp; paper; lignin removal; sugar; lignocellulose; disease resistance; feedstuff; ss. Esterase; thermostable enzyme; ester; chiral compound; cheese; /transl_except= /transl_except= /transl_except=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This DNA sequence codes for thermostable esterase VC16-16MC (W23076) of Archaeoglobus fulgidus VC16, an isolate that grows coptimally at 85 deg C and pH 7.0. It can be amplified from a pBluescript vector by PCR (see T79317-18). Claimed, newly identified polynucleotides (T79321-30) encoding esterases C (W23069-77, W23088) were recovered from genomic gene libraries. CC They can be used for recombinant production of the enzymes in host cells, and as probes to identify related sequences. The esterases CC are stable at high temperature and in organic solvents, making them superior for use in production of pure chiral compounds used in pharmaceutical, agricultural and other chemical industries. A method is claimed for transferring an amino group from an amino companied to an alpha-keto acid using a claimed esterase. The enzymes can did to an alpha-keto acid using a claimed esterase. The enzymes can be useful as ilpening starters in cheese making, in lignin removal in paper and pulp manufacture, in carbohydrate derivative synthesis, in fermentable sugar production from lignocellulosic vaste, in the study of plant wall structure, plant resistance to companic matter decomposition and to select plants bred for production of highly degradable animal feeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in cheese paper manufacture, and to study plant resistance to disease
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gctcctgagcacaagtttccccccccagtttatcattgctacgatgcgaccaagtgggtt
                                 GCTCCTGAGCACAAGTTTCCCCCCCCAGTTTATCATTGCTACGATGCGACCAAGTGGGTT
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              Page 50-51;
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Reid J, F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T79333 standard;
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                                                                                                                                                                                                                                                    (RECO-) RECOMBINANT BIOCATALYSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       resistance; feedstuff; ss.
                                                                                                                                                                          Robertson
                                                                                                                                                                       Kosmotka A,
bbertson DE,
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                                                                                                                                                                            Swanson RV,
                                                                                                                                                                                                   Link S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sugar; lignocellulose
                                                                                                                                                                          Maffia AM,
V, Warren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chiral compound;
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                                                                                                                                                                               PV;
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Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in chapaper manufacture, and to study plant resistance to disease

cheese

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Query Match
Best Local S
Matches 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This DNA sequence codes for esterase 23mc1 (W23080) of Metallosphae prunae. Newly identified polynucleotides (T79321-40) encoding esterases (W23069-88), some of which are claimed, can be used for recombinant production of the enzymes in host cells, and as probes to identify related sequences. The esterases are stable at high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 905
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                                                                             gtgatcactgcagagtatgatcccctaagggatcagggagagacctactctcactcccta
                                                                                                                             ATCATAACCGCCGAATACGACCCGCTGAGAGATGAAGGAGAAGTTTTCGGGCAGATGCTG
                                                                                                                                                                                  gcggtatccccctacgcctctccagccttggctgacctacataacctcccaccctcactg
                                                                                                                                                                                                                                  ttcctcaccaggtccatgatgaactggttcgggaccatgtacttctcctctggaagggaa
                                                                                                                                                                                                                                                                                                                                          ATTCTCGACCAGAAGATAATGAGTTGGTTCTCGGAGCAGTACTTCTCCAGAGAGGAAGAT
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Pred. No. 1.8e-61;
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241 GGTCTGGTTTACTATCACGGTGGTGGATTTGTGATTTGCAGCATCGAGTCGCACGACGCC 300

Matches 369; Query Match Best Local

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14.6%;

Score 137; DB 18; Pred. No. 5.1e-35;

Length 918; Indels

Sequence 918 BP;

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                                                                                              and in organic solvents, making them superior for use in production of pure chiral compounds used in pharmaceutical, agricultural and other chemical industries. A method is claimed for transferring an amino group from an amino acid to an alpha-keto acid using a claimed esterase. The enzymes may also be useful as ripening starters in cheese making, in lignin removal in paper and pulp manufacture, in carbohydrate derivative synthesis, in fermentable
                                                                                                                                                                                                                  This DNA sequence codes for thermostable esterase P1-8LC (W23077) of Sulfolobus solfataricus P1, which grows optimally at 85 deg C and pH 2.0. It can be amplified from a pBluescript vector by PCR (see T79319-20). Claimed, newly identified polynucleotides (T79321-30) encoding esterases (W23069-77, W23089) were recovered from genomic gene libraries. They can be used for recombinant production of the enzymes in host cells, and as probes to identify related sequences. The esterases are stable at high temperature and is considered to the production.
                                            sugar production from lignocellulosic waste, in the study of plant wall structure, plant resistance to disease and organic matter decomposition and to select plants bred for production of highly
                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in che paper manufacture, and to study plant resistance to disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T79330;
                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 52-53; 113pp; English.
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                                   degradable animal feeds.
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resistance; feedstuff;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robertson DE, Swanson RV,
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f; ss.
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V, Warren |
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                                                                                                 CDS
                                                                                                                                                    Esterase; structural gene;
           16-SEP-1997;
                                 23-MAR-1999.
                                                     JP11075860-A.
                                                                                                                                Acetobacter pasteurianus
                                                                                                                                                                          DNA enncoding an esterase protein.
                                                                                                                                                                                                 06-JUL-1999
                                                                                                                                                                                                                      x35306;
                                                                                                                                                                                                                                           X35306 standard; DNA; 954
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                                                                                                                                                                                                                                                                                                                                                                                                GAAGGAGAAGTTTTCGGGCAGATGCTGAGAAGAGCCGGTGTTGAGGCGAGCATCGTCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGTACTTCTCCAGAGGGAAGATAAGTTCAAGCCCCTCGCCTCCGTAATCTTTGCGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTCCTGAGCACAAGTTTCCCCCCCCAGTTTATCATTGCTACGATGCGACCAAGTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGATAAACCAGATTGCCGCTCT 920
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                                                                                                                                                                                                                                                                                                                                                                                   caaggagaagcgtatgcaaataaactactacaagctggagtctcagttactagtgtgaga
                                                                                                                                                                                                                                                                                                                                                                                                                                gatttcaacggattacctccagccttgataataacagcagaatacgatccactaagggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          caatacttacgaagccctgcagatttgctagactttaggttctctccaattctggcgcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ttgaagtatcaaatactggtttacccagcggtaagtttagataacgtttcaagatccatg
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          97JP-0268259
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                                                                           /product=
                                                                                                           Location/Qualifiers
                                                                                      rtag-
                                                                          "esterase"
                                                                                                                                                                                                                                           ΒP
                                                                                                                                                    aromatic vinegar; high grade sake flavour;
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Best Local S
Matches 167
                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents an esterase structural gene of Acetobacter pasteurianus. The esterase is used for preparation of an aromatic vinegar of high grade sake flavour from cheap
                                                                                                                                         Esterase; hydrolysis; 1,4-diacetoxy-cis-2,3-epoxybutane; (2S,3R)-4-acetoxy-2,3-epoxybutan-1-ol; pheromone; ds.
                                                                                                                                                                           Bacterial esterase genomic
                                                                                                                                                                                                  14-JUN-1999
                                                                                                                                                                                                                                           X23339 standard; DNA; 1973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 954 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2;
                    23-MAR-1999
                                          JP11075850-A
                                                                                                                       Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-257707/22
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                                                                                                                                                                                                                                                                                                                                                                                                    405 TGCGACCAAGTGGGTTGCTGAGAACCGGGAGGAGCTGAGGATTGACCCGTCAAAAATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                               345 CGTGGATTACAGGCTCCCTGAGCACAAGTTTCCCCCCCCAGTTTATCATTGCTACGA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                 348 agttgattatcgtctggcgccagaggtcaaataccccggcgcgattgaagactgctatgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288 agaagtggatgaccctaaatgccaaaagctggccagtgatctaggatttcagatttttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            285 CGAGTCGCACGACGCCTTATGCAGGAGAAYYGCGAGACTTTCAAACTCTACCGTAGTCTC
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Local Similarity 53.5%;
nes 167; Conservative
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                                                                                                                                                                                                                                                                                                 CAGCGGAGAAGA 536
                                                                                                                                                                                                                                                                                                                                           tgtggcgggtgaaagtgcgggtggtggtttaagtgccgcactgagcctgatggcgcggaa
                                                                                                                                                                                                                                                                                                                                                                                        cgtgctgaaatgggtgcatgaaaacgccagtaagcttggtatttcgcgcgataaggttgt
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                                                                                                                                                                                               (first entry)
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                                                                                    Location/Qualifiers 104..1263
                                                              /product=
                                                                           /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 C;
                                                                                                                                                                            DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 81.2; DB 20;
Pred. No. 1.4e-16;
1; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for preparation of vinegar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 G;
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                                                                                                                                                       insect;
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04-SEP-1997;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of 1,4-diacetoxy-cis-2,3-epoxybutane to (2S,3R)-4-acetoxy-2,3-epoxybutan-1-0.1, and has no lipase activity using p-nitropalmitic acid as the substrate and no esterase activity using Tween 20 as the substrate. The new enzyme can be used for the synthesis of an insect pheromone of high biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NITL )
Whale mat sample 11.801
                         pulp; paper; lignin
disease resistance;
                                     Esterase; thermostable enzyme; ester; chiral compound; pulp; paper; lignin removal; sugar; lignocellulose;
                                                                             DNA encoding
                                                                                                          16-FEB-1998
                                                                                                                                   T79336;
                                                                                                                                                              T79336 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1973 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 11-13; 16pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New esterase used to prepare insect pheromone of 1,4-d1:acetoxy-cis-2,3-epoxybutane to (2S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-257698/22
P-PSDB; W93498.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                         ရှ
                                                                                                                                                                                                                                                                                               CTAACTTACCCCGTTGTGAACTTTGTAGCCCCCACACCATCGCTTCTGGAGTTTTGGAGAG 615
                                                                                                                                                                                                                                                                                                                                   acagcagcattatcattattagcccgagatcgaaaatatccttcgatttgtttacaaatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 catggtggtggttatatcttagggtctatagatgataacgatgatacttgtatgaggttt 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention describes a novel esterase which catalyses
                                                                                                                                                                                                                                                                                 ccactctatccaatgattgatgatcgaaataatacaccttcagccaatgaaattaaagag
                                                                                                                                                                                                                                                                                                                                                                                       tcattaaacattgattcgaatcgaattggggttgcaggagtaagcgctggaggtggacta
                                                                                                                                                                                                                                                                                                                                                                                                                     GAGCTGAGGATTGACCCGTCAAAAATCTTCGTTGGGGGGGACAGTGCGGGACGGAATCTT 495
                                                                                                                                                                                                                                                                                                                                                               GCCCCGGCGCTTTCAATAATGGCGAGAGACAGCGGAGAAGATTTCATAAAGCATCAAATT 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTCCCCCCCCAGTTTATCATTGCTACGATGCGACCAAGTGGGTTGCTGAGAACCGGGAG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gcaaaagaagctggctgtgtggtcgtatctgtagactaccgcttagctcctgaacatcct 669
                                                                                                                                                                                                                                                                                                                                                                                                                                              tacccagcaccaattgaagattgttattcagctttaaaaatggattgctgataatgcagag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184;
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                                                                                                                                                                                                                                911
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                                                                              whale mat sample 11.801 esterase es2
                                                                                                       (first entry)
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                                                                                                                                                              DNA;
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                          feedstuff; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 79.6; DB 20;
Pred. No. 7.3e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 G; 634 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catalyses hydrolysis
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                                                   cheese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the hydrolysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in production of pure chiral compounds used in pharmaceutical, agricultural and other chemical industries. A method is claimed for transferring an amino group from an amino acid to an alpha-keto acid using a claimed esterase. The enzymes may also be useful as ripening starters in cheese making, in lignin removal in paper and pulp manufacture, in carbohydrate derivative synthesis, in fermentable sugar production from lignocellulosic waste, in the study of plant wall structure, plant resistance to disease and organic matter decomposition and to select plants bred for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This DNA sequence codes for whale mat sample 11.801 esterase es2 (W23083). Newly identified polynucleotides (779321-40) encoding esterases (W23069-88), some of which are claimed, can be used for recombinant production of the enzymes in host cells, and as probes to identify related sequences. The esterases are stable at high temperature and in organic solvents, making them superior for use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in cheese paper manufacture, and to study plant resistance to disease
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TTCATAAAGCATCAAATTCTAACTTACCCCGTTGTGAACTTTGTAGCCCCCACACCATCG
                             agcgcagggggcaatcttgccgccgttgtctgccaacaaaccgccatgaacggcgagcgc
                                                                                                gtgcgcccaacgcaacaaccttggcggcgatcctgaacgtatcggcgttggcggcgat
                                                                                                                    GTTGCTGAGAACCGGGAGGAGCTGAGGATTGACCCGTCAAAAATCTTCGTTGGGGGGGAC
                                                                                                                                                                 ctagcgcccgaacacaaatttccttgtgcgccgcttgatgcgattgcggcctataaatgg
                                                                                                                                                                                                                                   ggggtttgcggcaagctggcaaaatgggcgaactgcattgttatctcggtcgattatcgt
                                                                                                                                                                                                                                                                    GCCTTATGCAGGAGAAYYGCGAGACTTTCAAACTCTACCGTAGTCTCCGTGGATTACAGG 357
                                                                                                                                                                                                                                                                                                    ccaatwctagtgtattttcacggcggtggctgggttcagggcaatctggacagccatgac 387
                                                                 AGTGCGGGACGGAATCTTGCCCCGGCGCTTTCAATAATGGCGAGAGACAGCGGAGAAGAT
                                                                                                                                                                                                   CTCGCTCCTGAGCACAAGTTTCCCCCCCCCAGTTTATCATTGCTACGATGCGACCAAGTGG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                           914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of highly degradable animal feeds
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                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        Score 71; DB 18;
Pred. No. 3.3e-13;
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CC expression of genes in a first filamentous fungal (FF) cell relative to ceapression of the same genes in one or more second filamentous fungal (CC cells: The method uses fluorescence-labeled nucleic acids isolated from CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs CC are used in the methods for monitoring differential expression of genes CC in a first filamentous fungal (FF) cell relative to expression of the Same genes in one or more second filamentous fungal cells. Monitoring CC the global expression of genes from FF cells allows the production CC potential of the microorganisms to be improved. New genes may be CC discovered, possible functions of unknown open reading frames can be CC identified and gene copy number variation and stability can be CC identified and gene copy number variation and stability can be CC monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore CC morphogenesis, recombination, metabolic or catabolic pathway engineering. CC clones including elimination of redundancy as one spot on an array CC clones including elimination of the gene products to facilitate analysis of the results. F074/B to F11873 represents ESTs from According From Fusarium CC constitute. F11873 represents ESTs from According From Fusarium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                         venenatum; F11248 to F11853 represents ESTs from Aspergillus niger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 86; Page 747; 3161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          substrate of expressed sequence tags -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-594572/56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention describes a method for monitoring differential ression of genes in a first filamentous fungal (FF) cell relative to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acaccagatctgcaagtcctgatctatccggcgctggatgcacgcatgatctcgacctcg
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                             to F14878 represents ESTs from Aspergillo represents ESTs from Trichoderma reesel, ically claimed in the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene expression; filamentous fungal cell; EST;
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NORDISK AS.
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                                                                         ESTs from Aspergillus oryzae;
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Sequence 606

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138 T; 9 other;

expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses filuorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the

Claim

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expressed

sequence tags

88; Page 1952-1953; 3161pp; English.

present invention

describes

describes a method for monitoring differential a first filamentous fungal (FF) cell relative to

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Best Local Similarity
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                                                                                                               Monitoring differential expression of genes uses fluorescence-labeled nucleic acids isol
                                                                                                                                                                                                                                                                                                          Aspergillus oryzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         F12065 standard;
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                                                                                                                                                                                                                                                                  28-SEP-2000.
                                                                                                                                                                                                                                                                                                                              metabolic pathway engineering; catabolic pathway engineering;
                                                                                                                                                                                                                                                                                                                                                                                          Aspergillus oryzae EST SEQ ID NO:4588.
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                                                                                                                                                                    Rey MW,
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                                                                                                                                                                    Shuster JR,
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Pred. No. 3
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Best Local
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                           Claim 4; Page 6-8; 8pp; Japanese
                                                       New esterase for hydolyzing oleyl bezoate and and for preparing optically active substances intermediate materials for drugs -
                                                                                                                          P-PSDB;
                                                                                                                                                                                                      02-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                Acinetobacter calcoaceticus
                                                                                                                                                                                                                                                                                                                                                                              Esterase;
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                                                                                                                                                                       (NAGS ) NAGASE SANGYO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCGCTCCTGAGCACAAGTTTCCCCCCCCAGTTTATCATTGCTACGATGC 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccggtgatgctgtatttccacggnggtggatgggtcctggggaatataaacacggagaat 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ccggtttgcacaaatttgtgcgtgagagggaactgcgtcgtagtcacagttgattacagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94;
                                                                                                                           в35739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        638
                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                            oleyl benzoate; p-nitrophenyl
                                                                                                                                                                                                                                                                                                                                                              active drug intermediate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                             sequence
                                                                                                                                                                                                                                    99JP-0053823
                                                                                                                                                                                                      99JP-0053823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 A; 186 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.4%;
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Pred. No. 2e-06;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                              benzoate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75;
                                                                          p-nitrophenol necessary for
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                                                                          the
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Polynucleotide C66279 encodes an

esterase protein B35739. The esterase

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RESULT 10
F11486
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Best Local 9
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                                    Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hydrolyses oleyl benzoate and p-nitrophenyl benzoate. The invention includes a vector containing the esterase gene, and a method for preparing the esterase protein. The esterase is useful for the preparation of optically active substances necessary for the intermediate materials for drugs.
            Claim
                                                                                                                                                                                                                                                                                                                                          expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F11486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1189 BP;
                                                                                            WPI; 2000-594572/56
                                                                                                                                                                                           22-MAR-1999;
                                                                                                                                                                                                                                                                          WO200056762-A2
                                                                                                                                                                                                                                                                                                    Aspergillus niger
                                                                                                                                                                                                                                                                                                                             metabolic pathway
                                                                                                                                                                                                                                                                                                                                                                                   Multiple gene expression; filamentous fungal cell; EST;
                                                                                                                                                                                                                                                                                                                                                                                                              Aspergillus niger EST SEQ ID NO:4009
                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F11486 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   554 cttgggtatatcaaaatcgtagacaattaaaaatattaaaaggtcgaattgcggtagcgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aattacctcttcttgttttctaccatgggggggggtttgttgtaggtggtttagatactc 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTCCCCGGGTCTGGTTTACTATCACGGTGGTGGATTTGTGATTTGCAGCATCGAGTCGC 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTGGGTTGCTGAGAACCGGGAGGAGCTGAGGATTGACCCCGTCAAAAATCTTCGTTGGGG
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                                                                                                                       RM,
         87; Page 1773; 3161pp; English
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                                                                                                                    Rey MW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                         99US-0273623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA;
                                                                                                                                                                                                                                                                                                                               engineering; catabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391 A;
                                                                                                                     Shuster JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.18;
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Pred. No. 2.4e:
1; Mismatches
                                                                                                                                                                INC.
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                                                                                                                     Kauppinen
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                                                                                                                                                                                                                                                                                                                               pathway engineering;
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                                                                                                                       Clausen
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                                                                                                                     IG,
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                                                                                                                       Olsen
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                                                                                                                       PB;
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RESULT 11.
C32687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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    25-FEB-1999;
05-MAR-1999;
                                                             25-FEB-2000; 2000EP-0301439.
                                                                                                    06-SEP-2000
                                                                                                                                           EP1033405-A2
                                                                                                                                                                             Arabidopsis thaliana.
                                                                                                                                                                                                                        metabolic
                                                                                                                                                                                                                                           Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;
                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana DNA fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                         17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                               C32687;
                                                                                                                                                                                                                                                                                                                                                                                                                        C32687 standard;
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hes 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATCAATTACTATCCCGTGCTGAAG 885
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                                                                                                                                                                                                                      pathway; promoter; termination sequence;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 149 A; 132 C; 174 G; 130 T; 2
    99US-0121825.
99US-0123180.
                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
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Pred. No. 0.0001
0; Mismatches 1
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    03-JUN 1999
04-JUN 1999
07-JUN 1999
10-JUN 1999
110-JUN 1
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23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
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21-MAY-1999
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14-MAY-1999
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19-APR-1999,
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990S-0139460.
990S-0139462.
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990S-0139763.
990S-0139763.
990S-0140553.
990S-0140823.
990S-0140823.
990S-0141847.
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990S-0135124

990S-0135353

990S-0135629

990S-0136021

990S-0136021

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990S-0136782

990S-0137528

990S-0137528
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99US-0130891.
99US-0131449.
99US-0132048.
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99US-0132487
99US-0132863
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99US-0128714.
99US-0129845.
99US-0130077.
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99US-0132485
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990S-0125788
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15-JUL-1999; 16-JUL-1999; 16-JUL-1999; 19-JUL-1999; 19-JUL-1999;

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Best Local Similarity
Matches 116; Conserv
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25-OCT-1999;
25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
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29-OCT-1999;
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13-OCT-1999;
13-OCT-1999;
                                                     Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                17-OCT-2000
                                                                                                                                                      C37749 standard; DNA; 1190 BP
 06-SEP-2000
                   EP1033405-A2
                                      Arabidopsis thaliana
                                                                                             Arabidopsis thaliana DNA fragment SEQ
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21-OCT-1999
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14-OCT-1999;
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                                                                                                                                                                                                                                                                                                                               293 ACGACGCCTTATGCAGGAGAAYYGCGAGACTTTCAAACTCTACCGTAGTCTCCGTGGATT
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                                                                                                                                                                                                              TCGTTGGGGGGGACAGTGCGGGACGGAATCTTGCCC
                                                                                                                                                                                              ACAGGCTCGCTGAGCACAAGTTTCCCCCCCCAGTTTATCATTGCTACGATGCGACCA
                                                                                                                                                                                                                                         agtacatcgaggagaatcacggttcgattcttccggcgaacgctgatctctcgagatgct
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Pred. No. 0.00017
                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                             ID NO: 18530
                                                                                                                                                                                                                       499
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Best Local Similarity
Matches 116; Conserv
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28-SEP-1999
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          Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                  18-OCT-2000
                                                                                     C50447;
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                                                                                                     standard; DNA; 1210 BP
                                               thaliana
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990S-0156458
990S-0156596
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                                               DNA
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Pred. No. 0.00018;
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equence; ss.
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09-MAR 1999
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11-MAY 1999
11-JUN 1999
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Best Local Similarity 53.7%;
Matches 116; Conservative
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               17-OCT-2000 (first entry)
                                   C39057;
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Arabidopsis thaliana DNA fragment SEQ ID NO: 23208.
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                                                   standard; DNA; 1809
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Pred. No. 0.00018;
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			mapping; gene expression al transduction pathway; termination sequence; ss
			on control; ss.
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                                                                                                                                                       tataggcttgcgcctgagaataggtaccctgcggcgtttgaggatggagtcaaagtgctt
                    standard; DNA; 1366
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nilarity 55.3%;
Conservative
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99US-0152363
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Pred. No. 0.00041;
2; Mismatches 77;
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12-SEP-1999

22-SEP-1999

24-SEP-1999

24-SEP-1999

24-SEP-1999

24-SEP-1999

25-OCT-1999

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21-OCT-1999

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                                   513
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Local Similarity 53.3%;
nes 113; Conservative
        CATTGCTACGATGCGACCAAGTGGGTTGCTGA 425
                                gacgccgtcgaagctatcttatggctccgtga
                                                                  CAGCAGAAGCCCGATTCCCCCGGGTCTGGTTTACTATCACGGTGGTGGATTTTGTGATTTTGC
                                                                           AGCATCGAGT-----CGCACGACGCCTTATGCAGGAGAAYYGCGAGACTTTCAAACTCT
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                                                                                                                                        Score 42.4; DB 21;
Pred. No. 0.0012;
1; Mismatches 92;
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18-JUN 1999
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Search completed: June 2, 2001, 22:23:42 Job time: 30920 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-08-602-359A-32
US-08-232-463-14
US-09-073-354-5
US-09-073-259-5
US-09-073-259-6
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US-09-363-095-6
US-09-363-095-6
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US-08-491-988-15	US-08-702-572-15	US-09-075-904-1	US-08-247-901C-1	US-09-080-538-2	US-08-723-938-2	US-08-715-527-2	US-08-395-246C-1	PCT-US95-06406A-21	US-08-343-380-3	US-07-973-324A-3	US-08-459-065-1	US-08-459-146-1	US-08-993-380-3	PCT-US94-07926-33	US-08-888-497-33	US-09-517-584A-3	US-08-801-092-2
Sequence 15, Appl	Sequence 15, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 21, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 33, Appl	Sequence 33, Appl	Sequence 3, Appli	Sequence 2, Appli

ALIGNMENTS

1
TOPOLOGY: LINEAR
2
LENGTH: 936 NUCLEOTIDES
8-5099
TELECOMMINICATION INFORMATION:
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ATTORNEY /AGENT INFORMATION:
PRIOR APPLICATION DATA:
CLASSIFICATION: 435
FILING DATE: February 16, 1996
APPITCATION NUMBER: US/OB/602.359A
SOFTWARE: WORD PERFECT 6.0
SYSTEM: MS-DO
`
TYPE: 3
COMPUTER READABLE FORM:
TID: USA
STATE: CALIFORNIA
5
7.
ADDRESSEE: FISH & RICHARDSON P.C.
CORPECDONDENCE ADDRESS.
NIMBER OF SECTION: ESTERASES
CANT: KOSMOTKA,
WARREN, Patrick
SWANS
LINK, St
APPLICANT: MAFFIA, Anthony
MURPHY
GENERAL INFORMATION:
Patent No. 5942430
Sequence 31, Application US/08602359A
IS-08-602-359A-31

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                                    GCGGGACGGAATCTTGCCCCGGCGCTTTCAATAATGGCGAGAGACAGCGGAGAAGATTTC
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ATAAACCAGATTGCCGCTCTTCTTGTGTTCGACTAG
                                                                           CAGTACTTCTCCAGAGAGGAAGATAAGTTCAAGCCCCTCGCCTCCGTAATCTTTGCGGAC
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                  ATAAACCAGATTGCCGCTCTTCTTGTGTTCGACTAG 936
                                                                                               GGAGAAGTTTTCGGGCAGATGCTGAGAAGAGCCGGTGTTGAGGCGAGCATCGTCAGATAC
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RESULT 2 US-08-602-359A-32

Sequence 32,

Application US/08602359A

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; STRANDENNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: GENOMIC DNA
US-08-602-359A-32
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFLEXANCE INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKET MEDIUM TYPE: 3.5 INCH DISKET COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS SOFTWARE: WORD PERFECT 6.0

SOFTWARE: WORD PERFECT 6.0

CURRENT APPLICATION NUMBER: US/08/60

FILING DATE: FEBRUARY 16, 19

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KOSMOTKA, Anna
TITLE OF INVENTION: ESTEASES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P
STREET: 4225 EXECUTIVE SQUARE,
CITY: LA JOLLA
STATE: CALIFORNIA
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APPLICANT:
APPLICANT:
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APPLICANT: MURPHY, Dennis
APPLICANT: REID, John
APPLICANT: MAFFIA, Anthony
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 541 ATAAAGCATCAAATTCTAACTTACCCCGTTGTGAACTTTGTAGCCCCCACACCATCGCTT
                                                                                                                                               217 GTTCTAGTGTATCTTCATGGAGGCGGTTTTGTAATAGGCGATGTGGAATCTTATGACCCA 276
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                                                                       GCGGGACGGAATCTTGCCCCGGCGCTTTCAATAATGGCGAGAGACAGCGGAGAAGATTTC
                                    GCTGGAGGAAATTTGGCAGCGGTTGTAGCTCTTCTTTC-----AAAGGGTAAAATTAAT
                                                                                                              TATAACAATTTAGATAAATT---TGATGGAAAGATGGGAGTTGCGATTGCGGGAGATAGT
                                                                                                                                                                                       GCTCCAGAATACAAGTTTCCTTCTGCAGTTATCGATTCATTTGACGCTACTAATTGGGTT
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SWANSON, Ronald V.
WARREN, Patrick V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 137; DB 2; Pred. No. 8.1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 297;
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APPLICANT: DORNER
APPLICANT: SCHEIF
                                                                                 INFORMATION FOR SEQ ID NO:
                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                    REFERENCE/DOCKET NUMBER: 30.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                    FILING DATE:

APPLICATION NUMBER: EP 91

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                                                                     NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
         LENGTH: 7218 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                    (703)683-4109
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US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5,
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                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                            APPLICATION NUMBER: 08/65
FILING DATE: 24 MAY 1996
APPLICATION NUMBER: JP 13:
FILING DATE: 31 MAY 1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith 1
                                                                                                                                                                                                                                                                         MEDIUM TYPE: 3.5" Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 6.1 Windows CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" F1
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                                             REFERENCE/DOCKET NUMBER: 24:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
                                                                                                                                                                                                            CLASSIFICATION: 0506 PRIOR APPLICATION DATA:
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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Local Similarity 12.3%;
hes 23; Conservative
                                TELEFAX:
                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: Concur
                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington STATE: D.C.
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                                                                                              NAME: Toffenetti, Judith L. REGISTRATION NUMBER: 39,048
                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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1025 Connecticut Avenue, N.W., Suite 600
                                202-429-0796
                                                                                                                                                                                                                                                                                                                                                                                           USA
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TAKAGI, Masahiro
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                                                                                    39,048
BER: 241
                                                                                                                                                             JP 134096/95
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                                                                               2418/9
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Pred. No. 5.8e-05;
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RESULT 5
US-08-656-005A-5
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Best Local Similarity
Matches 101; Conserv
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                 NFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                           ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Floppy disk
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ORIGINAL SOURCE: Hyperthermophilic archaeon
                                                              REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 24:
TELECOMMUNICATION INFORMATION:
 SEQUENCE
                                                                                                                             APPLICATION NUMBER: JP 134096/95 FILING DATE: 31 MAY 1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: A Method of Amplifying Nucleic TITLE OF INVENTION: Acid and A Reagent Therefor
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                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 5.1
                                 TELEFAX:
                                              TELEPHONE:
                                                                                                 NAME: Toffenetti, Judith L. REGISTRATION NUMBER: 39,048
                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 24 MA
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1025 Connecticut Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                      USA
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TAKAGI, Masahiro
                               202-429-0796
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IMANAKA, Tadayuki
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24 MAY 1996
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                                                                                 2418/3
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Best Local Similarity
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                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                               CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" F]
COMPUTER: IBM PC con
                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                              TELEPHONE: 202-429-0796
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                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
STRANDEDNESS:
                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                             LENGTH:
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                 nucleic
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                             5342 base pairs
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46.8%;
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Sequence 5, Application US/09073259 Patent No. 6143536
                                                                                  APPLICATION NUMBER: 08/656,005
FILING DATE: 24 MAY 1996
APPLICATION NUMBER: JP 134096/95
FILING DATE: 31 MAY 1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WordPerfect 6.1 Windows CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/073,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: IMANAKA, Tadayuki
APPLICANT: TAKAGI, Masahiro
APPLICANT: MORIKAWA, Masaaki
TITLE OF INVENTION: DNA Enco
NUMBER OF SEQUENCES: 16
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        476 TGACATCTACGAGTACGACATACCCTTCGCCAAGCG 511
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                                                         NAME: Toffenetti, Judith L
REGISTRATION NUMBER: 39,041
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1025 Connecticut Avenue,
                                                                                                                                                                                                                                                                                                    Concurrent Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Encoding A Thermostable DNA Polymerase
16
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                      39,048
ER: 24:
                                   2418/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33.2;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
).77;
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; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE: Hyperthermophilic archaeon
US-09-073-259-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
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Best Local Similarity 46.8%;
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
TELEFAX: 212-4:
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tent No.
                                  REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-425-7200
                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1
FILING DATE: 29-JUL-1996
                                                                                                                                APPLICATION NUMBER: JP 200446/96
APPLICATION NUMBER: 30-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect 6.1 Windows CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.50 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: IMANAKA, Tadayuki
TITLE OF INVENTION: Modified Thermostable DNA Polymerase,
TITLE OF INVENTION: and DNA Polymerase Composition for Nucleic Acid
TITLE OF INVENTION: Amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        416 TACTCATCCGCAGGACGTCCCAGCGATAAGGGACAAGATACGAGAGCATGGAGCAGTTAT 475
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                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfert 6
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                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/902,632 FILING DATE: Concurrent Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                                                                                                                                                                                                                     10004
                                                                                                             GREASON, Edward W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Broadway
                  212-425-5288
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KAWAMURA, Yoshihisa
TAKAGI, Masahiro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAMIMURA, Hideki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KOMATSUBARA, Hideyuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kenyon & Kenyon
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                                                                                         18,918
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                                                                             2418/7
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; MOLECULE TYPE: genomic DNA US-08-902-632-3
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Best Local Similarity
Matches 101; Conserv
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PRIOR APPLICATION DATA: 08/656,005
APPLICATION NUMBER: 08/656,005
FILING DATE: 24 MAY 1996
APPLICATION NUMBER: JP 134096/95
FILING DATE: 31 MAY 1995
FILING DATE: 31 MAY 1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 2418/9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

COPETUANES: WORLD-FOST 6 1 41456
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                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MORIKAWA, Masaaki
TITLE OF INVENTION: A Thermostable DNA Polymerase and Kits for
TITLE OF INVENTION: Amplifying Nucleic Acids
NUMBER OF SEQUENCES: 16
TELECOMMUNICATION INFORMATION: TELEPHONE: 202-429-1776
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                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
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TAKAGI, Masahiro
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IMANAKA, Tadayuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARAKAWA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KITABAYASHI, Masao
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46.8%;
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Pred. No. 1.
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1.2;
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Best Local :
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE: Hyperthermophilic archaeon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
REFERENCE/DOCKET NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 241
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                  SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Floppy disk
                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MORIKAWA, Massaki
TITLE OF INVENTION: A Method of Amplifying Nucleic
TITLE OF INVENTION: Acid and A Reagent Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                              STREET: 1011
                                                                                                                                                                                              APPLICATION NUMBER: US/08/656,005A FILING DATE: 24 MAY 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 3.4%; Local Similarity 46.8%; nes 101; Conservative
                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 CAGGGAGGCGATAAATCGAATATACGAGGAGAGAAACCGGCAGCTGAGCCAGCATGAGAG 155
                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                     Toffenetti, Judith L.
                                                                                                                                                                                                                                                                                                                                                                                                            1025 Connecticut Avenue, N.W., Suite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMANAKA, Tadayuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAWAKAMI, Bunsei
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                                                                                                                          UMBER: JP 134096/95
31 MAY 1995
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US-09-073-259-6
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INFORMATION FOR SEQ ID NO:
                  INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Floppy disk
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1 Windows
CURRENT APPLICATION DATA:
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LENGTH: 5339 base pairs
TYPE: nucleic acid
                                                                                                                                        APPLICATION NUMBER: 08/65
FILING DATE: 24 MAY 1996
APPLICATION NUMBER: JP 1:
FILING DATE: 31 MAY 1995
ATTORNEY/AGENT INFORMATION.
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ORIGINAL SOURCE:
                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DNA Encoding A Thermostable DNA Polymerase NUMBER OF SEQUENCES: 16
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                        NAME: Toffenetti, Judith L. REGISTRATION NUMBER: 39,048 REFERENCE/DOCKET NUMBER: 241
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CITY: Washington
STATE: D.C.
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                                  TELEFAX:
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                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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1025 Connecticut Avenue,
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Imanaka, Tauni
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                                   202-429-0796
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                  ID NO:
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STRANDEDNESS: LENGTH:

double

nucleic acid

5339 base pairs

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; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE: Hyperthermophilic archaeon
US-09-073-259-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/363,095
CURRENT FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: US 09/073,259
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: US 08/656,005
EARLIER FILING DATE: 1996-05-24
EARLIER APPLICATION NUMBER: JP 134096/95
EARLIER FILING DATE: 1995-05-31
                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 101; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WordPerfect 6.1 Windows
SEQ ID NO 6
LENGTH: 5339
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Best Local Similarity
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APPLICANT: TAKAGI, Masahiro
APPLICANT: MORIKAWA, Masahiro
TITLE OF INVENTION: DNA Encoding A Thermostable DNA Polymerase
FILE REFERENCE: 2418/11
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                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Hyperthermophilic archaeon
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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216 TTACCAGCAGAAGCCCGATTCCCCGGGTCTGGTTTACTATCACGGTGGTGGATTTGTGAT 275
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                                                                ggttgaaaaggttcagaagaagttcctcgggagaccagttgaggtctggaaactctactt 415
                                                                                                           GGTTGAAAGAGTTGAGGACAGGACGATTAAGGGGAGGAACGGAGACATCAGAGTCAGAGT 215
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Sequence 1, NPF--
Sequence 1, NPF--
                                                                                                           Matches 101;
                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: IMANAKA, 7
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: 3.50 in
                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 212-425-7200
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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 156 GGTTGAAAGAGTTGAGGACAGGACGATTAAGGGGAGGAACGGAGACATCAGAGTCAGAGT 215
                                     296 CATTGAGGAAGTCAAGAAGATAACCGCCGAGAGGCACGGGACGGTTGTAACGGTTAAGCG 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276 TTGCAGCATCGAGTCGCACGACGCCTTATGCAGGAG 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 1
FILING DATE: 29-JUL-1996
                                                                      96 CAGGGAGGCGATAAATCGAATATACGAGGAGAGAAACCGGCAGCTGAGCCAGCATGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1 Broad CITY: New York STATE: NY
                                                                                                                                                                                                                   STRAIN:
                                                                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 18
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: JP 200446/96 APPLICATION NUMBER: 30-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: GREASON, Edward W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                         nucleic acid
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                                                                                                                                                                                                                     KOD1
                                                                                                                                                                                                                                                                                                                                          5342 base pairs
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                                                                                                       3.4%;
ilarity 46.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KITABAYASHI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAWAKAMI, Bunsei
                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAMIMURA, Hideki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KOMATSUBARA, Hideyuki
                                                                                                                                                                                                                                    hyperthermophilic archaeon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kenyon & Kenyon
                                                                                                                                                                                                                                                                     genomic DNA
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                                                                                                                                                                                                                                                                                                          double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tadayuki
Modified Thermostable DNA Polymerase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and DNA Polymerase Composition for Nucleic Acid
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                                                                                                                          Score 32; DB 3; Length 5342; Pred. No. 1.9;
                                                                                                         Mismatches 115; Indels
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                                                                                                       Gaps
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RESULT 14
US-08-614-770A-1
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; ORGANISM: Hyperthermophilic archaeon
US-09-363-095-5
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US-09-363-095-5
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                                                                                                                                                                   Sequence 1, Application US/08614770A Patent No. 5773267 GENERAL INFORMATION:
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LENGTH: 5342
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EARLIER APPLICATION NUMBER: US 09/073,259
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: US 08/656,005
EARLIER FILING DATE: 1996-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/363,095
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SOFTWARE: WordPerfect 6.1 Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: JP 134096/95 EARLIER FILING DATE: 1995-05-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: TAKAGI, Masahiro
APPLICANT: MORIKAWA, Masaaki
TITLE OF INVENTION: DNA Encoding A Thermostable DNA Polymerase
FILE REFERENCE: 2418/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: IMANAKA, Tadayuki
                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                           APPLICANT: WILLIAM R. JACOBS AND GRAHAM F. HATFULI TITLE OF INVENTION: D29 SHUTTLE PHASMIDS AND USES
  STREET: 90 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 GGTTGAAAGAGTTGAGGACGACGACGATTAAGGGGAGGAGCACGGAGACATCAGAGTCAGAGT 215
                                                                                                                                                                                                                                                                                                                         476 tgacatctacgagtacgacatacccttcgccaagcg 511
                                                                                                                                                                                                                                                                                                                                                                                                          416 tactcatccgcaggacgtcccagcgataagggacaagatacgagagcatggagcagttat 475
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                                                                                                                                                                                                                                                                                                                                             276 TTGCAGCATCGAGTCGCACGACGCCTTATGCAGGAG 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 TTACCAGCAGAAGCCCGATTCCCCGGGTCTGGTTTACTATCACGGTGGTGGATTTGTGAT 275
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Local Similarity 46.88;
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                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101;
NEW YORK
                                        90 PARK AVENUE
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                                                              AMSTER,
                                                              ROTHSTEIN & EBENSTEIN
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                                                                                                                             THEREOF
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ORGANISM: MYCOBACTI
; INDIVIDUAL ISOLATE:
US-08-614-770A-1
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                                                                                                                                                                                                                                                                                                         sequence 20, Application US/08361920
Patent No. 5457046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 286-0854 or 286-0082 TELEX: TWX 710-581-4766 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10185 TCCGCTGAGGCCATCAGGGCCGCAGAGAGCCGCCTGATCAAGAAGGTCGAGCGGAAGAAC 10244
                                                                                                     APPLICANE: SYCH, TETTLE OF INVENTION: An Enzyme Capable of Degree TITLE OF INVENTION: or Hemicellulose NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS: No. 545704601sk of No. Addressee: No. 5470460 No. 5457046d1sk of No.
                                                                                                                                                                                                                                                                                                                                                                                                                          10245 GCGATCTTCGGCGGTG 10260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10125 GTCGCTGCGTACACGGGACTCCCCTCCCCAGTACCTGAGTACCGCCGCTGACAATCCGGCC 10184
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COMPUTER REALABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
MEDIUM TYPE: IBM PC COMPATIBLE
MC-NOS
   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                    APPLICANT: Woeldike, Helle F.
APPLICANT: Hagen, Frederick
APPLICANT: Hjort, Carsten M.
APPLICANT: Sven, Hastrup
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FILING DATE: MARCH 7, 1996
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 49272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460 ATCTTCGTTGGGGGGG 475
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                                     COUNTRY: United States of America ZIP: 10174-6201
                                                                         STREET: 405 Le
CITY: New York
STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MS-DOS SOFTWARE: ASCII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 39,91
                                                                         New York
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Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          697-5995
                                                                                                                                                                                  An Enzyme Capable of Degrading Cellulose or Hemicellulose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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Pred. No. 6.
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6.7;
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                                                                                                                               5457046th America,
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US-08-361-920-20
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Search completed: June 2, 2001, 20:15:55
Job time: 23253 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 20
SEQUENCE CHARACTERISTICS:
LENGTH: 1695 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
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CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/940,860
FILING DATE: 28-OCT-1992
APPLICATION NUMBER: DK 1158/90
APPLICATION NUMBER: DK 1158/90
TTING DATE: 09-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/00124
FILING DATE: 08-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 34,728
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
NFORMATION FOR SEC TO ""
                                                                                                                                                                                                                                                                1504 CAGTGCGGTGGCCAGAACTACAGCGGCCCCACGACCTGCAAGTCTCCTTTCACCTGCAAG 1563
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,920
                                                                                                  1564 AAGATCAACGACTTCTACTCCCAGTGTCAGTAAAGGGGGCTGCCGAGCTATCTAGCATGAG 1623
                                                                                                                                                                                                           94 TACAGGGAGGCGATAAATCGAATATACGAGGAGAAACCGGCAGCTGAGCCAGCATGAG 153
                                                                                                                                                                                                                                                                                          34 CAGCTTGCTGAGTATTTCGACAGTCTGCCGAAGTTCGACCAGTTTTCCTCGGCCAGAGAG 93
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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5: gb_in3:*
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8: gb_ou:*
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Copyright (c) 1993 - 2000 Comp
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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96.8	99.4	115.4	5 116.6	122	157.6	2 228.6	916	Score
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AB029896 Petroleum Z80108 Mycobacteri		AL512977 Sulfolobu AP000993 Thermopla	AF034088 Pseudomon	AP001514 Bacillus	X62835 B.acidocald	AL512977 Sulfolobu	AE000985 Archaeogl	Description

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                                                                                  AUTHORS
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                                                                                                                                                                                         Klenk, H.P., Claycon, R.A., Tomb, J., White, O., Nelson, K.E., Ketchum, K.A., Dodson, R.J., Gwinn, M., Hickey, E.K., Peterson, J.D., Richardson, D.L., Kerlavage, A.R., Graham, D.E., Kyrpides, N.C., Fleischmann, R.D., Quackenbush, J., Lee, N.H., Sutton, G.G., Gill, S., Kirkness, E.F., Dougherty, B.A., McKenney, K., Adams, M.D., Loftus, B., Peterson, S., Reich, C.I., McNeil, L.K., Badger, J.H., Glodek, A., Zhou, L., Overbeek, R., Gocayne, J.D., Weidman, J.F., McDonald, L., Utterback, T., Cotton, M.D., Spriggs, T., Artlach, P., Kaine, B.P., Sykes, S.M., Sadow, P.W., D'Andrea, K.P., Bowman, C., Fujii, C., Garland, S.A., Mason, T.M., Olsen, G.J., Fraser, C.M., Smith, H.O.,
                                                                                                                              The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus Nature 390 (6658), 364-370 (1997)
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AE004380 Vibrio ch
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U70619 Rhodococcus
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AJ000482 Sus scrof
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Utterback,T., Cotton,M.D., Spriggs,T., Artiach,P., Kaine,B.P.,
Sykes,S.M., Sadow,P.W., D'Andrea,K.P., Bowman,C., Fujii,C.,
Garland,S.A., Mason,T.M., Olsen,G.J., Fraser,C.M., Smith,H.O.,
Woese, C.R. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (15-DEC-1997) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA In order to show the genes in ascending order on the genome, the origin of this version has been moved by TIGR to position 2093570 of the original version and the opposite strand is shown from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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/gene="AF1708"
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/gene="AF1708"
/transl_table=11
/product="A. fulgidus
/protein_id="AAB89539.
                                                                 putative"
                                                                                                                                                 complement(3731.
                                                                                                                                                                                                                                                                                                               TPIAKKGRDTYLAFGYPDEPYLDRYFILDSIDDGYTVKIAFQSRLDEVHLDRENLEIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , 1997 this sequence Location/Qualifiers
                                                                                                                                                              VQEIEREVLLYLIERGGFKDVKTARDEIVKFLKRQAEREEIGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAB89536.1"
/db_xref="GI:2648840"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKKRAEIESLAEEIKGKERMLLLNGKFYHLVKDSGFEIKEGEEVGVVKYYSLRNLKRN
LASILREELKRNVSFYSRLLGINYGRIFIKMQKTKWASCSSKGNLSFNLASLALPEKL
                                                codon_start=1
                                                                                                                              /gene="AF1709"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"type I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="similar to GB:L77117 SP:Q57588 PID:1592264 percent dentity: 38.95; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REYIVVHELVHLLEPKHSRLFWETVGFYYPEYEEAERELKKYWIFVERNEVWRMLRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'organism="Archaeoglobus
                                                                               note="hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MNVVVERKNVRNVRIQVLADGKVRVVAPPDFDVDSFISKHADWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .3609)
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                                                                                                                 .4645)
                                                                                                                                                 . 4645)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; identified
                                                                                 protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    version replaced gi:2648834.
      predicted coding region AF1709"
                                                                                 identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coding
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                                                                                 GeneMark;
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/note="hypothetical protein; putative"
                                                                                                                                                                                                     /note="hypothetical protein;
putative"
                                                                                                                                                                                                                                                                     complement(6678. .6857)
/gene="AF1713"
                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(6345. .6560)
/gene="AF1712"
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/gene="AF1712"
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/gene="AF1711"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(5915.
/gene="AF1711"
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VDEAIAKTERLKKGLMQELLIKGIGHKEFKDTEIGRIPKEWEVVRLGDVLELCQYGLS
VPLKDKGKYPVIRMDEIVNGYVVTDIAKYADLDEETFKNFKLEKGDVLFNRTNSLELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(4638. .5663)
/gene="AF1710"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MNKKGNTEEIIERLFSILSSEKDSIEFLKAVSEFSKFYEIDKKE
DERRSSEAKSFYKMALQDFESYKIIXOSKIYSLAVYHLQQAVEKYVKAYVLAFFGLSK
KEMKGYVGHDSPKAFIRLLDNYKRSLELFLKISJOKIGGLDTOPLKISDEDIRKLVFUN
NMSRKQIAEMDSNQIKGIINATIKIKIALENKEIKNQILGLLSKLKNEASEIKSSDPS
                            complement(6960. .7142)
/gene="AF1714"
                                                                                                                                                                                                                                        complement(6678.
/gene="AF1713"
                                                                                                                                                                                                                                                                                                     /translation="mGEIIEAVYQKGVLKPLRKVSLREGEIVKVEIRETKKVTGRFYA
KLRELEKRIERVEGAHRELEEIRDDRY"
                                                                                                                                                                                                                                                                                                                  /protein_id="AAB89537.1"
/db_xref="GI:2648841"
/translation="""
                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to
36.51; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MIVIDTSIFVDYLFDRDENRNEKARKFLNSIEGLTVFVPKIFVI
ELISVAKRLGIEISRKDIEELTYDFEILSEDFVFDEALNVAEKVHPRAADSYFIATAR
LTNSILISSDRLMVRNGKKYGIEAYCLLDELEKALEAIGKLKGEG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to 33.33; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRVKANE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRTGIFLLDGYYVFASYLIRLRPKHEILHPHFLTFYLIFSQSRLKQLATVAVHQANIN
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/gene="AF1710"
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                                                                          complement(6960.
                                                                                            KNGIPWEKLKAELGL"
                                                                                                                          /product="A. fulgidus predicted
/protein_id="AAB89543.1"
/db_xref="GI:2648847"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="conserved hypothetical
/protein_id="AAB89534.1"
/db_xref="GI:2648838"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATNLKKFKIPLPPLPEQQKIAEILSTVDKKLELERKRKEKLERIKKGLMNDLLTGRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAB89535.1"
/db_xref="GI:2648839"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identity: 33.01;
                                                              /gene="AF1714"
                                                                                                                                                                       /codon_start=1
/transl_table=11
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                                                                                                           translation="MKIIREELKKLSSKIELLEAGMIQEEEISEEEAKELDRLVEETK"
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661 CAGTACTTCTCCAGAGAGGAAGATAAGTTCAAGCCCCTCGCCTCCGTAATCTTTGCGGAC
                                                               CTGGAGTTTGGAGAGGGGCTGTGGATTCTCGACCAGAAGATAATGAGTTGGTTCTCGGAG
                                                                                                                                                                                                                                                                                                                                           CCGAAGTTCGACCAGTTTTCCTCGGCCAGAGAGTACAGGGAGGCGATAAATCGAATATAC
                                                                                                                                                                                                                                     GCGGGAGGGAATCTTGCCGCGGCGGTTTCAATAATGGCGAGAGACAGCGGAGAAGATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                            GCTCCTGAGCACAAGTTTCCCCCCCCAGTTTATCATTGCTACGATGCGACCAAGTGGGGTT
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                                                                                                                                                                                                                                                                              GCGGGACGGAATCTTGCCCCGGCGCTTTCAATAATGGCGAGAGACAGCGGAGAAGATTTC
                                                                                                                                                                                                                                                                                                                        GCTCCTGAGCACAAGTTTCCCGGCCGCAGTTTATGATTGCTACGATGCGACCAAGTGGGTT
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9201. .10136
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9201. 10175
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/protein_id="AAB89542.1"
/db_xref="G1:264846"
/translation="MGEVTIKYSVPDNAEKAFRKAVEETAKFFNERDRFFELMNELKG
VIKTDKSWMELKRDLV"
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/gene="tRNA-Val-2"
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98.5%;
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Pred. No. 1e-263;
2; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAAACCAGATTGCCGCTCTTCTTGTGTTTCGACTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAGGCGTGCTTCACGGATTCATCAATTACTATCCCGTGCTGAAGGCTGCGAGGGATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGAAGTTTTCGGGCAGATGCTGAGAAGAGCCGGTGTTGAGGCGAGCATCGTCAGATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAGAAGTTTTCGGGCAGATGCTGAGAAGAGCCGGTGTTGAGGCGAGCATCGTCAGATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTGAGAACCTACCTCCTGCGCTGATCATAACCGCCGAATACGACCCGCTGAGAGATGAA 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAGGCGTGCTTCACGGATTCATCAATTACTATCCCGTGCTGAAGGCTGCGAGGGATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (17-JAN-2001) Sensen C.W., Biosciences, 1411 Oxford St. Halifax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sulfolobus solfataricus
Archaea; Crenarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sulfolobus
AL512977
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                                                                                                                                                                                                                                                                                     complement(1499. 2212)
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complement(1499. 2212)
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500. .1243
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information regulator 2) homolog"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 to
                                                                                                                                                                              translation="MYVMHAVILAGGYGKRLRPLTDDRPKPLIEVAGRPIIEWQISWL"/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="ORF-bac03_017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Sulfolobus solfataricus"
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CANADA
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                                           gene
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  CDS
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ELVEINPLALTNDGRILALDSKVILEDNALYRHEDLLKELGRQBVRDSYVELEGGIG
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TLEVAKMFDQDPETEKIVVIGEIGGTMEERLAEAYKEGEIKKDIIAYIAGMTAPREKR
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complement(7350..8306)
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RVLGISIKKKNEVKRLVEENLERNVYEYKLLHAGIVTVGRAFCFIENPKCEDCILKKV
                                                                                                                                                                                                                                                                                                                                                     complement(6667.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGHAGAVVYMGMGTFESKIRAFKEAGIPIANTPYDIPKLLLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(4721.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="Hypothetical
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gene

CDS

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VQDDCHIFLREDQLREEIKMLISKTVEYWHKFGFKDDDIKPYLSTRDESIGSDELWE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KATNALISALQESGLKFGIKEKEGAFYGPKIDFEIRDSLGRWWQLSTIQVDFNLPERF
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                                                                                                                                                                                              /gene="ORF-bac03_006"
11638. .12402
                                                                                                                                                                                                                                                               GANMLPYNPNNKTVFIYLAVTATGPAFNYNGTSNGQMKIYVPAGWNVMIILTNEQSIP
HNANIVLNDTQIPNNPNISADGKILLYVGDSPSNFANNGILSGQTAVGILDNISAGYY
                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="soxE"
10807. .11592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mlvyglyksplgyITvakddkgrImldfcdcvegnsrddssfte
ffhkldlyfegkpInlrepInlkTypfrLsvfkevmkIpwgkvmTykqIadslgTspr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARGNIEVRNVKFEKFLELLITEIAQRDVEQTTVKALK"
                  LELWGISNKLSKSIVLIPSLGVVSGSSCCVFLPSIVMYSIALSISSITATILSILSSF
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/gene="ORF-bac03_006"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="Methylated-DNA-protein-cysteine"
/protein_id="CAC24284.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ogt"
10033. .104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="Threony1-tRNA synthetase (Threonine-tRNA")protein_id="CAC24283.1"
/protein_id="CAC24283.1"
/db_xref="G1:12313155"
/translation="MESYKPYMLKGAVILAINLIDKGYKPVAVGLGERDFYIDVKSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLSDPITWSDYNVLLEAIENANEPNVFDTGTPNLVKHVLSEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Hypothetical protein"
/protein_id="CAC24282.1"
/db_xref="GI:12313154"
                                                                                                                                           /transl_table=11
                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="soxE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="ogt"
/EC_number="2.1.1.63"
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/gene="thrs"
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/codon_start=1
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                                            amy gene; amylase.
Alicyclobacillus acidocaldarius.
Alicyclobacillus acidocaldarius
Bacteria; FirmLoutes; Bacillus/Clostridium group;
Alicyclobacillus group; Alicyclobacillus.
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Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (22-OCT-1991) H.O. Hemila, Institute of Biotechnology, Valimotie 7, 00380 Helsinki, FINLAND 2 (bases 1 to 7872) KGIVULA,T.T., Hemila,H., Pakkanen,R., Sibakov,M. and Palva,I.
                                                                        Similarity
                                                                                                                                                                 1615
                                                       Conservative
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SNPYDSWFQ IDTLPLTDTSNPAQRFVYGSDNSYARYWI REGADGWRLDSADNGWENT
AWWGGERQAVKSIDPNAA I IGEIWDNATNDNGTDWLTGSTFDSVMNYQFRANAVIDFER
GTYNDGNYQHHAVDAAGFNQELWRLYSBYPLGSFYSMMNLVDSQDTMRILTI ILENAPQ
PGDLSALQQDBYRPSFAAEQLGIERLKLYSDFQFSFPGDPTIFYGDEAGLTGYSDPLN
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VNGTNASWNSVQFTVPQSLPNGLYRVELDTVAKDAGGVVNVELDRSAELIVGPLPAWM
QAYAHDSGPQAFYRSPFGAVSTCTPITLAELAFLSVKSATLAELAGAADOGSEIDLEMQK
QAYAHDSFQAFYRSPFGAVSTCTPITLAELAFLSVKSATLAELAGAADOGSEIDLEMQK
CAMSGDELAQQTGQDINDYTWWTVTIPAADVTTPGTMWYQFVTETDTGQVVYYDDNG
AQLEGGCQVGLSSDGPSYQISVERGFGTPDWLKHAVITEIMPGTYNCNIATEENPN
TQKGITVGADGTESLCGIGFHENWDSSPPYDPNILFPLSDFKIASLAGNGQMUIDFFGGD
TQKGITVGADGTESLCGIGFHENWDSSPPYDPNILFPLSDFKIASLAGNGQMUIDFFGGD
TQKGITVGADGTESLCGIVATLYLMPVFEAESNHKYDTADXFKIDPGFGTQODWLNILVQAA
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DLSVTVERDAYAQTFAVQALFSASDHAQSPVSAPKTVSLAVDVPAVRLSQPIVSGRVV
GDRAWVSITPVSGATQYVIYQRQGDGSYAPVATVSTSGDSAAIGEVPAQGPANSPHAT
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GVPAEDATAIVAINNQNQAITVTIPTDGTVADGSTMLDELNNQWYKVQNGGITLTLQS
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QNKGFQVEMSPGRTFGPYQLWSATIPASNGGTIYYRFDIYDGTSFACLSGDGLHTSDD
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STNASPPTGASAGGGTAGETYSNAVQIVSGNGFRAGNGATVVLAVNGLNLNPSSFKVV
VSNSLNGVIDVTSDSVLTGPNSIALHLPAGDDGLGAGTYTVTVESGGDSVSTPSGQGL
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/protein_id="CAA44638.1"
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                                                                                                                                                                                                GKGPDVVFGMPHDNNGVFAEEGLMAPVPSGVLNTGLYAPNTIDAIKVNGTMYSVPVSV
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alpkgetitvwswqtgpelqdvkqiaaqwakahgdkvivydqssnpkgfqfyataart
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/protein_id="CAA44639.1"
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/clone_lib="lambda gt-
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Hirama,C., Fuji,F. and Takami,H.
Characterization and comparative study of the rrn opero
alkaliphilic Bacillus halodurans C-125
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                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (22-MAR-2000) Hideto Takami, Japan Marine
Technology Center, Deep-sea Microorganisms Research
Natsushima, Yokosuka, Kanagawa 237-0061, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtil Nucleic Acids Res. 28, 4317-4331 (2000)
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Horikoshi, K.
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URL:http://www.jamstec.go.jp/jamstec-e/bio/DEEPSTAR/FResearch.html
Tel:81-468-67-3895, Fax:81-468-66-6364)
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Reidentification of facultatively alkaliphilic Bacillus
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249-284; Springer-Verlag (1999)
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Nakamura,Y., Ogasawara,N., Kuhara,S.
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others"

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5681

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JOURNAL MEDLINE REFERENCE AUTHORS
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                           CGATGCGACCAAGTGGGTTGCTGAGAACCGGGAGGAGCTGAGGATTGACCCGTCAAAAAT
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TGCGGCCACTTGCTGGCTGGTCGAGCACGCTGCCGAACTCGGCGTCGATGGCCGTCGCCT
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Choo,D.W., Kurihara,T., Suzuki,T.,
Direct Submission
Submitted (11-NOV-1997) Institute
University, Uji 611, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFU34088 927 bp DNA BO
Pseudomonas sp. B11-1 lipase (lipP) gene,
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oo,D.W., Kurihara,T., Suzuki,T., Soda,K. and Esaki,N
                                                                                                                                                                                                                                                                                                                                                                 151
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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ALAVSRLAAQRQGFKISYQCLFYPVTDARCDSQSYEEFABGYFLTGAMMYWFWQQYLQ
DTGQGDDPLASPLRAETLADLPPTTLITAEFDPLRDEGEAFALRLQQAGVSVRVQRCE
GMIHGFISMAFFVERAHALSDAADLRRALN"
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AL512977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-JAN-2001) Sensen C.W., Institute for Marine Biosciences, 1411 Oxford St. Halifax, NS, B3H 3Z1, CANADA
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Archaea; Crenarchaeota;
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/gene="ORF-bac03_016"
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DSIADYVVREPVEISLPKILENVRQKILS"
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                                                                                                                                                                                                                                                                                                                                                                         /country="Italy:Naples"
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                                                                                                                                                                                                                                                                                                                                                                      /gene="sucC"
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                                                                              complement(6667.
                                                                                                              complement(6667.
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                               codon_start=
                                                                                               /gene="ntH"
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                                                                                                                                                                                                                                                                                                           /codon_start=:
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SREGGIDVEQAKDVKKNIIPLERGVRSYDIVEAEKYLGVKGLGQIIQGLYKLFVDVDA
ELVEINPLALTNDGRILALDSKVILEDNALYRHEDLLKELGRQEVRDSYVELEGDIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(5569. .6582)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Succiny1-CoA synthetase, alpha subunit"
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TLEVAKMFDQDPETEKIVVIGEIGGTMEERLAEAYKRGEIKKPIIAYIAGMTAPREKR
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TAAAGTPSGFLETGKEFTTYNGIPAVEFLDYNNYTYISLQYMIPLKSYYSINIDPASN
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VALNITGLKFISLLVPITTFHDLLGVSKFIYNGSPYIIILTSTGSTGSAYYYNTSVPI
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VFILYVIFRYILVLTLFIIPILVYLFTIAISLHLYKPEIYEKITRVEIKDKIIKIHTS
NKTFIIHRGKILGFTDQI"
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                                                                                                                                                                                                                           3GITRCDEVALGIIDALKEVKKPIFVRLLGTNEELGKKILRENGVNVYDDVLKMIGDA
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                                                                                                                                                                                                                                                                      GNGAGLTMASMDLVKLNGGNPANFLDVGGGANREHVKESVLKVGSNPRVKKIVINIY
_number="4.2.99.18"
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/10033. .1045
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8358. °
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QYANKIYEIPKGREPDESSLVLFKRLFSIIVKSASIKKYDLIIATGSNHSIFSSFEQF
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DLEKWIANASLVITHQGKTAMEAVVMYRKPVIMVYNNDWKSATTLSDAKKYAEILGAT
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complement(7350...8306)
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AVQMALSKNPILLIIPCHRVIAENGIGGYSRGVKLKRALLELEGVKIPE"
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SITLDEVKKAINENVLANVSIENNQIVYKGNKVSIIEDKYSISVNLNRXYFEILNIST
HHPMPNEQYVRIRGVAFETIEBOLKDYLSWLEKALEFDHRLIGEKLDLEFSHEERAGSGL
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11638. .12402
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ARGNIEVRNVKFEKFLELLITEIAQRDVEQTTVKALK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KATNALISALQESGLKFGIKEKEGAFYGPKIDFEIRDSLGRWWQLSTIQVDFNLPERF
KLEYIDKDGIKKRPVMVHRAIYGSIDRFVAILLEHFKGKLPTWLSSVQVRVLPITDEV
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Query Match
Best Local Similarity
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                                                                                                                                GCCGGTGTTGAGGCGAGCATCGTCAGATACAGAGGCGTGCTTCACGGATTCATCAATTAC
                                                                                                                                                                                                                              ACCGCCGAATACGACCCGCTGAGAGATGAAGGAGGAGGTTTTTCGGGCAGATGCTGAGAAGA
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/product="Hypothetical protein"
/protein_id="CAC24286.1"
/db_xref="G1:233136"
/translation="MIKRLTISPLFLILSLIAYYLSRNDILLYSTLSTILFWTFIILI
/translation="MIKRLTISPLFLILSLIAYYLSRNDILLYSTLSTILFWTFIILI
/translation="MIKRLTWFTYGILSYHYLLYSFFYLLLYSTLAGSKNISWFSF
NAGIGYSIPPJTYFLEWPUSNSPAIWFFIGPYEEGDVIF#STFLGVVLALLGLHVMKI
LELWGISNKLSKSIVLIPSLGVVSGSSCCVFLPSIVMYSIALSISSITATILSILSSF
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hes 326;
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                                                                   TIGAGGGAATCTTGCAGCCGTAGCAAGCCTGATGGCGAGGGATAAAGGTATAAAGCTTCC 116866
                                                                                                                                             GAAAAGAAGCGAGGAATTAGGTGTGGACAGCGATAAGATAGCATTAATGGGAAGACAGCGC 116806
                                                                                                                                                                               GTGCAGGCGGATAGCGAAGTATTCTGGATCGAAGGTAATATCAGTAGGCTATAGGCTAGG 116686
                                                                                                                                                                                                                                                                                                              ATGCAGGAGAAYYGCGAGACTTTCAAACTCTACCGTAGTCTCCGTGGATTACAGGCTCGC 362
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                                                                                                                                                                                                                                                                                                                                                                                                 TCTGGTTTACTATCACGGTGGTGGATTTGTGATTTGCAGCATCGAGTCGCACGACGCCTT 302
                                                                                            GGGACGGAATCTTGCCCCGGCGCTTTCAATAATGGCGAGAGACAGCGGGAGAAGATTTCAT 542
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                                 AAAGCATCAAATTCTAACTTACCCCGTTGTGAACTTTGTAGCCCCCACACCATCGCTTCT 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermoplasma volcanium (strain:GSS1) DNA.
Thermoplasma volcanium
Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (20-DEC-1999) Masashi Suzuki,
Bioscience and Human-Technology, Centre
Higashi 1-1, Tsukuba, Ibaraki 305-0046,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaeal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanium proc. Natl. Acad. Sci. U.S.A. 97 (26), 14257-14262 (2000)
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Thermoplasma volcanium o
AP000993 BA000011
AP000993.1 GI:11990452
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Watanabe,K., Yamazaki,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 11.2%;
Similarity 48.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          URL:http://www.aist.go.jp/RIODB/archaic/, Tel:81-298-54-6582
Fax:81-298-54-6041)
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Kanehori,K.,
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AF294430
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Cloning and characterization of a novel
esterase (estA) gene in Escherichia coli
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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                                                                  /product-"carboxyl esterase A"
/protein_id-"aaG09918.1"
/db.xref-"G1:9964294"
/translation-"MNLEEQIKIAASLRQPSEGSLASQSELKPVNPPEVNKMEYDIPT
/translation-"MNLEEQIKIAASLRQPSEGSLASQSELKPVNPPEVNKMEYDIPT
/SAGETEVWYFKPVNTOKQLLPVFVNLHGGGFINGSAEMDNPWCTVVIADRAQCITVNVE
YOLAPEHPFPAALHECYDVLKWLYEHPEELQIDIRNALAIGHSAGGNLAFAACLLNO
RGNTLPIAYQVLDYPPLDLATDPAQKPAFEEAIPVELARLFNSFYLQGQDPHNPLVSP
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                                                                                                                                                                                                                                                                                                                          /organism="Bacillus pumilus"
/db_xref="taxon:1408"
                                                   FADRSSLAQMPPALVITAERDSLAQEADQYAKKLKEAGVDVTYSSLKEFLTASHTPE
                                                                                                                                                                                                 codon_start=1/
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Query Match Best Local Similarity

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Direct Submission
Submitted (05-DEC-2000)
Institute, The First La)
                                                                              Complete genome structure of the bacterium Mesorhizobium loti DNA Res. 7, 331-338 (2000)
                                                                                                                        Kaneko,T., Nakamura,Y., Sato,S., Asamizu,E., Kato,T., Sasamoto,S. Watanabe,A., Idesawa,K., Ishikawa,A., Kawashima,K., Kimura,T., Kishida,Y., Kiyokawa,C., Kohara,M., Matsumoto,M., Matsuno,A., Mochizuki,Y., Nakayama,S., Nakazaki,N., Shimpo,S., Sugimoto,M., Takeuchi,C., Yamada,M. and Tabata,S.
                                                                                                                                                                                                                                                   Mesorhizobium loti (strain:MAFF303099)
Mesorhizobium loti
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Mesorhizobium loti DNA,
                                                Kaneko, T
                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae Phyllobacteriaceae; Mesorhizobium.
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Fax:81-438-52-3934)
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                                                              AB029896
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Pred. No. 2.9e-18;
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CTTCTGGAGTTTGGAGAGGGGCTGTGGATTCTCGACCAGAAGATAATGAGTTGGTTCTCG
                                                                                                   AAGATCGTCTTCCAGTTGCTGATCTATCCGGCGACCGACGCCCTGCACGAAGGCCTGTCG
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                                                                                                                                                                                                                                                                                                                                                                    GTCGCCCGCAACGCCGAGATCAACGCCGACCCGACCCGCATCGCCGTCGGCGGCGAT 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCTTATGCAGGAGAAYYGCGAGACTTTCAAACTCTACCGTAGTCTCCGTGGATTACAGG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                     Life Science; Yamadaoka 2-1, Suita, Osaka 565-0871, Japan (E-mail:satoru@mls.eng.osaka-u.ac.jp, URL:http://www.mls.eng.osaka-u.ac.jp/Mater&LifeScience.html, Tel:85-6-6879-7443(ex.7443), Fax:85-6-6879-7443)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-JUL-1999) to the DDBJ/EMBL/GenBank databases. Satoru Mizuguchi, Graduate School of Engineering Osaka Univ., Material and Life Science; Yamadaoka 2-1, Suita, Osaka 565-0871, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 954)
Mizuguchi,S., Kanaya,S.
Direct Submission
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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petroleum-degrading bacterium HD-1.
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/protein_id="BA82510.1"
/protein_id="BA82510.1"
/db_xref="G1:5509944"
/translation="MTLDAQAKAILDQIARSPMPKLHQVPASVARQMFEISCKLTEIK
/translation="MTLDAQAKAILDQIARSPMPKLHQVPASVARQMFEISCKLTEIK
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/translation="MTLDAQAKAILDQIARSPMPKLHQVPASVARQMFEISCKLTEIK
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/translation="MTLDAQAKAILQUIARSPMPKLHQUIARSWFFIT"
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/codon_start=1
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/db_xref="taxon:89018"
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Lipase, from an Oil-degrading
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Pred. No. 2.5e-18;
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(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackts after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome
                                                                                                                                                                                                                                                                                                                                                        Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhillesanger.ac.uk On Jun 26, 1998 this sequence version replaced gi:1542891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erratum:[{published erratum appears 12;396(6707):190]] 2 (bases 1 to 39150)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E., Tekala, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium to Z80108 AL123456
                                                                                                                                                                                                                                                                         available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parkhill, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 393 (6685), 537-544 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deciphering the biology of Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barrell, B.G.
                                                                                                                                                                                                                                                                                                     Details of M. tuberculosis sequencing at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            initiation codon
                                                                                                                                                                                                                                                                                           2027. .3646
/gene="ppE"
2027. .3646
/gene="ppE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Rv1386, (MTCY21B4.03), len: 102. Member of M. tuberculosis PE family, similar to many e.g. G913039 ORE 3.0F PGRS TANDEM REPEAT (polymorphic GC-rich sequence)(100 aa), fasta scores, opt: 149, E(): 0.0013, (31.5% identity in 92 aa overlap), also G699138 U1756A (aa) (34.7% identity in95 aa overlap) and G466937 U1620K (100 aa) (36.2% identityin69 aa overlap)"
                          /note="Rv1387, (MTCY21B4.04), len: 539, Member of M. tuberculosis PPE family of protein, similar to many e.g. r05F_MYCTU 010892 hypothetical 46.9 kd protein cy231.15 (463 aa), fasta scores; E(): 4.2e-26, 37.7% identity in 531 aa overlap; contains PS00343 Gram-positive cocci surface proteins 'anchoring' hexapeptide; similar also t MTCY274.23c (37.5%identity in 168 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="PE"
1722. .2030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDICVRAFADFAVVKPOVAFFESYGAAGFAVLERTIAELRAADVLVLADAKRGDIGAT
MSAYATAWVGDSPLAADAVTASFYLGFGSLTEPLEVAAAHGRGVEVVLAATSNPEGAAV
QNAAADGRSVAQLVVDQVGAANEAGAGFGGSLTEVVVGATAPQAFDLSAFTGPVLVPGV
GVQGGRPEALGGLGGAASSQLLPAVAREVLRAGPGVPELRAAGERMRDAVAYLAAV"
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/note="Rv1355, (MTCY21B4.02), pyrF, len: 274. orotidine
5'-phosphate decarboxylase, identical to M. bovis,
DCOP_MYCBOP42610 (274 aa); contains PS00156 Orotidine
5'-phosphate decarboxylase active site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mtlrvvpeslagasaaieavtarlaaahaaaapfiaavippgsd
svsvcnavefsvhgsqhvamaaqgveelgrsgvgvaesgasyaardalaaasylsggl
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/protein_id="CAB02190.1"
/db_xref="GI:1542893"
/db_xref="SWISS-PROT:p77898"
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/strain="H37Rv"
/db_xref="taxon:1773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mycobacterium tuberculosis"
/strain="H37Rv"
/db_xref="taxon:1773"
/clone="Y21B4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAB02191.1"
/db_xref="GI:1542894"
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/product="PE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="PE"
       /codon_start-J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="PS00156 Orotidine 5'-phosphate decarboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MTGFGLRLAEAKARRGPLCLGIDPHPELLRGWDLATTADGLAAF/
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1527
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3952. .4524
/gene="mIHF"
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/translation="myepmiappevhsamlnygagygpmiisatqngelsaqyaeaa
/translation="myepmiappevhsamlnygagygpmiisatqngelsaqyaeaa
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/translation="myepmiappevhiisaty"
/translation="myepmia
                                         5351. .5683
/gene="Rv1390"
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/gene="gmk"
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/gene="gmk"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="SWISS-PROT:P71659"
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IPMLHESVSATTRAPRGEVUGVDYLHFIDPTREQQLLDQGELLEWAEIHGGLHRSGTL
AQPVRAAAATGVPVLIEVDLAGARAIKKTMPEAVTVFLAPPSWQDLQARLIGRGTETA
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/product="PPE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAB02172.1"
/db_xref="GI:1542897"
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PQNQGVGLDFVRKPEYGRLRWPAYPAGTNNDRLISMRDGGIVALPQLTDEQRAAALEK
AAAARRARAELKDRLKRGGTNLTQVLKDAESDEVLGKMKVSALLEALPKVGKVKAQEI
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/protein_id="CAB02193.1"
/db_xref="GI:1542896"
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/db_xref="GI:1542895"
                                                                                                    'gene="Rv1390"
                                                                                                                                                                                                                                                                                                                                                              'note="PS00017 ATP/GTP-binding site motif A (P-loop)"
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anchoring' hexapeptide"
note="Rv1390, (MTCY2184.07), len: 110. Unknown."
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Richardson, D.L.,

M., Shen,M., Zalewski,C.,

Research,

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                                                                                                                                                                  Deinococcus radiodurans
                                                        Deinococcus radiodurans
                                     Bacteria;
                                                                        Deinococcus radiodurans
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         Thermus/Deinococcus group; Deinococcales; to 16440)
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/protein_id="CAB02173.1"
/db_xref="GI:1542898"
Elsen, J.A., Heidelberg, J.F.,
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48.4%;
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section 130 of 2
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Hickey, E.K.,
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Peterson, J.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (08-NOV-1999) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          White,O., Eisen,J.A., Heidelberg,J.F., Hickey,E.K., Peterson,J.D., Dodson,R.J., Haft,D.H., Gwinn,M.L., Nelson,W.C., Richardson,D.L., Moffat,K.S., Qin,H., Jiang,L., Pamphile,W., Crosby,M., Shen,M., Vamathevan,J.J., Lam,P., McDonald,L., Utterback,T., Zalewski,C., Makarova,K.S., Aravind,L., Daly,M.J., Minton,K.W., Fleischmann,R.D., Ketchum,K.A., Nelson,K.E., Salzberg,S., Smith,H.O., Venter,J.C. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                radiodurans R1
Science 286 (5444), 1571-1577 (1999)
20036896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dodson, R.J., Haft, D.H., Gwinn, M.L., Nelson, W.C., Richardson, Moffat, K.S., Qin, H., Jiang, L., Pamphile, W., Crosby, M., Shen, Vamathevan, J.J., Lam, P., McDonald, L., Utterback, T., Zalewsk, Makarova, K.S., Aravind, L., Daly, M.J., Fraser, C.M. et, al. Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases
                               /translation="MTLNTDQLSRRLSWSGILAGLVMGVVTFLT]IALGTVITALTGL
TLSGVGIAAVIWSAIAALVGAYAAGILAVRASAPATRNSDGIAAMTHDDATLTGLVTA
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                                                                                                                                                                                                                                                           complement(1921.
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DTALFEKGEQHRGNLRGELKDGELNGQLRTVVFGKELLSYSLRLQRVTDAAAEENEGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLSWLLASGLTLLATVMGARSAATTRRGVVTTVNTTTTRR*
                   SQGRWRNAEYRPGPGMIHGYANMTAFSPVAAQLIDEAGVWLGEQLRG
                                                                                                                                                                                                                                                                                                                  complement(1921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1393. .1884)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1393. .1884)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KALSGEQFVTRLERQGLSNAEAREVQTTINNTVNRVETQAQQAAKVAEDNARIAARNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Deinococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="DR1484"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="DR1484"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="DR1483"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene='
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:1299"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                        dentified by sequence
                                                                                                                                                                                                                                          note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to 16440)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DR1483*
                                                                                                                                                                                                                      GB:AL123456 percent identity:
uence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by Glimmer2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              þу
                                                                                                                                                                                                                                                                               2892)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         putative,
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gene
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                                                                                                                                                                                                                                                                                  is not the result of a sequencing artifact; sim GB:M80458 SP:P26646 PID:145173 PID:606193 GB:U0 percent identity: 64.40; identified by sequence similarity; putative" 7777. .8433
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DQBRKYDDNAGH.HIDLQPGRQRLSGEQAEGFLRFRKDNMGDIGRVGRQQQFLTALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVNEGAKILEEGIAQRASDIDVIYIYGYGFPAYRGGPMQYASEQGLKNVAADLEKYGQ
TPAPVLKQLADEGKTFSDYDREHAGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEGARPEDVDAAMNALGLPMGPFQMSDMAGLDIGYSIRQHQAKVRGEPEPDGWLDRIV
KTGRKGQKTQGGIYDYGEDRKPKPNADVQKLIEDYRAEQGTQSREISQEEITKRLAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVETSQEALDRGLGVIRKNYENTAKKGRMTQDDVEKRMGLLTPTLKMEDLAGADIIIE
AVFENMDVKKDIFTRLDKIAKPGAILASNTSTLDVNEIASVTGRPEQVIGLHFESPAN
VMKLLEIVRADKTSDSVLATSLALAKRIKKVGVVVGVCDGFVGNRMVHRYGDEARKIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MGRHHKQEALPMTQDTPNRVDQSRDGDVEILTINNPPVNAFGPG
VPEGLKAGLDAAAADSVKAVVIIGGGRFYAKADIKGFGLPRGQAPDLRGTVAKLDA
YEKPTVAALHGFALGGGLELALGCTYRVAVKDAQLGLPEVKLGVLPGAGGTQRLPRV
GAQKALEMMLSGNPIKAPAAKELGLVDEIVDGDLLAGAVAFARAHADARPLPRVSERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="enoy1-CoA hydratase/3,2-trans-enoy1-CoA isomerase/3-hydroxyacy1-CoA dehydrogenase" /protein_id="AsF11052.1" /db_xref="G1:6459246"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(3215. .5341)
/gene="DR1487"
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complement(2951.
/gene="DR1486"
                                                                                                                                                                                                                                    /gene="DR1490"
7777. .8433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANEQKPWPVTTVSGPATPAAALLRDLGYGQLDNAPSLPGSELTIRLGRDTPAQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEIRRÞANVWKLPKVIAÄLDÁNÁKTNLTRAQTAELLGAAQRGPQYSTFTVÞGNFGMYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(5424. .6593)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEGGSPEVFAAAREGLKKTHRGQHSPSHIVDLAEMAATKPFQEGWDAEADRFVDSLNS
PQSRGLRHIFFAEREAGKIRGLSKDTPTTDIKSAGIIGAGTMGGGIAMNFLNVGIPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to 63.02; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(3215. .5341)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MPEGTVTREEAIWQFCGFHRHLLKRSAQCGCFYCLRLFSPSEIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="DR1489"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to PID:1653307 percent identity: 55.46; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="DR1488"
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                                                                                                                                                        codon_start=1
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                                                                                                                                                                                                            'gene="DR1490"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _table=11
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by sequence similarity; putative"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                          408
                                                                                                                                                                                                                                                                                                                                                                                                          348
  588 CACACCATCGCTTCTGGAGTTTGGAGAGGGGC---TGTGGATTCTCGACCAGAAGATAAT 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283;
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MPASDRPAPVWAGAEGRVAVIDLPSFLSTDTAAAFLAQVRQLQAAGVRSLIVDLRFNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="DR1491"
8574. .9911
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                                                                         FAGFFAKYLAIQVAFQAGYLLISVLAVLSSVAALVYYLRPAMLMFMPDRTPAREYAHG
QRPATNVAVALSLIGIVVLGLLPNLWYGWVASPEIWRLLAGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGDVALPARLTPDVPAPLDIDLLTTQGRDTGLEAALIVLGEAVTSPPTLTTSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSSAPGAKGYGVVTLDLTRGNKVGKALAGQVTNGMASKSFEGRAWIYTDQATTLSGTV
DCQKLVGIGIAIPATVNVTTQAGWNVLKVSGTGSLFGVNAKVENGTKEPTTWRTLLDEL
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/db_xref="GI:6459249"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(9980. .11458)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLIGPDTASCAEVFAYYAQKGGARLVGEATKGVANSGVLLRNLPDGGLIAVTVFRGYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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'transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ldentity: 43.96;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="DR1491"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="similar to GB:AL123456"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ppiD:1226042 piD:1651804 percent identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cl23456 percent identity:
    similarity; putative"
Length 16440;
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2341 GGGCGGCCCGGCTTTGCGGGCGCAGCTTCTCATTTACCCCGCCGCCGATTTCGAGCACCC
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                                                  528 CGGAGAAGATTTCATAAAGCATCAAATTCTAACTTACCCCGTTGTGAACTTTGTAGCCCC
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                                                                                                         GGCGGGCGACAGCGCGGGGGCCAACCTCGCCACCGTCACGGCGCTGCGGTCGCGTGACGA
                                                                                                                                                        TGGGGGGGACAGTGCGGGACGGAATCTTGCCCCGGCGCTTTCAATAATGGCGAGAGACAG 527
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Sequencing of three lambda clones from the genome of alkaliphi
Bacillus sp. strain C-125
Extremophiles 3 /12 - - -
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                                                                                        (in) Extremophiles in deep-sea
  HORIKOSHI, K. TSUJII;
  249-284; Springer-Verlag (199
                                                                                                                                                                                                                                                                   Takami,H., Takaki,Y., Nakasone,K., Sakiyama,T., Maeno,G., Sasaki,R., Hirama,C., Fuji,F. and Masui,N. Genetic analysis of the chromosome of alkaliphilic Bacillus halodurans C-125
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Replication origin region of the chromosome of alkaliphilic
Bacilus halodurans C-125
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An improved physical and genetic map
Bacillus sp. C-125
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Bacillus halodurans genomic
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                                 Takami, H. and Horikoshi, K. Reidentification of facultatively alkaliphilic Bacillus
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Takami,H.,
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Technology Center, Deep-sea Microorganisms Research
Natsushima, Yokosuka, Kanagawa 237-0061, Japan
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Hirama,C., Fuji,F. and Takami,H.
Characterization and comparative study of
alkaliphilic Bacillus halodurans C-125
Extremophiles 4 (4), 209-214 (2000)
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         /protein_id="BAB06292.1"
/db_xref="G1:10175194"
/db_xref="G1:10175194"
/translation="MD1KRAATHKRAVLMLVLFIVVFSVLIARFLYLQIEKEVKGYSL/translation="MD1KRAATHKRAVLMLAEEVTSYSYYAVLDNSHQDAVEDDERTAQ
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LLAEHINMSEERLLELLTRDVYQVELGAGARNLTQEQRDKIADLDLPGIYFTEEPRRY
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RLTIDSRVQTIIERELDIAEATYSPDGAIAIANNPNTGEILGMSSRPHYNDENFREVK
PEVYNQNKPIMMQYEBGSTFKIITLAAALENEVDLTNDRFHDPGFIEVAGHRLRCWK
KGGHGSQTFLEVVENSCNPGFVVLGERLGKDRLFDYIEAFGFGQKTGIDLQGEAKGII
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LENNHIVSFIGFAPADDPQIVVYVAIDNPKDTVQFGGVVAAPIVGKIIGDSLQALGIE
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EPAKTGNDVYLTLDSNIQTALDQVMTQVEEEYKPERIIAIVADPKTGQILAMSNRPTF
                                                                                                                                                 /product="penicillin-binding
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NPNEYEOITNYMNYAVSDRYEPGSTMKVFTLAAALEEGVLNVNEQYQSGTYAIRNDTN
PPIRDHNQGRGWGTISYLEAMQRSSNVGFSKTALEKLGPEKLEYLDEEGGEGEPTGID
LPNEAASVYAKGALRDAASTAFGQGTAVTP1QQTQAMTAIANDGKMMKPYVVDRIVDS
ETGEVIEEKEPEVVGEPISKETAKEVRDILETVVTSSSCTGRPFYLEGFDVAGKTGTA
QVRNPDGPGYLNGHGKNIFSFIGMAPKDDPSVIVYVAYDRPSLNTNQVGSEPVAKIEN VMQDALFPVLAFVAGPGEISYWATLKRVFHECGMKMSPVVPRISATCVPSAVQKWFAE KQYSYEEAIAHGLEKEKEGWLEEQTPWPIDQVVEEAITQIRHSHKPIKDLAEQIGETP GKLANKNWSIIESQLRFMERRMKRHVRERFEHELSKFDEAERWLKPNGLLQERHDHVI RKRIASEAGLNKETLAKWLATVFRSLPETEHTLPLYERVKTLAGRSNTYTDFFAELLL YLFRDEGLVVFDSGDPSFRTLEKSCFHMLIQKTKNVQGAFAHQVKKLEQAGYGRPIIT EETNAHLFYVEEGSRYRIDYTGENYELNGKNQTFSREELLEHLTLHPERFSNNVVTRP /translation="MIVEELKLLPSSKAAKDYLNNQNDMLSFFDYNIHQPTVFQQRLS DLQEQPYDRDALSKALLSYQKRFAFHDKAAQQVEKLKDPRSVVVIGGQQAGLLTGPLY TIYKAVTIVLLAREQERALGVPVVPVFWIAGEDHDLDEINAVPIEKNGRWRSHRIEEK QVEWKKLEESLKNLPFTKKDARAFTRFFFSGATECELDKQGRVNIASPLREFAQLKKE CVVIGVSNRVEIWSKELWEEYFAESEESFSEIAENIVDFDL* /translation="mfehytvlknesviglnikpdgiyvdctlggaghsgeivkqltg GGHLYAFDQDQYALSHAKETLSPYRGSFTLIESNFRYMREKLEELGVHHVDGVLFDLG /protein_id="BAB06293.1" /db_xref="G1:10175195" /tabslation="MONVARSIEHVRROPGQAPQQPAPRPRRORGKITKGEKMLLGML TVAFILFIGFSVHNYATMYSVNREIHELEQTVAAQEQINDGLSIQVVELSSPERILKI complement(4529. .4891) /gene="BH2574" TVEGQQPYSGHKLLEGERVILRTESESYTLPSMIGWSLRDVLKVANVLDVNVNLFGQG FVVGQSIEEGDTITPGDYMVVELASPTRKKTKTDEKEEDEE" QLLNIVGDDFIPRLISMNINKMGVHYLVKL" unknown conserved protein complement(6487. .8103) /gene="BH2577" complement(6487. .8103) unknown conserved protein" comprement complement(5901. .6332) TLKLITKKPIVPTAEEIELNNRARSAKLRIAEKQ" KQTARKTEQSREKKPTRTTGELVDTTKEATPAPARRTGGHPAKRTFQATRTAVNDELG AFEEALEAATDLTAPKGRTCVTTFHSLEDRTCKEMFREASKGPDVPPGLPVTPEEYKA VSSPQLDEDERGFSYHRDAPLDMRMNRSQSLSAYEVVNQWDFIELMKIISRYGEERFA unknown conserved protein" complement(4939. .5871) complement (4939. AKSLGMKLEDENVKVVQN" unknown conserved protein" complement(4529. .4891) TIMNHSLQYLNISPSVEELKDEEEEGYELADFIGESARSAREELEQAGMKVYVLGEGD /protein_id="BAB06296.1" /db_xref="GI:10175198" /protein_id="BAB06295.1" /db_xref="GI:10175197" complement(5901. .6332) /gene="BH2576" /protein_id="BAB06294.1" /db_xref="GI:10175196" /gene="BH2574" /transl_table=11 /note="BH2577 /gene="BH2577" /transl_table=11 /gene="BH2576" /transl_table=11 /note-"BH2575 /gene="BH2575" /gene="BH2575" /transl_table=11 /codon_start-1 /note="BH2574 translation="MFMGEYRHNVDEKGRMIIPAKFREELGETFVVTRGLDRCLFVYP/ /codon_start=1 /note="BH2576 codon_start=1 .5871) in B. subtilis"

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A set of ordered cosmids and a detailed
for the 8 Mb Streptomyces coelicolor A30
Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                     Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                   polymerase sigma factor; fdxA, ferredoxin; ferredoxin reductase; hydroperoxide resistance protein; integral membrane protein; lipase; membrane protein; oxidoreductase; pyruvate dehydrogenase component; qcrB2, ubiquinol-cytochrome C reductase cytochrome B subunit; RNA polymerase sigma factor; secreted protein; transcriptional regulator; transcriptional regulatory protein;
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                                                                           Redenbach, M., Kieser, H.M.,
                                                                                                                                                                                                    transmembrane efflux protein.
                                                                                                                                                                                                                                                                                                                                            acetyltransferase; acyltransferase; dehydrogenase; ECF-family RNA
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                                                          Kinashi, H. and Hopwood, D.A.
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                                                                             Denapaite, D., Eichner, A.,
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                led genetic and physical map A3(2) chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional beginner preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta o is given for CDS which show significant similarity to other CDS in the database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cosmid 4B10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation correct initiation codon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Colney, Norwich, Norfolk NR4 7UH, Notes:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cerdeno, A.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-AUG-2000) Streptomyces coelicolor sequencing project,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMPORTANT: This sequence MAY NOT be the entire insert of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The more significant matches with motifs in the PROSITE database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strand)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bases
                                                                                                                                                                                                                                                                                            coelicolor possible oxidoreductase SCF11.06, 277 aa; fasta scores: opt: 208 z-score: 258.9 E(): 5.9e-07; 25.5% identity in 243 aa overlap. Contains Pfam match to entry pF00561 abhydrolase, alpha/beta hydrolase fold"
                                                                                                                                                                                                                                                                                                                                                                                                                    /note="SC4B10.01, probable oxidoreductase, len: 2. similar to TR:09RK83 (EMBL:AL132662) Streptomyces
         DLVRTWAGGNGPVNAGYVWHPLARIWQDRVQGDRYMAELRAEPFAEEVAAGFDVPLHL
AREMASRVDEPMKDAVLRLYRSALTMGAEWEPELSAVSAPCVVFWGARDPACQIEFGR
                                                                     EAWDLPGFGAERPAGFGSTKEEYVDWLVRRLERVGEPVDLVGHDWGCILTLRVASLRP
                                                                                                                                 /product="putative oxidoreductase"
/protein_id="CAC04206.1"
/db_xref="GI:9885198"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="SC4B10.01"
173. .955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SC3A4"
                                                                                                                                                                                                                                       /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:100226"
/clone="cosmid 4B10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Streptomyces
/strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SC4B10.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="nominal overlap with Streptomyces coelicolor cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 to 40007)
                                                                                                      translation="MSPTARDLVPPTKGFTMPAILIHGVPDTHHVWDGVRRRLTRSDV/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to 40007)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coelicolor A3(2)*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             덖
                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 aa;
                                                                                                                                                                                                                                                           gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
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/note="SC4B10.05, possible RNA polymerase sigma factor, len: 292 aa; similar to TR:CABB9771 (EMBL:AL534616)
Streptomyces coelicolor putative RNA polymerase sigma factor SC3A4.25c, 300 aa; fasta scores: opt: 901 z-score: 941.4 E(): 0; 51.7% identity in 290 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="SC4B10.03c, conserved hypothetical protein, le 184 aa; similar to TR:CAB89770 (EMBL:AL354616) Streptomyces coelicolro hypothetical 191 kD protein SC3A4.24c, 178 aa; fasta scores: opt: 394 z-score: 4(E(): 5.4e-15; 55.5% identity in 182 aa overlap. Conticolled-coil region at approx. residues 18. .45"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLPEVVAGSVEARHAAVSLRRHLHRTRLIAGSVTEIRDSAHTATVRPQSGPEFDLHYD
ILVMTAGAVTRTFPIFGLSDQAYGLKHVEEAVAIRDRLLTSFDRAATLPHGPERRRLL
TATVVGGGFSGVEGFELLSLASALLKHY PEIGAEELAFHLVERAGRILDEVTDGPGE
WVVRSLEKRGARVHLNTQLVSAKDGRVVLSDGSEYDSELLWTAGNAANPIVHNHTDL
PVDARGLLMVRADLRVGTESEVVADWAAGDDASVPDLAAGRPDARTVPNAQHAVRGY
KLLAKNILASLRGRPAKDYVHHSLGVVATLGLGRGIFQYRRLVIKGFPAMLMHRGYHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(3200. .3499)
/gene="SC4B10.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3011. .3014)
complement(3200. .3499)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVQRALSALQALMPESVPPAPAARPADVVAEAPATVAPAPVPSADEAEDGVGDGDEDR
TEDASGAGDADGSKSYGKLTEQILAYFADAGNTDVRARDVASALGRDTDSGSINAVRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(2451. .3005)
/gene="SC4B10.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(2451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similar to SW:DHNA_ECOLI (EMBL:V00306) Escheri
NADH dehydrogenase (EC 1.6.99.3) Ndh, 433 aa;
scores: opt: 472 z-score: 552.4 E(): 2.7e-23;
identity in 377 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  approx, residues 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hydrophilic. Contains a possible approx, residues 41. .59"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLDRLVGQSRVRRVGRGLYRAAKR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="conserved hypothetical protein"
/protein_id="CAC04208.1"
/db_xref="G1:985200"
/translation="MVSVTPKARNIEITAEGLQEDLARLEIQKQALERELAAVTAHFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="
1052. .
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/protein_id="CAC04207.1"
/db_xref="GI:9885199"
/translation="MREILIYGGGYAGFYTAWGLEKKLRRDEARVTVVDPRPYMTYQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Pfam match to entry PF00561 abhydrolase, alpha/beta
hydrolase fold, score 27.70, E-value 7.8e-05"
                                                                                                                                                               'gene="SC4B10.05"
                                                                                                                                                                                                                                 /gene="SC4B10.05"
                                                                                                                                                                                                                                                                                                                          /translation="MSTVHEPTARAEEGRGMSRSTDRQTDPAAATASLAAEAALLEGR
LSLLREAIDSVDARIDAVSETLRRLQRPATGPTDGETPEERKRGTGPDRSKRGRA"
                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical
/protein_id="CAC04209...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SC4B10.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SC4B10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAIPSWERKARVFAVWVTAAFFGRDVISLASVQHPREAFVSSGDPRRGEKSADADAVA
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                   db_xref="GI:9885201"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="SC4B10.04c, unknown,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="SC4B10.02, probable dehydrogenase, len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .2407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2407
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                                                                                                                                                                                                                                                                                                                                                                                                                    9.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 aa. Highl
coiled-coil
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Contains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
mes 317; Conserv
                                                                                                                                                                                            TACCGGCTCTTCGCGCACGGACCGCACCTGACCG----CGAAGGCCATGGAGTGGTTCTGG
ATCTTTGCGGACCTTGAGAACCTACCTCCTGCGCTGATCATAACCGCCGAATACGACCCG
                                                                          AACGCCTACGCCCCGATCCGGCGGAGCGGGACCAGATCACGGCCTCGCCGCTGCGCGCCC
                                                                                                                                GAGCAGTACTTCTCCAGAGAGGAAGATAAGTTCAAGCCCCTCGCCTC------CGTA
                                                                                                                                                                                                                                                  CTTCTGGAGTTTGGAGAGGGGCTGTGGATTCTCGACCAGAAGATAATGAGTTGGTTCTCG
                                                                                                                                                                                                                                                                                                           ACCTTCCTGCACCAGTCCCTCTACTACCCCGTCACCGACGCCGGGCAGGACACCGAGAGC
                                                                                                                                                                                                                                                                                                                                                                 TTCATAAAGCATCAAATTCTAACTTACCCCGTTGTGAACTTTGTAGCCCCCACACCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                          TCCGTCGGCGGCAACATGAGCGCCGCCCCTCACCCACATGGCCCAAGCGGCGCGGTGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTGCGGGACGGAATCTTGCCCCCGGCGCTTTCAATAATGGCGAGAGACAGCGGAGAAGAT 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCTCCCCGGAGGCGAAGTACCCCGTCGCCATCGAGCAGGCCTACGCCACCGCGCAGTGG 33140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCGCTCCTGAGCACAAGTTTCCCCCCCCCAGTTTATCATTGCTACGATGCGACCAAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGTCTGGTGCGGGAGCTGGCCGTGGCCGGAGGCGGCCGTGGTCTTCGTCGAGTACGAC 33080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCTTATGCAGGAGAYYGCGAGACTTTCAAACTCTACCGTAGTCTCCGTGGATTACAGG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGGGTCTGGTTTACTATCACGGTGGTGGATTTGTGATTTGCAGCATCGAGTCGCACGAC 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCACCACCAAGGGCGCCGAGGAAGGCCTGGACGGCTCCCGCATGGTCGTCGCCGGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="SC4B10.06c, possible RNA polymerase sigma factor, len: 301 aa; similar to TR:Q9SIV5 (EMBL:ALI0950)
Streptomyces coelicolor putative sigma factor SCJ24.18c, 250 aa; fasta scores: opt: 877 z-score: 1049.7 E(): 0; 54.7% identity in 236 aa overlap and to Streptomyces coelicolor St4B10.13c, 298; fasta scores: opt: 1112 z-score: 1131.2 E(): 0; 57.3% identity in 288 aa overlap. Also contains a possible helix-turn-helix motif at residues 133. .154 (+3.38 SD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MAGDLSEAVSVFVELRPRLFGIAYRVLGSAVEAEDVVQEVWLRW
QRTDRTLVISPVAFLSSTTTRLAINVAQSARVRRETYIGPWLPEPVDTSNDPEVGAER
AEALELALLLVLQRLSPTERAAYVLREAFDYAYPDIARILGLSPVNVRKIVSRARKHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mepvydmpigellderrhlldvahwmlgsgivaehvideayre
wyalsehqrrigaprawltrygsislarlapspegdphepesbegsgasgpaleddl
dalwaealdaltpaeraltyllmealggabarpygtagpartbrepeldbarhs
lrvraarptppcvedalvdavrqacadedadrlatlihpdavafydgggkvrtltrpv
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complement/#PF?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative RNA polymerase sigma factor"
/protein_id="CAC04210.1"
/db_xref="GI:9885202"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative RNA polymerase sigma
/protein_id="CACO4211.1"
/db_xref="GI:9885203"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="SC4B10.06c"
/note="sc4B10.06c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VGGPRVARSLLTLLARHPRTTVHTRPVNGRTGLVARYDGQVAAVICLDLAGSRVVQVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
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1; Mismatches 322;
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AGTTGATTATCGTCTGGCCCAGAGGTCAAATACCCCGGCGCGATTGAAGACTGCTATGC
                                                                         AGAAGTGGATGACCCTAAATGCCAAAAGCTGGCCAGTGATCTAGGATTTCAGATTTTTTC
                                                                                                            CGAGTCGCACGACGCCTTATGCAGGAGAAYYGCGAGACTTTCAAACTCTACCGTAGTCTC
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                                                                                                                                                                                                                               168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cloning and Characterization of Ethanol-Regulated Acetobacter pasteurianus
J. Biosci. Bioeng. 87, 19-27 (1999)
2 (bases 1 to 1080)
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Acetobacter pasteurianus
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PTEVMYVPGAYHVEDMYVPDARLSRFWDAYCAALKRTLNL"
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CQKLASDLGFQIFSVDYRLAPEVKYPGAIEDCYAVLKMVHENASKLGISRDKVVVAGE
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

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US-09-739-449-208
US-09-270-849B-59602
US-09-270-849B-172488
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US-09-270-849B-1171
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US-09-270-849B-15736
US-60-248-505-429
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US-09-737-223-8281
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US-09-737-223-3652
US-09-737-223-4180
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                  Sequence
                                   e 429, App
e 202, App
e 299, App
e 488, App
e 1533, Ap
e 153762,
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e 1, Appli
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281, App

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US-09-270-849B-132036
; Sequence 132036, Application US
; GENERAL INFORMATION:
; APPLICANT: Swimmer et al.
; TITLE OF INVENTION: Insect get
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Sequence 4073, Ap	Sequence 94922, A	Sequence 435, App	Sequence 34244, A	Sequence 30708, A	Sequence 21924, A	Sequence 7076, Ap	Sequence 15456, A	Sequence 19827, A	Sequence 19894, A	Sequence 27, Appl	Sequence 22, Appl	Sequence 19, Appl	Sequence 21, Appl	Sequence 20, Appl	Sequence 43166, A	Sequence 23239, A	Sequence 486, App

ALIGNMENTS

genome survey devices

US/09270849E

Sequence 3652, Application US/09737223

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/737,223
CURRENT FILING DATE: 2000-12-13
PRIOR FILING DATE: 1909-06-04
NUMBER OF SEQ ID NOS: 38054 RESULT 2 US-09-737-223-3652 US-09-270-849B-132036 CURRENT APPLICATION NUMBER: US/09/270,849B CURRENT FILING DATE: 1999-03-17 NUMBER OF SEQ ID NOS: 195450 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 132036 LENGTH: 452 TYPE: DNA Best Local Similarity Query Match FEATURE: OTHER INFORMATION: ORGANISM: Artificial Sequence 421 GGCGCAGTCAAAGCCATC 438 224 gccgcgttacacaacgttaccttagcccgatttaactcgtggcagattgacccagtgctg 361 GGCGACACCTACCACTTAAACCGCGGCATATTTAACTCATCGCTGATTGACGAAGTAGTG 420 301 GCTGGCAGCACGCTTTTCGACAATGGGTTCGACACTTTTCGCCTTAATTTTCGCGATCAC 360 164 gatgcaagcaagttgggcgacgaaggctctgccactcggggagcgccatagcgctatatg 223 gccggaccataaccaagc 74; Conservative Description 3.5%; 53.6%; 0; Score 35.6; DB Pred. No. 0.41; of Artificial Sequence: Synthetic Mismatches DB 64; 5. Length 452; Indels 0 Gaps 283

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; ORGANISM: Homo sapiens
US-09-737-223-3652
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GENERAL INFORMATION:
APPLICANT: Hyseq, 1
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Best Local Similarity
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Best Local Similarity
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NAME/KEY: misc_feature
LOCATION: (1)...(421)
OTHER INFORMATION: n = A,T,C or
-09-737-223-4180
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218 caggagtcctccagaccctcaccc
                                                                           158 tgctggatttaggcagccccaactggccatgcactctatccgggagatggcctgcacca 217
                                                                                                                  521 AACAGCATCTCGCTAAACCGCTAGCGGGCGTGCTCGCCGTATGCCCGGTACTCGACCCCG
                                                                                                                                                                                 461 AGTATTGCCTGATGGGGTTCTCACTGGGTGGGGAACTTTGCCCTTGCGCGTGCGGGTGCGGG 520
                                                                                                                                                                                                                                                                401 CGCTGATTGACGAAGTAGTGGGCGCAGTCAAAGCCATCCAGCAGCAAACCGACTACGACA 460
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                                     581 CACACACCATGATGGCCCTAAACC 604
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                                                                                                                                                                                                                                                                                                                       0; Mismatches
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241
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBJ
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 2041-756
CURRENT APPLICATION NUMBER: US/09/737,223
CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 09/332,782
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8281
LENGTH: 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 17926
; TYPE: DNA
; ORGANISM: human
US-60-248-505-201
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; ORGANISM: Homo sapiens
US-09-737-223-8281
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                                                                                                                       Query Match
Best Local Similarity
Matches 97; Conserv
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Best Local Similarity 47.0
Matches 102; Conservative
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CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hyseq,
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                                                                               401 CGCTGATTGACGAAGTAGTGGGCGCAGTCAAAGCCATCCAGCAGCAAACCGACTACGACA 460
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                                     ccctgatccgagaggtggccaacaaaggcaaggtccccctgcaggatcccatggtacgga 122
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                                                                                                                         Conservative
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RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN
PROTEINS, AND USES THEREOF
                                                                                                                                          3.2%;
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47.0%;
                                                                                                                     0; Mismatches 107;
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                                                                                                                                          Score 32.8; DI
Pred. No. 2.7;
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                                                                                                                                                             DB 5;
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                                                                                                                                                             Length 365
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Length 187892;

Indels

0;

Gaps

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RESULT 6
US-09-739-449-3397/c
; Sequence 3397, Application US/09739449
; GENERAL INFORMATION:
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; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-3397
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                                                                                                           NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 208
LENGTH: 187892
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Best Local Similarity 46.5%;
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SEQ ID NO 3397
LENGTH: 780
                                                                                                                                                                                                                                                                                                                                                          Sequence 208, Application US/09739449 GENERAL INFORMATION:
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APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
                                                                                                                                                                                                                                                             APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(11490)C
                                                                 ORGANISM: Agrobacterium tumefaciens
                                              FEATURE:
                                                                                          TYPE: DNA
LOCATION: (1)..(187892)
                  NAME/KEY: unsure
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Pred. No. 3.3;
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; Sequence 57449, Application US/09270849B; GENERAL INFORMATION:
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APPLICANT: Swimmer et al.
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Best Local Similarity
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                  CURRENT APPLICATION NUMBER: US/09/270,849B
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
                                                                                                    APPLICANT: Swimmer et al.
TITLE OF INVENTION: Insect genome survey devices
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CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
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                                                                                        FILE REFERENCE:
SOFTWARE: PatentIn
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Pred. No. 1
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US-09-270-849B-172488
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US-60-281-593-226
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                                                                                       Sequence 172488, Application US/09270849B GENERAL INFORMATION:
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SOFTWARE: PERL Program
SEQ ID NO 226
LENGTH: 1835
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Best Local
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Best Local Similarity
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                                     APPLICANT: Swimmer et al.
TITLE OF INVENTION: Insect genome survey devices
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Amy Lasek
TITLE OF INVENTION: GENES EXPRESSED IN LUNG
FILE REFERENCE: PA-0045 P
CURRENT APPLICATION NUMBER: US/09/270,849B CURRENT FILING DATE: 1999-03-17
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OTHER INFORMATION: Incyte ID No: 569648CB1
-60-281-593-226
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ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                   309 CACGCTTTTCGACAATGGGTTCGACACTTTTCGC 342
                                                                                                                                                                                                                                                                    440 cagggtgcatcgaggctgcaagtcctgcaggcccaactcacctgggtccgcgtcagccat
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78; Conservative
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Pred. No. 3.7;
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US-09-270-849B-168048; Sequence 168048; Application US/09270849B; GENERAL INFORMATION:
APPLICANT: Swimmer et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-270-849B-54582
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CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 54582
LENGTH: 556
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APPLICANT: Swimmer et al
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SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 172488
LENGTH: 1899
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/270,849B
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 168048
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Best Local
                                                                                                          TITLE OF INVENTION: Insect genome survey devices
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Insect genome survey devices
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                                                                                                                                                                                                     920 agataccgtccaagcgtgtcgaatga
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Local Similarity 55.4%;
es 62; Conservative
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Pred. No. 5.2;
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Pred. No. 5
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RESULT 15
US-09-270-849B-12787/c
US-09-270-849B-12787, Application US/09270849B
Sequence 12787, Application US/09270849B
GENERAL INFORMATION:
APPLICANT: Swimmer et al.
TITLE OF INVENTION: Insect genome survey devices
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/270,849B
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
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US-09-270-849B-15171
Sequence 15171, Application US/09270849B
GENERAL INFORMATION:
APPLICANT: Swimmer et al.
TITLE OF INVENTION: Insect genome survey devices
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-849B-15171
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CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15171
LENGTH: 354
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 53.7%;
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Best Local Similarity 53.78;
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SOFTWARE: PatentIn Ver.
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Pred. No. 5.3;
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Matches 66
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                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                               LENGTH: 416
278 AGA 276
                               236 AGA 238
                                                              338 AATTGGACGCAGAGGTTAAACCCCTCGCCTGGTGGAATGGCATCCGTACGCAGGCCGCACA 279
                                                                                398 CACACAAGCGATACATCGTAAAAGCGTCTAAATGTAAACAGCGTTGCGTATGACGTAGATG 339
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les 66; Conserv
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Pred. No. 5.6;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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1017
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em_esthum27:*
em_esthum28:*
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em_esthum11:*
em_esthum12:*
em_esthum13:*
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em_estov1:*
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em_estro20:*
gb_est25:*
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em_esthum17:*
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em_estro10:*
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em_estro3:*
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em_esthum21:*
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em_esthum19:*
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gb_est27:*
gb_est28:*
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                                                            gb_est30:*
gb_est31:*
gb_est32:*
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                                                gb_est41:*
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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                        38
38
38
38
37
36
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Match
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9b_9ss26:**
9b_9ss26:**
9b_9ss28:**
9b_9ss28:**
9b_9ss31:**
9b_9ss31:**
9b_9ss31:**
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em_gss_pln2:
em_gss_prod1:
em_gss_rod1:
em_gss_rod4:
em_gs_rod4:
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      438
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      166
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17
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    110 AW100329
121 AW937427
121 AW937427
123 BE792596
129 CNS00100
117 AW613791
151 BF665915
1 AA038984
7 AA458955
7 AA458955
166 BE362704
166 BE362704
166 BE426503
168 AI128118
168 AI128158
167 BE490137
167 BE489166
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AW100329 sd23a12.y
AI213B92 gm35h01.x
AW937427 OV3-DUT004
BE792596 601585388
ALD688607 DYOSOPhil
AW613791 hh81f07.x
BF665915 602119071
AA038984 m196f10.r
AA038984 m196f10.r
AA458955 zx88ee06.s
BE1862704 DG1_88_E0
BE426503 WHE0318_H
AI128158 qc43a12.x
BE490137 WHE0365_A
BE490137 WHE0365_A
BE490137 WHE0315_H
BE425329 WHE313_B0
BE470901 WHE0261_D
BE470901 WHE0261_D
BE470901 WHE0260_G
AZ317931 1M0036010
                                                                                                                                                                                                                                                                                                                                                                                                          Description
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9b_est88:
9b_est99:
9b_est100:
9b_est100:
9b_est100:
9b_est103:
9b_est104:
9b_est106:
9b_est69:
9b_est70:
9b_est71:
9b_est71:
9b_est79:
9b_est71:

em_gss_hum8: *
em_gss_hum9: *
em_gss_inv1: *

em_gss_inv2:*
em_gss_inv3:*
em_gss_other:*

em_gss_hum4:*
em_gss_hum5:*
em_gss_hum6:*
em_gss_hum7:*

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RESULT 1
AW100329/c
                               FEATURES
                                                                                                                                                                                    COMMENT
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35.8
35.4
35.2
35.2
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                                                                      This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                Unpublished (1999)
Contact: Shoemaker R/Public Soybean
                                                                                                                                                                                                                                                                     Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J.,
                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.

1 (bases 1 to 438)
                                                                                                                                                Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                    Wylie,
                                                                                                                                                                                                                                                                                                                               Glycine max
                                                                                                                                                                                                                                                                                                                                                      EST
                                                                                                                  Email: est@watson.wustl.edu
                                                                                                                                                                       Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                    sequence.
                                                              info@genomesystems.com web site: www.genomesystems.com
                                                   primer: -40RP from Gibco
                                                                                                                             314 286 1800
314 286 1810
                             quality sequence stop: 415
Location/Qualifiers
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/organism="Glycine max"
/db_xref="taxon:3847"
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18 AI291019
9 AA557978
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AA558042
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59 Z81162
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AL061656 Drosophil
BG239945 OV1_31_A0
BE490185 WHE0366_D
AA477162 zu41c03.r
Z81162 SSC5C08 Por
AA459166 zx88e06.r
AI291019 qm09g08.x
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AI736695 sb3zd02.y
AW596158 si98f12.y
BF008863 ss70d03.y
AL520408 AL520408
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AA410639 zv33g05.s
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AA558042 nl18d12.s
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AA479662 zu41c03.s
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AI355102 qt97g03.x
T96433 ye49a06.rl
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KEYWORDS
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Matches 129;
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                                                                                                                                 JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 ACCACTTAAACCGCGGCATATTTAACTCATCGCTGATTGACGAAGTAGTGGGCGCAGTCA 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCTCTCCTTCAGACTCGCTATCGCCTATCATGGCGAAGGTAGGATGGGAGAGGG
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                                                                                  Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 391)
                                                                                                                                                                                                                                                                                                                                                                                                       qm35h01.x1 NCI_CGAP_Lu5
                                      Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                               AI215892.1 GI:3784933
                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
                    Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                     National Cancer Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
cDNA Library Preparation: M. Bento Soares,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepared using the Stratagene pBluescript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XL10-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolatifrom the appical shoots of 9 to 10 day old etiolated seedlings. The shoot tips including any emerged leaves were harvested for mRNA isolation. The cDNA library was
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seedlings"
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49.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                           mRNA EST 21-DEC-1998 Homo sapiens cDNA clone IMAGE:1883857 3',
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                                          Ph.D., Michael R.
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l (bases 1 to 496)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                 QV3-DT0043-090200-080-a04 DTC
                                                            Contact: Simpson A.J.G.
                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                   Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
  Rua Prof. Antonio Prudente 109,
                     Laboratory of Car
Ludwig Institute
                                                                                                                          sequence rags
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                       M.J., Soares, F., Brentani, R.R., Reis, L.F.,
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quality sequence stop: 377.
    Location/Qualifiers
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                                                                                                     Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-*Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           constructed by Bento Soares and M. Fatima Bonaldo.
137 c 103 g 89 t
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/clone="IMAGE:1883857"
/clone_11b="NCI_CGAP_Lu5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="carcinoid"
/lab_host="DH10B"
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  01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Primates; C.
1 (bases 1 to 667)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, J
Unpublished (1999)
               found through the I.M.A.G.E. Consortium/LLNL plate: LLCM788 row: p column: 21 High quality sequence stop: 667.
Location/Qualifiers
                                                                                                    Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
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601585388F1 NIH_MGC_7
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                                                                                                                                                                                                           Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue mRNA and cDNA amplification were performed under low stringency conditions."
104 c 158 g 95 t
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/db_xref="taxon:9606"
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Local Similarity 54.7%;
                                                                                                - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP's pland EST libraries. A more detailed description of the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://becom.med.puffalo.gen.de/Joroepac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                               at http://bacpac.med.buffalo.edu/drosophila_bac.htm
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                                                    Location/Qualifiers
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/cell_line="MGC3"
/organism="Drosophila melanogaster"
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/clone="IMAGE:3939716"
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                                                                                                                Genome Sequencing Center
Clone distribution: WCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40Up from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
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                                                                                                                                                                                                                                  Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D., cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University
                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
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                                                                                                                                                                                                                                                                                                               Robert_Strausberg@nih.gov
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/clone="BACR32D23"
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/clone_lib="NCI_CGAP_GU1"
/tissue_type="2 pooled hi
                                  /clone="IMAGE: 2969221"
                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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pooled high-grade transitional cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plate: LLCM1096 row: m column: High quality sequence stop: 664. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF665915 671 bp
602119071F1 NIH_MGC_56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL http://lmage.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                       /clone_lib="NIH_MGC_56"
/tissue_type="primitive neuroectoderm"
/lab_host="DH10B (TI phage-resistant)"
/lab_host="DH10B (TI phage-resistant)"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgttaggcc); Site_2: SfiI (ggccattatggcc);
SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAAAGGCCGAGCGCCCACATG-dT(30)BN-3'
(where B = A, C, Or G and N = A, C, G, Or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-*Torgan: genitourinary tract; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Technologies. Solution of the state of the 
full-length clones and was constructed by Clontech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:4276409"
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                             Fax: 314 200 10.10
Email: mouseest@vatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone ''-- ''-- ''-- 64 mage.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
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m196f10.rl Soares mouse p3NMF19.5 Mus musculus cDNA
IMAGE:474475 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1996)
Contact: Marra M/Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of MedicineP
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               double-stranded cDNA was size selected, ligated to Eco Ri adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by
                                                                                                                      Laboratories (Palo Alto, CA)."
a 207 c 188 g 164 t
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/clone="IMAGE:474475"
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                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA458955 393 bp mRNA EST 09-JUN-199
zx88e06.sl Soares ovary tumor NbHOT Homo sapiens cDNA clone
IMAGE:810850 3' similar to WP:F01F1.9 CE01235 VACUOLAR
                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
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/db_xref="GDB:6041656"
/db_xref="taxon:9606"
/clone="IMAGE:810850"
                                                                                                                                                           /sex="Female"
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                                                                                                                                                                                                                                           Seq primer: PolyTMix
High quality sequence
                                                                                                                                                                                                                                                                                                                                                       The University of Georgia Plant Sciences Building, I Tel: 706 542 1860 Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukāryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.

1 (bases 1 to 574)
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Sorghum bicolor
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DG1_88_E04.g1_A002
                                                                                                                                                                                                          High quality sequence POLYA=No.
                                                                                                                                                                                                                                                                                                  Sequences have been trimmed below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                      Email: mmpratt@uga.edu
Sequences have been tr
                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Botany
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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             /db_xref="taxon:4558" [ (DG1)" (Clone_lib="Dark Grown 1 (DG1)" (Clone_lib="Dark Grown 1 (DG1)" (DG1)" (Portor: /note="Organ: 5-day-old dark-grown seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision." a 189 c 175 g 100 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence have been trimmed to remove vector quality sequence with phred score less than Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE426503 260 bp mRNA EST 24-JUL-2000 WHE0318_H11_H112S Wheat unstressed seedling shoot cDNA library Triticum aestivum cDNA clone WHE0318_H11_H11, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE426503 260
WHE0318_H11_H11ZS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The structure and function of the expressed portion of the wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bread wheat
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76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          510559577
                                                                                                                                                     /lab_host="E. coli SOLK".
//otce="Vector: Lambda Uni-ZAP XR, excised phagemid;
//otce="Coor: Site_2: XhoI; Seeds were surface-sterilized
Site_1: EccRI; Site_2: XhoI; Seeds were surface-sterilized
, germinated and grown aseptically in the dark at room
temperature on filter paper with water, nystatin and
cefotaxime in covered crystallization dishes. Shoots were
harvested. The tissue, total RNA, and poly(A) RNA were
prepared, a cDNA library was made, and the CDNA clones
were in vivo excised to give pBluescript phagemids in the
TJ Close lab (Choi, Close, Fenton) at the University of
TJ Close lab (Choi, Close, Fenton) at the University of
                                                                                                                      California, Riverside. Plasmid DNA preparations and sequencing were performed in the OD Anderson lab (other authors)."
                                                                                                                 other authors)
                                                                                                                                                                                                                                                                                                                                                                                       /clone="WHE0318_H11_H11"
/clone=lib="Wheat unstressed seedling shoot cDNA library"
/tissue_type="Etiolated shoot"
/dev_stage="Five day old seedling"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cultivar="Chinese Spring"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Triticum aestivum"
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δõ

401 CGCTGATTGACGAAGTAGTGGGCGCAGTCAAAGCCATCCAGCAGCAAACCGACTACGACA 460

Matches Query Match Best Local

99;

Similarity 48.9 99; Conservative

48.5%;

Score 36; DB 1 Pred. No. 5.7; 0; Mismatches

DB 16; 5.7; 105;

Length 527; Indels

0,

Gaps

0

0;

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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTCTTCGTCACCGAGGGCACCATCCTGGCGGGCTTCATCAGCTCCTCCTCCAACACCG 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI128158 527 bp mRNA EST 9C43a12.x1 Soares_pregnant_uterus_NbHPU Homo sa IMAGE:1712350 3' similar to WP:F01F1.9 CE01235
                                                                                                                                                                                                                                                                                                                                                                              Email: Robert_Strausberg@nih.gov
This clone is available royalty free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length; 603 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                              rel: (301) 496-1550
Email: Robert 7
                                                                                                                                                                                                                                                                                                                                               Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMINOPEPTIDASE ;, mRNA sequence
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                120
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          went through one round of normalization. constructed by M. Fatima Bonaldo."
134 c 156 g 117 t
                                                              /note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I
oligo(dT) primer [5'
                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                        /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                            /sex="female"
                                                                                                                                                                                                                                         /clone_lib="Soares_pregnant_uterus_NbHPU"
                                                                                                                                                                                                                                                           /clone="IMAGE:1712350"
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
West Area, Western Regional, Research Center
West Area, Western Regional Research Center
West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West Area, West A
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The structure and function of the expressed portion of the wheat genomes - Cold-stressed seedling cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence with phred score less than Seq primer: Stratagene SK primer.
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Eukaryota; Viridi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
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Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
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                                              77
                                                                                                                                                                                                                                                                                            /tissue_type="Seedling"
/dev_stage="Five-day old seedling"
/lab_host="E. coll SOUR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized
/germinated and grown asseptically in the dark at room
temperature on filter paper with water, nystatin and
cefotaxime in covered crystallization dishes. Five-day
old seedlings were transferred to 5 C cold room and kept
for 48 hr. The tissue, total RNA, and poly(A) RNA were
prepared, a cDNA library was made, and the cDNA clones
                                          California, Riverside. P. sequencing were performed other authors)."
224 c 149 g 93 1
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/db_xref="taxon:4565"
/clone="WHE0365_A11_B21"
                                                                                                                         were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., H., P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wh genomes - Normalized shoot cDNA library
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: oandersn@pw.usda.gov
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                   dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Chol, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo
                                                                                                                     /tissue_type="Etiolated shoot"
/tissue_type="Etiolated shoot"
/dev_stage="five day old seedling"
/lab_host="E. coll DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water,
                                                                                                                                                                                                                                                                                   cDNA library"
                                                                                                            nystatin and
                                                                                                                                                                                                                                                                                                /cultivar="Chinese Spring"
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/clone="WHED1075_H12_023"
/clone_lib="Wheat unstressed seedling
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Location/Qualifiers
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give pBluescript phagemids before
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Pred. No. 5.8;
0; Mismatches
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normalization was carried out.

The mass excision of

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VERSION
KEYWORDS
SOURCE
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BE425329
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        535
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                                                                                                                                                                                                                                                                                                                                                                Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Triticum aestivum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae;
                                                                                                                                                                                                                                                         Email: oandersnepw.usda.gov
Sequence have been trimmed to remove vector
quality sequence with phred score less than
Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE425329 571 bp mRNA EST 24-JUL-2000 WHE313_B09_B092S Wheat unstressed seedling shoot cDNA library Triticum aestivum cDNA clone WHE313_B09_B09, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 571)
Anderson,O.D., Chao,S., Choi,D.W., Clc
,P.S., Hsia,C.C., Kang,Y., Lazo,G.R.,
Seaton,C.L. and Tong,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Triticum aestivum cDNA
BE425329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The structure and
                                                                                                                                                                                                                                                                                                                                                  Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bread wheat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares', Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                        /clone="WHE313_B09_B09"
/clone=11b="Wheat unstressed seedling shoot cDNA library"
/tlssue_type="Etiolated shoot"
/dev_stage="Five day old seedling"
/lab_host="E. coli SOLR"
                                                                                                                                                /cultivar="Chinese Spring"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                             organism="Triticum aestivum"
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Pred. No. 5.8;
0; Mismatches 105; Indels
Lambda Uni-ZAP XR, excised phagemid; Site_2: XhoI; Seeds were surface-sterilized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Close,T.J., Fe
R., Miller,R.,
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, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Shoots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

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BASE COUNT ORIGIN

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Best Local :
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                                                                                                                                                                                                                   254 TGCTGCACGGCTGGGAAGGCTCCAGCCAGTCGGCCTATGCGACCTCCGCTGGCAGCACGC
CCGGCCTGCAGATCACTGACTACG
                               CCATCCAGCAGCAAACCGACTACG 457
                                                                                  ACTTAAACCGCGGCATATTTAACTCATCGCTGATTGACGAAGTAGTGGGCGCAGTCAAAG 433
                                                                                                                                                       TTTTCGACAATGGGTTCGACACTTTTCGCCTTAATTTTCGCGATCACGGCGACACCTACC
                                                                                                                          TGTACACCAAGACGCTCTACAAGGGCGACATCATGGTGTTCCCCCAGGGCCTGCTACT 453
                                                             ACCAGTACAACGGCGGCGGCTCGGCAGCGGTGGCGCTCGTTGCGTTCAGCGGCCCCCAACC
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48.5%;
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                                                                                                                                                                                                                                                    Score 36; DB 166;
Pred. No. 5.8;
0; Mismatches 105;
537
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Search completed: June 2, 2001, 21:50:09 Job time: 28907 sec

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Title:
Perfect score:
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Maximum DB seq
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Maximum Match 100%
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1413.542 Million cell updates/sec
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: /cgn2_6/ptcdata/2/pna/US082_COMB.seq: *
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/cgn2_6/ptodata/2/pna/USO6_COMB.seq:*
/cgn2_6/ptodata/2/pna/USO7_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US081_COMB.seq:*
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44: /cgn2_6/ptodata/2/pna/US6012_COMB.seq:*
45: /cgn2_6/ptodata/2/pna/US6014_COMB.seq:*
46: /cgn2_6/ptodata/2/pna/US6014_COMB.seq:*
47: /cgn2_6/ptodata/2/pna/US6015_COMB.seq:*
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49: /cgn2_6/ptodata/2/pna/US6016_COMB.seq:*
50: /cgn2_6/ptodata/2/pna/US6019_COMB.seq:*
51: /cgn2_6/ptodata/2/pna/US6019_COMB.seq:*
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59: /cgn2_6/ptodata/2/pna/US6025_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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Score

Match

Length

Description

Query

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; MOLECULE TYPE: US-09-382-242-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30, Applicat GENERAL INFORMATION:
                                                                                                                                                                                                                                      Query Match 100.0%; Score 1017; Best Local Similarity 100.0%; Pred. No. 0; Matches 1017; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WAKKEN, ANDA APPLICANT: KOSMOTKA, ANDA APPLICANT INVENTION: ESTERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1017 NUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WORD PERFECT 6.0 CURRENT APPLICATION DATA:
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                181
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                                                                                                                                                                                                                                                                                                                                      LENGTH: 1017 NUCLEOTI
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/382,242 FILING DATE:
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REID, John
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APPLICANT: Bower, Stanley G. APPLICANT: Hinkle, Gregory J. TITLE OF INVENTION: 38-10(15804)C; FILE REFERENCE: 38-10(15804)C
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        PRIOR FILING DATE: 2000-02:
NUMBER OF SEQ ID NOS: 18992
SEQ ID NO 715
LENGTH: 20487
TYPE: DNA
ORGANISM: Xanthomonas campestris
                                                                                                                       FILE REFERENCE: 38-10(15804)C
CURRENT APPLICATION NUMBER: US/09/703,708
CURRENT FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/164
                                                                                             PRIOR APPLICATION NUMBER:
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FEATURE:
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; NAME/KEY: unsure; LOCATION: (1)..(20487); OTHER INFORMATION: unsure US-09-703-708-715
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US-60-164-320-715/c
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APPLICANT: Bower, Stanley G.
APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Xanthomonas campestris Genome
FILE REFERENCE: 38-10(15804)A
CURRENT APPLICATION NUMBER: US/60/164,320
CURRENT FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 18992
SEQ ID NO 715
LENGTH: 20487
                                                                                                                                                           Sequence 715, Application US/60164320 GENERAL INFORMATION:
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Best Local Similarity
Matches 349; Conserv
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Pred. No. 4e-28;
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US-60-183-791-715/c ; Sequence 715, Application US/60183791 ; GENERAL INFORMATION:
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CURRENT APPLICATION NÜMBER: US/60/183,791
CURRENT FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 18992
SEQ ID NO 715
LENGTH: 20487
TYPE: DNA
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Best Local Similarity
Matches 349; Conserv
                                                                                                      APPLICANT: Bower, Stanley G.
APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Xanthemonas campestris
FILE REFERENCE: 38-10(15804)B
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nilarity 48.9%;
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Pred. No. 4e-28;
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RESULT 5
US-09-703-708-8388
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                                                                                                                                                              GENERAL INFORMATION:
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Best Local Similarity
Matches 349; Conserv
PRIOR APPLICATION NUMBER: PRIOR FILING DATE: PRIOR APPLICATION NUMBER: PRIOR FILING DATE:
                                                            FILE REFERENCE: 38-10(15804)C
CURRENT APPLICATION NUMBER: US/09/703,708
CURRENT FILING DATE: 2000-11-02
                                                                                               APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Xant
FILE REFERENCE: 38-10(15
                                                                                                                                             APPLICANT:
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                            : US 60/164,320
1999-11-10
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Pred. No. 4e-28;
                  60/183,79
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; TYPE: DNA
; ORGANISM: Xanthomonas campestris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-60-164-320-8388
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LENGTH: 471
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APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Xanthomonas campestris Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15804)A
CURRENT APPLICATION NUMBER: US/60/164,320
CURRENT FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 18992
SEQ ID NO 8388
LENGTH: 471
TYPES NAS
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Best Local Similarity
Matches 193; Conserv
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Best Local Similarity
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                                                ccgcagttctacgattggtatttccgccgcaaatggcgtgaatcgctgctacgcaagcgc 120
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                                                                                  GCGTTTTTCTACGGCCGCTATTTTGCGCATAAATGGAAGCGCTCGTTAACCGCAAAACTT
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Pred. No. 4.6e-08;
0; Mismatches 217;
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RESULT 8
US-09-252-991A-10659/c
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; CURRENT FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 18992
; SEQ ID NO 8388
; LENCTH: 471
; TYPE: DNA
; ORGANISM: Xanthomonas campestris
US-60-183-791-8388
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Best Local :
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APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Xanthemonas campestris Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15804)
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Pred. No. 4.6e-08;
""matches 217;
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RESULT 9
US-09-252-991A-10414
, Sequence 10414, Application US/09252991A
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 10659
LENGTH: 2862
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LENGTH: 2910
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE:
                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1876 GATCGTTGCCGGGATGATCGTGTTCAACGCCGGCTTCATGGTGTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   432 AGCCATCCAGCAGCAAACCGACTACGACAAGTATTGCCTGATGGGGTTCTCACTGGGTGG 491
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                                          432 AGCCATCCAGCAGCAAACCGACTACGACAAGTATTGCCTGATGGGGTTCTCACTGGGTGG 491
                                                                                                                              372 CCACTTAAACCGCGGCATATTTAACTCATCGCTGATTGACGAAGTAGTGGGCGCAGTCAA 431
cgccttcacccagcaactctggttcagctggctgatctacctgctggtgatcctcagttc
                                                                                   ccgcctgaaccgcctcctgcaaggcgaggcgctgttgatcctggcggtcggcgatcat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGCCTGAACCGCCTCCTGCAAGGCGAGGCGCTGTTGATCCTGGCGGTCGGCGCGGTCAT 1997
                                                                                                                                                                           110;
                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS ON: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS 107196.136
                                                                                                                                                                                             3.9%;
48.2%;
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BER: US_60/074,788
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Pred. No. 1.5;
                                                                                                                                                                                             Score 39.2; D
Pred. No. 1.6;
                                                                                                                                                                         Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 118;
                                                                                                                                                                                                                    DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16;
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US-09-726-791-461; Sequence 461, Applic; GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 10504
LENGTH: 3111
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10504, Application US/09252991A GENERAL INFORMATION:
                                                                                     SEQ ID NO 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                 APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: MOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2009-001
CURRENT APPLICATION NUMBER: US/09/726,791
CURRENT FILING DATE: 2000-11-30
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                                                                                                         PRIOR APPLICATION NUMBER: 60/168,127
PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 1870
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR ETILING DATE: 1998-U2-10
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR AFFILING DATE: 1998-07-27
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                        ORGANISM: Homo sapiens
                                                 TYPE: DNA
    FEATURE:
                                                                   ENGTH: 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1236 gctcagcgtcccgctgatcgcggcctggcactggtatcgcggctaccagccggcgcgcct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1116 ccgcctgaaccgcctcctgcaaggcgaggcgctgttgatcctggcggtcggcgcgatcat 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1296 gatcgttgccgggatgatcgtgttcaacgccggcttcatggtgttcct 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1176 cgccttcacccagcaactctggttcagctggctgatctacctgctggtgatcctcagttc 1235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 48.2%; Pred. No. 1.6; Length 3111; res 110; Conservative 0. M. 1.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCCATCCAGCAGCAAACCGACTACGACAAGTATTGCCTGATGGGGTTCTCACTGGGTGG 491
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                                                                                                                                                                                                                                                                                                                                                                          Application US/09726791
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; LOCATION: (1)...(329)
; OTHER INFORMATION: n =
US-09-248-797-20977
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US-09-248-797-20977
; Sequence 20977, Appl
; GENERAL INFORMATION:
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; LOCATION: (1)...(466)
; OTHER INFORMATION: n =
US-09-726-791-461
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US-09-346-956-7430
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Best Local Similarity
""" hes 76; Conserva
                 Sequence 7430, Application US/09346956
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARAIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-758CON1
CURRENT APPLICATION NUMBER: US/09/346,956
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CURRENT FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 48909
SOFTWARE: FastSEQ for Windows Version 3.9
SEQ ID NO 20977
LENGTH: 329
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
CURRENT FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                  123 GAGCTACCTCAGCACTGCC 141
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                                                                                                                                                                                                                                                                                                                                                 197 agcccctgccattgtagcgtctttctttttttggccatctgctccttggatctccctgagat
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                                                                                                                                                                                                                                                              257 gggcttcccaagggctgcc 275
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Local Similarity 54.7%;
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  1999-07-02
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54.7%;
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 Mismatches

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Indels Length 329;

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Gaps

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270 agcccctgccattgtagcgtctttcttttttggccatctgctcctggatctccctgagat 329
                                                                            210 gcctgctattggccgaaccanaaccaattattttcatccttgtcttattcccttcctgcc 269
                                       GCCAGCTAATGACTCACCCACGATCGACTTTAATCCTCGCGGCATTCTTCGCAACGCTCA 62
                                                                                                                                                           63;
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                                                                                                                                                                                                  Length
                                                                                                                                                           0;
                                                                                                                                                         Gaps
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; LENGTH: 329
; TYPE: DNA
; ORGANISM: Homo sapiens
; PEATURE:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(329)
; OTHER INFORMATION: n = A,T,C o:
US-09-346-956-7430
                    RESULT 15
US-09-652-355-9114
: Sequence 9114, Application US/09652355
: GENERAL INFORMATION:
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-248-797-22826
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Best Local S
Matches 76
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-764
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.8%;
Best Local Similarity 54.7%;
Matches 76; Conservative
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CURRENT FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 48909
    APPLICANT:
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Shyjan, Andrew W.
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SEQ ID NO 9114
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CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,136
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 11227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 1600.1192-001
                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (1)...(1660)
OTHER INFORMATION: n = A,T,C
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                               Score
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1250.617 Million cell updates/sec
                    Human Fchd540 gene
S. lavendulae MitS
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Complete nucleotid
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J, Ro 1997-4 DB; W23		FEB-1996;	FEB-1997;	AUG-1997.	WO9730160-A1.	Teredinibacter sp.	<pre>rrase; thermostable enzyme; ester; chiral compound; ; paper; lignin removal; sugar; lignocellulose; ase resistance; feedstuff; ss.</pre>	encoding Teredinibacter esterase 42L.	FEB-1998 (first entry)	28;	1 28 standard;		₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩	2
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PTX

Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in cheese

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paper manufacture, and to study plant resistance to disease

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amplified from a paluescript vector by PCR (See T79314-16).
Claimed, newly identified polynucleotides (T79321-30) encoding cesterases (W23069-77, W23088) were recovered from genomic libraries. They can be used for recombinant production of the enzymes in host cells, and as probes to identify related sequences. The esterases care stable at high temperature and in organic solvents, making them superior for use in production of pure chiral compounds used in ceptacial, agricultural and other chemical industries. A competitor for use in production of pure chiral compounds used in machined is claimed for transferring an amino group from an amino certain compounds used in selful as ripening starters in cheese making, in lignin cremoval in paper and pulp manufacture, in carbohydrate derivative contents, in the study of plant wall structure, plant resistance to contents. The study of plant wall structure, plant resistance to contents and organic matter decomposition and to select plants bred contents.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1017 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1017;
Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG
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The patent discloses methods for the treatment and diagnosis of cardiovascular diseases by novel human genes which are differentially expressed in different cardiovascular disease states. Compositions who

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                                                            Identifying s
                                                                                                                                                                                                                                                                                                                                               diabetic retinopathy;
TGF-beta signalling pa
pancreatic cancer; and
                                                                                              WPI; 2000-205414/18
P-PSDB; Y45014.
                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z50708
                                                                                                                                                                                             30-JUL-1999;
                                                                                                                                                   (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                        30-JUL-1998;
                                                                                                                                                                                                                                       WO200006206-A1
                                                                                                                                                                                                                                                                                                                                     vascularisation;
                                                                                                                                                                                                                                                                                                                                                                                fchd540
                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of human fchd540 gene
                                                                                                                                                                                                                  10-FEB-2000
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                                                                                                                                                                                                                                                                                                                sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                              gene; human; cardiovascular disease; oncogenic disorder; cretinopathy; fibroproliferative disorder; artherosclerosis; a signalling pathway; TGF; Transforming growth factor; a signaling pathway; TGF; Transforming growth factor; tic cancer; anglogenesis; inflammation; fibrosis; tumour grow
                                        Fig
                                                             substances for ameliorating symptoms oncogenic related disorders -
                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                        98US-0126640
                                                                                                                                                                                             99WO-US17394
                                       214pp; English
                                                                                                                                                                                                                                                                                 Location/Qualifiers 288..1568
                                                                                                                                                                                                                                                            /product= "fchd540 protein"
                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                     cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                     antidiabetic; opthalmological;
                                                                         of fibroproliferative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cc can modify TGF-beta signalling pathway are identified by screening.

Cc These are used therapeutically to treat fibroproliferative and oncogenic disorders, especially TGF (Transforming growth factor)-beta related concer, angiogenesis, inflammation, fibrosis, tumour growth and concer, angiogenesis, inflammation, fibrosis, tumour growth and concer, angiogenesis, inflammation, fibrosis, tumour growth and considered in endothelial cells subjected to laminar shear stress, can be used to design cardiovascular disease treatment strategies. Both fields to design cardiovascular disease treatment strategies. Both cf cdh540 and rchd534 are specifically expressed in vascular tissue.

Cc Interaction of the two proteins inhibits TGF-beta signalling.

Cc overexpression of fcdh540 expression constructs in pancreatic cells results in complete loss of TGF-beta response. Depending on whether the cc can be designed to increase or decrease the activity of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                               shear stress; cardiovascular disease; atherosclerosis; ischaemia; reperfusion; hypertension; restenosis; arterial inflammation;
             P-PSDB; W36003
                            WPI; 1997-424966/39
                                                                                                                                                                      14-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                              Fchd540 gene; differential expression; endothelial cell; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Fchd540 gene differentially regulated in endothelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T94468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T94468 standard; cDNA; 3105
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                                                           Falb DA;
                                                                                         (MILL-) MILLENNIUM PHARM INC
                                                                                                                         13-FEB-1997;
16-FEB-1996;
                                                                                                                                                                                                     21-AUG-1997.
                                                                                                                                                                                                                                      WO9730065-A1
                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                 therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2268 agcccctgccattgtagcgtctttcttttttggccatctgctcctggatctccctgagat 2327
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                                                                                                                         97US-0799910.
96US-0011787.
                                                                                                                                                                       97WO-US02291.
                                                                                                                                                                                                                                                                   Location/Qualifiers
289..1569
/*tag= a
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54.7%;
                                                                                                                                                                                                                                                                                                                                                                drug screening; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 874 G; 713 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
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12-MAR-1999;

99US-0266965

10-MAR-2000; 2000WO-US06394.

14-SEP-2000. WO200053737-A2 Streptomyces lavendulae

fungicide;

pesticide;

ds.

anti-inflammatory; immune-enhancer; immunosuppressant; asthma; chronic obstructive pulmonary disease; respiratory inflammation;

Mitomycin; biosynthesis; mitosane ring system; antibiotic; anti-cancer;

S. lavendulae MitS encoding DNA sequence.

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RESULT
C55796,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atherosclerosis, ischaemia/teperfusion, hypertension and restenosis. Methods are provided for the diagnosis, monitoring in clinical trials, screening for therapeutically effective compounds, and treatment of cardiovascular diseases based on discoveries regarding the expression patterns of novel genes fchd531, fchd540, fchd545, fchd602 (see T94470) and fchd605 (see T96711). Antisense oligonucleotides (see T94486-93) and ribozymes (see T94497-99) have been designed to inhibit expression of the fchd540 gene. The gene, deposited as ATCC 69984, encodes a novel intracellular protein (see W36003) that interacts with the rchd534 gene product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endothelial cells subjected to fluid shear stress in vitro. Shear stress is thought to be responsible for the prevelence of atherosclerotic lesions in areas of unusual circulatory flow. Also identified were novel genes fchd531 (see T94467), which is down-regulated in endothelial cells under turbulent and laminar shear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stress, and fchd545 (see T94469), which is down-regulated in endothelial cells under laminar shear stress. These genes provide fingerprint for the study of cardiovascular diseases, including
                                                                                                                                                                                                                                                                                                                                                   C55796 standard;
                                                                                                                                                                                                                                                                                 19-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3105 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fchd540 is a novel human gene that is up-regulated in endothelial cells subjected to laminar shear stress. Differential display wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease, e.g. atherosclerosis, restenosis, hypertension, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New genes differentially expressed in cardiovascular disease for diagnosis, drug screening and treatment of cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agcccctgccattgtagcgtctttcttttttggccatctgctcctggatctccctgagat 2328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcctgctagtggccgaaccagaaccaattattttcatccttgtcttattcccttcctgcc 2268
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54.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     874 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     713 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 18;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                C55857;
                                                                                                                                                           C55857 standard; DNA; 18331 BP
                       Complete nucleotide sequence of the mitomycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acid molecule comprising mitomycin biosynthetic gene cluster useful for cloning mitomycin biosynthetic genes for elucidating the molecular basis of mitosane ring system biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MINU )
(SHER/)
(MAOY/)
                                                                 19-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 948 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SHEL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HEMM/)
                                                                                                                                                                                                                                                                                                                                                                   131
                                                                                                                                                                                                                                                                                                                                                                                                             548
                                                                                                                                                                                                                                                                                                                                                                                                                                                          191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (VARO/)
                                                                                                                                                                                                                                                                            71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the cloning of the mitomycin biosynthetic genes.
                                                                                                                                                                                                        ហ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGGGAACTTTGCCTTGCGCGTCGCGGTGCGGGAACAGCATCTCGCTAAACCGCTAGCGG 547
                                                                                                                                                                                                                                                                            GTGACGTCGCCGGCGGCGG
                                                                                                                                                                                                                                                                                                                    GTGCGTTTTTCTACGGCCG
                                                                                                                                                                                                                                                                                                                                                                GCGTGCTCGCCGTATGCCCGGTACTCGACCCCGCACACACCATGATGGCCCCTAAACCGAG 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGCGGACCGTCCCGGCCGCGTCGCAGATCGCCGGCGATGGCCACGCCGACCCCGGCGAGG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to isolated and purified nucleic acid the mitomycin biosynthetic gene cluster. Mitomycins are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-601980/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.4%;
Similarity 53.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e mitomycin biosynthetic gene cluster. Mitomycins are a group of products that contain a variety of functional groups, including enzoquinone and axiridine ring systems. The S. lavendulae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNIV MINNESOTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHELDON P C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHERMAN D H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAROGLU M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAO Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               мао У,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 A; 344 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Varoglu M,
                                                                                                                                                                                                                                                                         53
                                                                                                                                                                                                                                                                                                                    626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 21
Pred. No. 0.47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           383 G; 127 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 He M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length 948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sheldon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65;
                     gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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δÃ 뫄 ş 밁 Ş

608 GTGCGTTTTTCTACGGCCG

13374

GGGTCCTCGCCGTGTCCCAGAAGACCGCGCGACCCGCGCGGCGAGCAGGTCCAGATCCGCG 13315

GCGTGCTCGCCGTATGCCCGGTACTCGACCCCCGCACACCACCATGATGGCCCCTAAACCGAG GTGCGGACCGTCCCGGCCGCGTCGCAGATCGCGGGCATGGCCACGCCGACCCCGGCGAGG

607 13375 Query Match Best Local S Matches 74

Local Similarity

3.4%;

Score 35; DB 2 Pred. No. 2.2; 0; Mismatches

21; 65;

Length 18331; Indels

0

Gaps

0

74;

Conservative

0;

13434

488

GTGGGAACTTTGCCTTGCGCGTCGCGGTGCGGGAACAGCATCTCGCTAAACCGCTAGCGG

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amino benzoquinone and axiridine ring systems. The S. lavendulae micomychn biosynthetic gene cluster comprises 47 mitomych genes spanning CC 55kb of DNA. The invention includes an expression cassette comprising a micomych biosynthetic gene operably linked to a promoter, and host cells CC transformed with the cassette. The nucleotide, and protein sequences and the transformed host cells of the invention result in antiasthmatic, antiinflammatory, cytostatic, immunomodulatory, and antibiotic cativitles. The nucleotide sequences are used to elucidate the molecular CC activitles. The nucleotide sequences are used to elucidate the molecular compines for the biosynthesis of novel natural products, e.g. antibiotics, anti-inflammatory agents, anti-cancer agents, immune-enhancers, cimmunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other disease involving respiratory inflammation, or cholesterol-lowering agents or a crop protection agents (e.g. fungicides or insecticides) as well as bipolymers, e.g., in packaging or biomedical applications, or to engineer pHA monomer synthases. Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from the mitomycin biosynthetic gene cluster. Mitomycins are a ginatural products that contain a variety of functional groups, incamino benzoquinone and axiridine ring systems. The S. lavendulae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid molecule comprising mitomycin biosynthetic gene cluster useful for cloning mitomycin biosynthetic genes for elucidating the molecular basis of mitosane ring system biosynthesis -
Sequence 18331 BP;
                                                                biosynthetic gene cluster DNA sequences and encoded proteins. C55812-C55814, C55850-C55856 and C55862-C55869 represent PCR p in the cloning of the mitomycin biosynthetic genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Figure 21; 399pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-601980/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sherman DH, Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces lavendulae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fungicide; pesticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chronic obstructive pulmonary disease; respiratory inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitomycin; biosynthesis; mitosane ring system; antibiotic;
anti-inflammatory; immune-enhancer; immunosuppressant; asti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SHEL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SHER/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MINU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (VARO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to isolated and purified nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNIV MINNESOTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHELDON P C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAO Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAROGLU M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHERMAN D H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000WO-US06394.
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2523 A; 7003 C; 6343 G; 2462 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Varoglu M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 He
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sheldon
   0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-cancer;
                                                                                                         primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecules
                                                                                                                                               Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        group of
                                                                                                             used
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B

13314 GTGACGTCGCCGGCGGCGG 13296

Best Local Similarity Matches 74; Conserv

Conservative

0;

Pred. No. 3.8; 0; Mismatches

65;

Indels

0;

Gaps

0

53.2%;

Qy В δÃ

548

1285

GTGCGGACCGTCCCGGCCGCGTCGCAGATCGCGGGCATGGCCACGCCGACCCCGGCGAGG GTGGGAACTTTGCCTTGCGCGTCGCGGTGCGGGAACAGCATCTCGCTAAACCGCTAGCGG

1226 607

547

GCGTGCTCGCCGTATGCCCGGTACTCGACCCCGCACACCATGATGGCCCTAAACCGAG

488

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RESULT
C55842/c
  CC from the milcomycin biosynthetic gene cluster Mitomycins are a group of CC mitomycin biosynthetic gene cluster Comprises 47 mitomycin biosynthetic gene cluster comprises 47 mitomycin biosynthetic gene cluster comprises 47 mitomycin genes spanning CC mitomycin biosynthetic gene cluster comprises 47 mitomycin genes spanning CC fish of DNA. The invention includes an expression cassette comprising a CC mitomycin biosynthetic gene operably linked to a promoter, and host cells CC transformed with the cassette. The nucleotide, and protein sequences and CC antiinflammatory, cytostatic, immunomodulatory, and antibiotic activities. The nucleotide sequences are used to elucidate the molecular basis for the biosynthesis of the mitosane ring system, as well as to cengineer the biosynthesis of novel natural products, e.g. antibiotics, and infilammatory agents of novel natural products, e.g. antibiotics, and infilammatory agents to treat asthma, chronic obstructive pulmonary disease as well as other disease involving respiratory inflammation, or cholesterol-lowering agents or as crop protection agents (e.g. fungicides or insecticides) as well as bipolymers, e.g., in packaging or biomedical applications, or to engineer PNA monomer synthases. Sequences CC 55782-C55814, C55815-C55849 and 832485-B3242 represent mitomycin biosynthetic gene cluster DNA sequences and encoded proteins. Sequences (c. 55812-C55814, C55850-C55865 and C55862-C55869 represent PCR primers used (c. 55812-C55814) and c55863-C55869 represent PCR primers used (c. 55812-C55814).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acid molecule comprising mitomycin biosynthetic gene cluster useful for cloning mitomycin biosynthetic genes for elucidating the molecular basis of mitosane ring system biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitomycin; biosynthesis; mitosane ring system; antibiotic; anti-cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C55842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C55842 standard; DNA; 53500 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to isolated and purified nucleic acid molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Figure 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAR-2000; 2000WO-US06394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200053737-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces lavendulae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anti-inflammatory; immune-enhancer; immunosuppressant; asthma; chronic obstructive pulmonary disease; respiratory inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JAN-2001 (first entry)
Sequence 53500
                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHEL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MAOY/) MAO Y.
(VARO/) VAROGLU M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MINU ) UNIV MINNESOTA. (SHER/) SHERMAN D H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEMM/)
                                            the cloning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HE M.
SHELDON P C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pesticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0266965
                                          the mitomycin biosynthetic
7481 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Varoglu M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               399pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the mitomycin biosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            He M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sheldon PC;
                                          genes.
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Query Match

ω

. 48;

Score

35;

DB

21;

Length 53500

Sequence 697 BP;

180

A.

201 C;

162 G;

154 T; 0 other;

BP;

19740 C;

19126

G;

7153 T; 0 other;

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RESULT X7068/7 (1) X270 (1) X270 (1) X270 (1) X270 (1) X270 (1) X2 XX (1) XX (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                   autoimmune diseases (e.g. rheumatoid arthritis, psoriasis, multiple sclerosis, systemic lupus erythematosus, type I diabetes, allergy) or viral, bacterial or parasitic infections (e.g. human immune deficiency virus, Helicobacter pylori, Porphyromonas gingivalis, or Candida albicans). A panel of cells (or cell lines) each genetically modified to express different antigens can be maintained as a repository, for treatment or prevention of the appropriate tumour type, e.g. based on histological analysis. Membrane-bound (I) provides a vaccine with increased receptor-cytokine avidity, and thus stimulates a stronger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric - Mus sp.
Chimeric - Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                   linked to a heterologous membrane attachment domain. The vaccines are used to treat or prevent a wide variety of cancers (e.g. of colon, breast or prostate, melanoma, glioma), alone or as adjunct to other therapies;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to a vaccine comprising a cell having a membrane-bound fusion protein (FP) consisting of a non-antibody immunomodulator (I) linked to a heterologous membrane attachment domain. The vaccines are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine having a membrane-bound fusion protein - comprising an immunomodulator and heterologous membrane attachment domain use for modulation of immune response against a disease-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAY-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence encodes the pHOOK-1.GM-CSF fusion protein. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 2a-b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMU-) IMMUNE RESPONSE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane-bound
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0902516.
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Best Local
                                                                                          Alternatively the effect of a candidate agonist or antagonist compound on the production of mRNA encoding METPRO02 may be detected using an ELISA assay. Diseases or conditions arising from altered expression or activity of METPRO02 may be diagnosed by detecting METPRO02 in a sample from a patient or detecting a mutation in the nucleotide encoding METPRO02 in the genome of a patient. These diseases or conditions include cancers, asthma, Parkinson's disease, Alzheimer's disease, and appears of the patient of the 
                                                                                                                                                                                                                                                                                 The present sequence encodes human aminopeptidase METPRO02. METPRO02 may be used to screen for its agonists or antagonists by contacting METPRO02 with the candidate compound and detecting any alteration in activity of METPRO02 or in a label attached to the candidate.
                     depression, diabetes, hypertension, stroke, respiratory diseases and inflammatory disorders. Detection of the nucleotide sequence may be used for chromosome mapping and tissue localization. METPRO02 and its
     nucleotide sequence may
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 13; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human aminopeptidases useful for thrombosis, diabetes and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burgess N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM PLC
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09-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METPRO02; therapy; diagnosis; aminopeptidase; cancer; asthma; Parkinson's disease; Alzheimer's disease; depression; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human aminopeptidase METPRO02 encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .Chapman
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98GB-0002824.
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/note= "amino"
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  be administered to patents as
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1434
                                                                                                                                                                                                                                                                                                  21-APR-1998;
09-FEB-1998;
                         New human aminopeptidases useful for diagnosing and treating thrombosis, diabetes and cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human aminopeptidase METPRO02 nucleotide sequence derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X90599 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1637 BP; 348 A; 486 C; 463 G;
                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM PLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACACACCATGATGGCCCTAAACC 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACAGCATCTCGCCTAAAACCGCTAGCGGGGCGTGCTCGCCGGTATGCCCCGGTACTCGACCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atgacaccccctgtggaaccaccattggacctatcttggcttctcggctggggctgcggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ccctgatccgagaggtggccaacaagtcaaggtccccctgcaggatctcatggtccgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCTGATTGACGAAGTAGTGGGCGCAGTCAAAGCCATCCAGCAGCAAACCGACTACGACA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgctggatttaggcagccccaactggccatgcactctatccgggagatggcctgcacca
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                                                                                                                                                                                       Chapman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stroke;
                                                                                                                                                                                                                                                                                                    98GB-0008478.
98GB-0002824.
                                                                                                                                                                                                                                                                                                                                                                                   98EP-0203211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 230..1606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_except= (pos:494..496,aa:Xaa)
/transl_except= (pos:887..889,aa:Xaa)
/note= "Xaa= unspecified; no stop cod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "METPRO02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cdna;
                                                                                                                                                                                       Ç
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    respiratory disease; inflammatory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34.4; DB Pred. No. 0.97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         340 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              no stop codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; asthma;
ression; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METPRO02 with the candidate compound and detecting any alteration
in activity of METPRO02 or in a label attached to the candidate.
Alternatively the effect of a candidate agonist or antagonist compound
on the production of mRNA encoding METPRO02 may be detected using an
ELISA assay. Diseases or conditions arising from altered expression or
activity of METPRO02 may be diagnosed by detecting METPRO02 in a sample
from a patient or detecting a mutation in the nucleotide encoding
METPRO02 in the genome of a patient. These diseases or conditions
conclude cancers, asthma, parkinson's disease, Alzheimer's disease,
depression, diabetes, hypertension, stroke, respiratory diseases and
inflammatory disorders. Detection of the nucleotide sequence may be
used for chromosome mapping and tissue localization. METPRO02 and its
nucleotide sequence may be administered to patents as vaccines or as
part of a gene therapy regime respectively, to treat the diseases and
conditions listed above. Antibodies against METPRO02 may be used to
isolate or identify clones expressing METPRO02 or to purify METPRO02 by
affinity chromatography. METPRO02 may also be used to identify molecules
which interact with it in or on the surface of cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.4%;
Best Local Similarity 48.0%;
Matches 98; Conservative
                                                                                                                                                                              BLM gene cluster; bleomycin gene cluster; polyketide metabolite; bleomycin; bleomycin analogue; holo-carrier protein; thiazolidine; thiazoline; microbial metabolite; sugar; ss.
                                                CDS
                                                                                                         CDS
                                                                                                                                                     Streptomyces verticillus
                                                                                                                                                                                                                                                                           31-OCT-2000
                                                                                                                                                                                                                                                                                                                                   A58471 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                             1536 caggagtcctccagaccctcaccc 1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1476 tgctggatttaggcagccccaactggccatgcactctatccgggagatggcctgcacca 1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1416 atgacacccctgtggaaccaccattggacctatcttggcttctcggctggggctgcggg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from EST (expre
                                                                                                                                                                                                                                         Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 8-30
                                                                                                                                                                                                                                                                                                        A58471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2019 BP; 417 A; 589 C; 571 G; 436 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 18; Page 13-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 CGCTGATTGACGAAGTAGTGGGCGCAGTCAAAGCCATCCAGCAGCAAACCGACTACGACA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  461 AGTATTGCCTGATGGGGTTCTCACTGGGTGGGAACTTTGCCTTGCGCGTGCGGGTGCGGG 520
                                                                                                                                                                                                                                                                                                                                                                                                                                         581 CACACCATGATGGCCCTAAACC 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    521 AACAGCATCTCGCTAAACCGCTAGCGGGCGTGCTCGCCGTATGCCCGGTACTCGACCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence encodes human aminopeptidase METPRO02 do m EST (expressed sequence tag) sequences. METPRO02 may be d to screen for its agonists or antagonists by contacting
                                                                                                                                                                                                                                                                         (first entry)
                                             /transl_except=
/note= "ORF 30; of 561..2309
   /transl_except=
/note= "ORF 29;
                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34.4;
Pred. No. 1
   (pos: 1..3, aa: Met)
encodes B07557"
                                                            (pos: 1..3, aa: Met) encodes B07556"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 20; Length 2019;
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/transl_except=
/note= "ORF 14;
52383..52946
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/note= "ORF 18;
39301..47181
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/note= "ORF 26; (
12291..15491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= d
/transl_except=
/note= "ORF 27;
5806..12294
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/note= "ORF
3527..5593
                                                                                                                                                  /note= "ORF 11;
55821..56093
                               57583..58857
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/note= "ORF 24;
21010..24666
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 'note=
                                           /transl_except=
/note= "ORF 9; e
                                                                                                     /transl_except=
/note= "ORF 10;
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/note= "ORF 15;
                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_except=
/note= "ORF 16;
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/note= "ORF 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                           note= "ORF 12;
                                                                                                                                                                                                                                                                                                                                                                                                            9982..51001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "ORF 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transl_except=
note= "ORF 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5818..37302
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note= "ORF 20;
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                                                                                        6090..57586
                                                                                                                                                                                                                                                       note= "ORF 13;
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"ORF 8; encodes B07578"
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                                             = (pos: 1..3, aa: Met)
encodes B07577"
                                                                                                     (pos: 1..3, aa: Met) encodes 807576"
                                                                                                                                                                 encodes B07575"
                                                                                                                                                                                                                                                                                                 (pos: 1..3, aa: Met) encodes B07572"
                                                                                                                                                                                                             encodes B07574"
                                                                                                                                                                                                                                                       encodes B07573"
                                                                                                                                                                                                                                                                                                                                                             (pos: 1..3, aa: Met)
encodes B07571"
                                                                                                                                                                                                                                                                                                                                                                                                                          (pos: 1..3, aa: Met) encodes B07570"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encodes B07569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (pos: 1..3, aa: Met) encodes B07568"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (pos: 1..3, aa: Met) encodes B07567"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (pos: 1..3, aa: Met) encodes B07566"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (pos: 1..3, aa: Met)
encodes B07559"
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RESULT 11
Q25975/c
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Best Local
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                                                                                                                                                                              57121
                                                       57241 gctcgtcgtcggcgtcaactccgacgcgagcgtccgacgcctcaaggg 57288
                                                                                                                                                                                                                                                                                           57001 actggcctccgccgccggcacggccgtcgccaccccggcaccagcacctggcacgc
                                                                                                                                                                                                                                                                                                                                                           56941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; B07556, 1
B07563, B07564, 1
B07571, B07572, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JAN-1999;
05-FEB-1999;
05-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents the BLM (Bleomycin) gene cluster, containing open reading frames (ORFS) 8-30. The proteins encoded by the gene cluster are useful for producing peptides and/or polyketide metabolites, especially bleomycin or bleomycin analogues. They are also useful for chemically modifying biological molecules to produce branched methyl groups, and for coupling amino acids and fatty acids. They may be reacted with an apo-carrier protein and coenzyme A to produce a holo-carrier protein. The BLM gene cluster or catalytic domains can be used individually or collectively to produce thiszolidine, thiszoline, bithiszoline and bithiszoline-containing microbial metabolites. The BLM gene cluster may also be used to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New bleomycin gene cluster components useful for peptide and/or polyketide metabolites, especially bleomycin, production and for chemically modifying biological molecules -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shen
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                                                                                                                                                                                                                                                                                                                                                                                       129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 58857 BP; 7256 A; 25139 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                             189
                                                                                                                                                                                                                                                                                                                                                                         CCTCAGCACTGCCCAATGGCTGGAGCTCGATGCCGGGCAACGGAGTTACCTTGGCCGGAGA 188
                                                                                                                                                                                                                                  cgacgaactgccgactgctcggcggcaccggcaaggtctgccggaccggcaccctgcc
                                                                                                                                                                                                                                                        TATTGTGCTGCACGCCTGGGAAGGCTCCAGCCAGTCGGCCTATGCGACCTCCGCTGGCAG
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                                                                                    CAAAGCCATCCAGCAAACCGACTACGACAAGTATTGCCTGATGGG
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                                                                                                                                             CTACCACTTAAACCGCGGCATATTTAACTCATCGCTGATTGACGAAGTAGTGGGCGCAGT
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; 99US-0118848.
; 2000US-0477962.
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, B07565, B07566, I
, B07573, B07574, I
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43.7%;
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Pred. No. 6.3;
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B07567, B07568, B07569,
B07575, B07576, B07577,
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B07578.
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                                                                                                                                                                                                                                                                                                                                       release channel gating. Analysis of surrounding sequences suggests that this mutation lies within a beta strand domain comprising roughly of amino acids 520 to 830. RYR1 is the calcium release channel of the sarcoplasmic reticulum and is a large protein which spans the gap between the transverse tubule and the sarcoplasmic reticulum. The cannel is activated by ATP, calcium, caffine, and micro-molar ryanodine. It is inhibited by ruthenium red, tetracaine, calmodulin,
                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence given is the mutant pig ryanodine receptor (RYR1) gene from swine cDNA. The polymorphic sites were observed in comparisons of Pietrain and Yorkshire breeds. There are 17 polymorphisms between the two breeds. The polymorphism at position 1972 causes a mutation from Arg to Cys and this is thought to be the molecular basis of porcine malignant hyperthermia (MH). This mutation lies within the region of RYR1 that is concerned with the binding of regulators of Ca2+
                                                                                                                                                        2414
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                                                                                                                                                                                                                                                                                             Sequence 15377 BP; 3197 A; 4630 C; 4755 G; 2774 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 2; 96pp; English.
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20-MAY-1991;
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   CCGCACACACC
                                                             GGGAACAGCATCTCGCTAAACCGCTAGCGGGGGGGGTGCTCGCCGTATGCCCGGTACTCGACC 577
                                                                                           TCCTCGGGGGCCAGAAGGTGCTGCCCTGGGGAAGTCACCAGGCGTGGCACGTGTCCTGTC
                                                                                                                        ACAAGTATTGCCTGATGGGGTTCTCACTGGGGTGGGAACTTTGCCTTGCGCGTCGCGGTGC
                                                                                                                                                        CAGCCGTTGATGCGGAAGGAGGATGGACGGCACGCTGAGGTCCAGGCAGCAGCTGACCACG
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Similarity 48.7%;
93; Conservative
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91GB-0019250.
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Pred. No. 3.6;
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Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                              The COUP-TF protein was isolated from nuclear extracts of HeLa cells and acquired mRNA used to construct a cDNA library.

The COUP-TF gene and antibodies are used in assays for determining the amt. of COUP-TF, its binding ability and promoter interaction.

These assays can be used to detect defects in the COUP-TF binding system that result in diabetes. Additionally promoters associated with e.g. very low density lipoprotein gene and the pro-opiomelanocortin gene can also be assayed to detect lipoprotein abnormalities (e.g. atherosclerosis) and neurogenic and adrenal disorders, resp. See also Q06156, -57, -59 and Q06427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chicken ovalbumin upstream promoter transcription factor; COUP-TF; antibodies; diabetes; very low density lipoprotein gene; insulin; pro-opiomelanocortin gene; atherosclerosis; adrenal dysfunction; ss
                                                                                                                                                                                                                                       Sequence 1513 BP; 319 A; 519 C;
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 14-16; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chicken ovalbumin transcription factor gene and antibodies for assaying COUP-TF, its binding ability and its promoter
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                          X34024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterial DNA vectors containing reporter constructs identifying coding or promoter sequences involved in infection-associated protein expression
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                                                                     X34024 standard; DNA;
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P-PSDB; Y04773.
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14-AUG-1997;
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97FR-0010404.
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Pred. No. 1.6;
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RESULT 15
X34023
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Best Local
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                         06-JUL-1999
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 Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 315
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P-PSDB; Y04772.
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14-AUG-1997;
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97FR-0010404
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Best Local Similarity 48.6%;
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P-PSDB; Y04771.
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14-AUG-1997;
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0; Mismatches
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Result
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Perfect score:
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      Issued_Patents_NA:*
1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
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1017
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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                      US-08-602-359A-30
US-08-946-3
US-08-944-495-3
US-09-126-640-2
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US-09-160-494-3
US-09-160-494-3
US-09-160-494-3
US-09-160-494-3
US-09-160-494-3
US-09-249-200-5
US-08-794-795-1
US-08-794-795-1
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US-08-110-129A-2
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Sequence 30, Appli
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US-08-602-359A-30 Sequence 30, Application US/08602359A Patent No. 5942430 GENERAL INFORMATION APPLICANT: MURPHY, Dennis APPLICANT: MURPHY, Dennis APPLICANT: MURPHY, Dennis APPLICANT: MEID, John APPLICANT: MAFFIA, Anthony APPLICANT: MAFFIA, Anthony APPLICANT: MAFFIA, Anthony APPLICANT: WARREN, Patrick V. APPLICANT: WONGYRA, Anna APPLICANT: WONGYRA, Anna TITLE OF INVENTION: ESTERASES NUMBER OF SEQUENCES 42 CORRESPONDENCE ADDRESS: APPLICANT: WONGYRA, ANDA APPLICANT: WONGYRA, ANDA TITLE OF INVENTION: ESTERASES CORRESPONDENCE ADDRESS: APPLICANT: MONDLA TITLE OF INVENTION: STETENSES CORRESPONDENCE ADDRESS: APPLICANTON INVENTION STETENSES COMPUTER: ASLIFORNIA COUNTRY: USA ZIP: 92037 COMPUTER: IBM PS/2 COMPUTER: AND DATA: APPLICATION NUMBER: US/08/602,359A FILING DATE: FEBUARY 16, 1996 CLASSIFICATION NUMBER: US/08/602,359A FILING DATE: FEBUARY 16, 1996 FILING DATE: FEBUARY 16, 1996 FILING DATE: MUMBER: 09010/010001 TELEFONNE: ATTONNEY/AGENT INFORMATION: ATTORNEY/AGENT INFORMATION: ARTORNEY/AGENT INFORMATION: TELEPHONE: 619-678-5070 TELEPHONE: 619-678-6020 TOROLOCATION UNDERS: 0910/010001 TELEPHONE: 619-678-6020 TELEPHONE:	C 28 30.6 3.0 1956 3 US-08-867-352-20 C 29 30.6 3.0 4951 2 US-08-752-307B-1 C 30 30.6 3.0 8299 1 US-08-462-014-2 C 31 30.6 3.0 8299 3 US-08-923-137-3 C 32 30.6 3.0 8299 3 US-08-923-137-3 C 33 30.2 30.2 3576 4 US-09-320-878-19 3 30.2 30.2 3169 2 US-08-588-27 C 35 30 2.9 3169 2 US-08-588-27 C 35 30 2.9 3169 2 US-08-588-27 C 37 29.8 2.9 1514 1 US-08-381-433A-1 C 38 29.8 2.9 1626 1 US-08-381-433A-1 US-08-481-435-1 US-08-381-433A-1 US-08-381-433A-1 US-08-381-433A-1 US-08-381-433A-1 US-08-381-433A-1 US-08-381-433A-1 US-08-381-433A-1 US-08-481-435-1 US-08-481-45-1 US-08-381-435-1 US-08-481-45-1 US-08-381-435-1 US-08-481-75-10 US-08-481-75-10 US-08-481-775-10 US-08-481-775-10 US-08-481-775-10 US-08-481-775-10 US-08-481-775-10
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Best Local Similarity
Matches 1017; Conserv
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ATTCTGGCAGCTGGCGACGACCCAATAATTCCAGCATCCGACTTTCAGAAAATAGCCAAG
                                                                                                               CTTGATGAGTTAAACAACTATTTCATTCCCCGCTACACCGGCTTCAACTCAGTCTCCGAA
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                                                                                                                                                   GCAAAACTTGCAGCTTTCCCCAGACTACAAATACGGCAAAGATTTAAAATCGATACACACG
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                                                                                                                                                                                                   CTAGCGGGCGTGCTCGCCGTATGCCCGGTACTCGACCCCGCACACACCATGATGGCCCTA
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Pred. No. 0;
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LOCATION: 288...1565;
OTHER INFORMATION:
US-08-826-246-3
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FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,787
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 70853-078-999
TELECOMMUNICATION: 11FORMATION:
TELEPHONE: (212)790909
TELECHONE: (212)790909
TELECAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3103 base pairs
TYPE: nicleic acid
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US-08-826-246-3
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                                                                                                                                                     Matches
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Best Local Similarity
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TITLE OF INVENTION: COM
TITLE OF INVENTION: THE
TITLE OF INVENTION: CAR,
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
 2328
                                                                                                   2208
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                  MOLECULE TYPE: FEATURE:
                       123 GAGCTACCTCAGCACTGCC 141
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1155 Avenue
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ZIP: 10036-2711
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STATE: NY
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                                                 AGCCCCTGCCATTGTAGCGTCTTTCTTTTTTGGCCATCTGCTCCTGGATCTCCCTGAGAT 2327
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28-MAR-1997
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Patent No. 6087477

Application US/08944495

APPLICANT:

Falb, Dean

INFORMATION:

TITLE OF INVENTION: COMPOSITIONS AT TITLE OF INVENTION: THE TREATMENT TITLE OF INVENTION: CARDIOVASCULAR

CARDIOVASCULAR DISEASE COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS

OF.

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RESULT 4
US-09-126-640-2
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           Sequence 2, Application US/09126640A Patent No. 6099823
GENERAL INFORMATION:
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Best Local Si
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APPLICANT: FALB, Dean A.
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                                                                                                                            2328
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LENGTH: 3103 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
                                                                                                                                                                                                                                                       2208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
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ADDRESSEE: PENNIE & EDMONDS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                         123 GAGCTACCTCAGCACTGCC 141
                                                                                                                                                                                                                       LOCATION: 288...1
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: both
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TELEX: 66141 PENNIE
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ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                     3 GCCAGCTAATGACTCACCCACGATCGACTTTAATCCTCGCGGCATTCTTCGCAACGCTCA 62
                                                                                                                          GGGCTTCCCAAGGGCTGCC
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Similarity 54.7%;
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SEQ ID NO 3
; LENGTH: 3111
TYPE: DNA
ORGANIEM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/487,444
CURRENT FILING DATE: 2000-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD7 EXPRESSION FILE REFERENCE: RTS-0133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Brett P. Monia APPLICANT: Lex M. Cowsert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 60/011,787
EARLIER FILING DATE: 1996-02-16
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 08/870,434
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 08/799,910
EARLIER FILING DATE: 1997-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE FILE REFERENCE: 7853-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 1998-07-30
                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: CDS
LOCATION: (296)...(1576)
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                   2276 agcccctgccattgtagcgtctttctttttttggccatctgctcctggatctccctgagat 2335
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54.7%;
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RESULT 7
US-09-160-494-1
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US-08-902-516-1
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                                                                                                                                                                                                                                                      Sequence 1, Apprased 1, Appras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08902516 Patent No. 5891432
                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: "LATION: ATTORNEY/AGENT INFORMATION: NAME: Campbell, Cathryn A. NAME: SINDHER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
                                      CORRESPONDENCE
                                                                     NUMBER OF SEQUENCES:
                                                                                                    TITLE OF INVENTION:
                                                                                                                                APPLICANT:
                                                                                                                                                               APPLICANT: BURGESS,
                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2336 gggcttcccaagggctgcc 2354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        578 CCGCACACCATGATGGCCCTAAACCGAGGTGCGTTTTTCTACGGCCGCTATTTTGC 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518 GGGAACAGCATCTCGCTAAACCGCTAGCGGGCGTGCTCGCCGTATGCCCGGTACTCGACC 577
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ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/(FILING DATE: 29-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGCCCACAGCATTCAGATCCTCTTCTGAGATGAGTTTTTTGTTCGTCGACTTTTTGGC 464
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                                                                                                                                                                                                                                                                                                   Application US/09160494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            660 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: CAMPBELL & FLORES, LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                CHAPMAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                     SOUTHAN,
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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   Ratner & Prestia
                                         ADDRESS
                                                                        NOVEL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.48;
                                                                                                                                                                                                     CHRISTOPHER
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COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE RESPONSE USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     William
                                                                                                                                       CONRAD
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Pred. No. 0.06;
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Best Local S
Matches 98
                                                                                                                                                                                                                 Sequence 8, Application US/09071709 Patent No. 6171790
                                                                                                                                                                                                GENERAL INFORMATION:
                                                                           APPLICANT: Hillman, Jennifer APPLICANT: Tang, Y. Tom APPLICANT: Lal, Preeti APPLICANT: Corley, Neil C. APPLICANT: Guegler, Karl J. APPLICANT: Patterson, Chandr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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LENGTH: 1637 base pairs
TYPE: nucleic acid
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FILING DATE: 02-FEB-1998
APPLICATION NUMBER: UK 9808478.3
FILING DATE: 21-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1314 ATGACACCCCCTGTGGAACCACCATTGGACCTATCTTGGCTTCTCGGCTGGGGCTGCGGG
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TELEPHONE: 601-407-0700
TELEFAX: 610-407-0701
                                      NUMBER OF SEQUENCES:
                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      461
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REGISTRATION NUMBER: 23
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09 FILING DATE: 24-SEPT-1998
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                                                                                                                                                                                                                                                                                                                                                                            CACACACCATGATGGCCCTAAACC 604
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98; Conserv
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                                                                                                                                                   Hillman, Jennifer L.
Tang, Y. Tom
                                    PATTERSON, Chandra
VENTION: HUMAN PROTEASE ASSOCIATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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INCYTE PHARMACEUTICALS, INC
                ADDRESS:
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                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                               Sequence 3, Application US/09160494 Patent No. 6180384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.4%;
Best Local Similarity 48.0%;
                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (650) 845-4166
NFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1395 CCCTGATCCGAGAGGTGGCCAACAAAGTCAAGGTCCCCCTGCAGGATCTCATGGTCCGGA 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
                                                                                                                                                                                                                                                                                                                                                                       1575 CAGGAGTCCTCCAGACCCTCACCC 1598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                              APPLICANT: BURGESS,
                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               461 AGTATTGCCTGATGGGGTTCTCACTGGGTGGGAACTTTGCCTTGCGCGTCGCGGTGCGGG 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401 CGCTGATTGACGAAGTAGTGGGCGCAGTCAAAGCCATCCAGCAGCAAACCGACTACGACA 460
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LIBRARY: UVEL.
ONE: 2058485
                                                                                                                                                                                                                                                                                                                                                                                           581 CACACACCATGATGGCCCTAAACC 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         521 AACAGCATCTCGCTAAACCGCTAGCGGGCGTGCTCGCCGTATGCCCGGTACTCGACCCCG 580
                                                   COUNTRY: US
                                                                       STATE:
                                                                                     STREET: P.O. CITY: Valley
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                                    19482-0980
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                                                                       PA
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                                                                                                                                                                                        CHAPMAN,
                                                                                                                                                                                                                          SOUTHAN,
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Diskette
                                                                                     Forge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34.4; DB Pred. No. 0.17;
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US-08-785-420-1/c
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                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08785420 Patent No. 6001976 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 02-FEB-1998
APPLICATION NUMBER: UK 980
FILING DATE: 21-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,0:
                                         ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                      1536 CAGGAGTCCTCCAGACCCTCACCC 1559
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MOLECULE TYPE:
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LENGTH: 2019 base pairs
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PRIOR APPLICATION UNMBER: UK 9802824.4
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,494
                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1476 TGCTGGATTTAGGCAGCCCCCAACTGGGCCATGCACTCTATCCGGGAGATGGCCTGCACCA 1535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 521 AACAGCATCTCGCTAAACCGCTAGCGGGCGTGCTCGCCGTATGCCCGGTACTCGACCCCG 580
                 COMPUTER:
OPERATING
                                                                                       COUNTRY: U
ZIP: 28234
                                                                                                                                  STREET: P.O. D.C. CITY: Charlotte,
                                                                                                                             STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: UK 9
FILING DATE: 02-FEB-1998
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                                                                                                                                                                              ADDRESSEE:
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                                                                                                                         No. 6001976th Carolina 28234
                                                                                                                                                             P.O. Drawer 34009
               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                          U.S.A.
                                                                                                                                                                                                                                                                     MacLennan,
O'Brien, P
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PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                Bell, Seltzer, Park & Gibson
                                                 Floppy disk
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DIAGNOSIS FOR PORCINE MALIGNANT
                                                                                                                                                                                                                                     HYPERTHERMIA
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                                                                                                                                                                                                                                                                                          David H
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PRIOR APPLICATION DATA:

FILING DATE:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/785,420

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US-08-785-420-1
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL: N
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                            2234 CAGCCCTCGCC 2224
                                                                        CORRESPONDENCE ADDRESS: SmithKline Beecham Corporation
                                                                                                                 TITLE OF INVENTION: Human
                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                        2294 CAGAGATGCAGCCCGTCAAAGCCGTAGGAATAGAGGTCATCGCCGACCCCGTTGCCGCCC 2235
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ATTORNEY/AGENT INFORMATION:
                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                           578 CCGCACACACC 588
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                COUNTRY:
                            STATE:
                                        CITY: King of Prussia
                                                           STREET:
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Gross, Mitchell
Lysko, Paul
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                                                           Road
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Best Local
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                               SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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LENGTH: 1560 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: ATG50009P
FILING DATE: 22-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 610-270-5219
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 GCTGAGGACAGCCCGTCCTTCTCCTTGCTGCAGTCAGCACCCCTGGAGAACACCCTGGCT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 GAGCACTTGCTGCAGCGGGTAGACAACTTCACTC 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 CACGCTTTTCGACAATGGGTTCGACACTTTTCGC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 TATTGTGCTGCACGGCTGGGAAGGCTCCAGCCAGTCGGCCTATGCGACCTCCGCTGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 GCTTAACACAGCGCCTGCAACTGCATCCTCCTCCCACCCGGCGCACAAGAACACTCTGGT 248
                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                  STREET: P.O. Box 91
CITY: Valley Forge
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 78; Conserv
                                                                                                                                   COUNTRY: UZIP: 19482
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                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 610-270-4026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                      DDRESSEE:
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                                                                                                                                                                                                   E: Ratner & Prestia
                                                                                                                                                                                                                                                                                      ADAMOU, JOHN
GROSS, MITCHELL
LYSKO, PAUL
                                                                                                                                                    USA
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MBER: US/09/249,200
12-FEB-1999
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: 0

08/794,795 -1997 60/017,699

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Best Local Similarity
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                                                                                                                                                      ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 22-MAY-
                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 610-407-0700
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ATTORNEY/AGENT INFORMATION:
                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                         OPERATING SYSTEM:
SOFTWARE: FastSE(
                                                                                                                                      COMPUTER: IBM Compatible
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                                                             APPLICATION NUMBER: US/08/794,795 FILING DATE: 04-FEB-1997
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                                              CLASSIFICATION: 435
                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                     ADDRESSEE:
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TOPOLOGY: linear
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                                                                                                                                                                                                                                  King of Prussia
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Lysko, Paul
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                                                           04-FEB-1997
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   22-MAY-1996
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Best Local Similarity 50.6
Matches 78; Conservative
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                              APPLICATION NUMBER: 08/794
FILING DATE: 04-FEB-1997
APPLICATION NUMBER: 60/017
FILING DATE: 23-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23.03
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: GROSS, MITCHELL APPLICANT: LYSKO, PAUL
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TELECOMMUNICATION INFORMATION:
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                   REGISTRATION NUMBER: 23,031 REFERENCE/DOCKET NUMBER: AT
                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 12-FEB-1999
                                                                                                                                                                                                                                                      OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                   ZIP: 19482
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O. Box 980
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                                                                                                        60/017,699
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                                                                                                                                      08/794,795
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                   ATG-50009-1
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TELEX: 846169
INFORMATION FOR SEQ ID NO:

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SEQUENCE CHARACTERISTICS: LENGTH: 1703 base pairs

MOLECULE TYPE: cDNA

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

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RESULT 15
US-09-103-429A-1
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Best Local Similarity 50.6%;
Matches 78; Conservative
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                                                                                                                                                                        TELEFAX: (607) 256-3628

NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2455 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Granados, Robert R
APPLICANT: Wang, Ping
TITLE OF INVENTION: A No. 6187558el Invertebrate Intestinal Mucin
TITLE OF INVENTION: CDNA and Related Products and Methods
                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Michaels, Christopher A
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: BTI-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (607) 256-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Pinnisi & Michaels, P.C.
STREET: 118 No. 6187558th Tioga
                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
                                         RAGMENT TYPE:
                                                         HYPOTHETICAL: R
                                                                                            OLECULE TYPE:
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ORGANISM:
                                                                                                                                                        TYPE: nucleic acid
                                                                                                                   STRANDEDNESS:
TOPOLOGY: 11r
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                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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                                     N-terminal
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                                                  GCCAGCTAATGACTCACCCACGATCGACTTTAATCCTCGCGGCATTCTTCGCAACGCTCA 62
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Score 38.2; DI Pred. No. 13; O; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGCTACCTCAGCACTGCC 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 4, 2000 this sequence version replaced gi:7767817.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens chromosome 18 clone RP11-756018 map 18, WORKING DRAFT
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1 (bases 1 to 188727)
Birren,B., Linton,L.,
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iomo sapiens chromosome 18, clone RP11-756018
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                                     NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces
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                                                                                                                                                                                                                                                                               Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator B1g Dye; 100% of re Assembly program: Phrap; version 0.960731 consensus quality: 176297 bases at least 030 consensus quality: 182355 bases at least 030 consensus quality: 184582 bases at least 020
                                                                                                                                         Quality coverage: 4.1 in Q20 bases; Quality coverage: 4.3 in Q20 bases;
                                                                                                                                                                                                               Insert size: 196000; agarose-fp
Insert size: 186427; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: L6562
Center clone name: 756_O_18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    site: http://www-seq.wi.mit.edu
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172508 188727: contig of
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1219 2716:
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                                                                                                                                                               /note="
2817. .
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                        note="assembly_fragment"
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                      note-"assembly_fragment"
                                                                                                                                                                                                                                                                                                clone_lib="RPCI-11 Human Male BAC"
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12277: gap of 100 bp
16179: contig of 3902 bp in
16279: gap of 100 bp
16279: gap of 2859 bp in
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119435: cont
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11129: contig of 7057 bp
11129: gap of 100
48279: contig
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07874: contig of 11252 bp in
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25744. 29860
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107975. .119435
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74011. .83534
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29961. .33872
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132248. .145585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University Of Washington, Box 352145, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stover, C.K., Pham, X. Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrook-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Saler, M.H., Hancock, R.E.W., Lory, S. and Olson, M.V.
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VYLVLAFHSVVLAPASWGQPAGWLVAACALLGSACALLSGRIGHTRHAGVYHAE
ERHGESLLEVTCRLQGWSHRAGQFAFLTCDRLEGAHPFTIASADRGCGEVRFSIKAL
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/transl_table=11
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/gene="PA0547"
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/gene="PA0547"
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complement(6989. .7786)
/gene="PA0550"
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ELPPVLALRLNCLDACVILDGHCRLRAGLLENVAPEILVLCAYDEQPMPVDTAQRERV
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GPLRGLLAYTELPHASCDFNHDPHSAIVDGSQTRVSGPRLVNLLAWFDNEWGFANRMI
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DWLAARERLDALEPIIRRYE"
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AWSRYFVETLRTSPGSCLEAGRWLLRLSLAEQVPAWQPPQSHDPRERVLERWRYRSVG
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LADALQDAAEPADCVVLNWVLHHFAAPAEALKQLARLVHPGGSLLVTDLCRHNQGWAR
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/gene="PA0549"
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                                                                                                         Stover.C.K., Pham.X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrook-Wadman, S., Luan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Saler, M.H., Hancock, R.E.W., Lory, S. and Olson, M.V.
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University of Washington Genome Ce
Box 352145, Seattle, WA 98195, USA
Location/Qualifiers
                                           Submitted (16-MAY 2000) Department of Medicine and University of Washington Genome Center, University
                                                                                                                                                                                                                                                                                                         Complete genome sequence of Pseudomonas opportunistic pathogen Nature 406 (6799), 959-964 (2000)
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AE004899.1 GI:9951126
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FSIAGGGDTLAAIDKYGIAERISYISTGGGAFLEFVEGKVLPAVEILEQRAKG"
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NVSAVSSGKEALAQLRTKAHLREYFDVYLLDQDMPGWTGMQLAAKIKEDPNLNHDILL
IMLTGISNAPSKIIARNAGIKRILAKPYAGYTLKATLADELAQRGVSGVTNYLQPAKE
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DYVQTIHSAGNELLTLINEILDISKLESGQIELDEVQPDLNALLEDCLDIFRVKAEQQ
RIELLSFTOPOVPRVLGGDPTRLROVVLSLLDNAFKQTEEGEILLVVALDQGETPGI
RIKLISFTOPOVPRVLGDDTTRLAFLHSGDFLSASKLGSHLGLIIARQLVRLMGGEFGIQ
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ESRLNRLLQGEALLILAVGAIIAFTQQLWFSWLIYLLVILSSLSVPLIAAWHWYRGYQ
PARLIVAGMIVFNAGFMVFLFYLFGTKQLDPGWLVLGVFSFATLAGLVLSVSLTERQR
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LAAGGYPGDYAKGEVIEGLAEAAALDGKVFHAGTALKDGQVVTSGGRVLCATAIGESV
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1476. .4304
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                                                                                                                                                                                                                                                           /gene="PA4858"
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Match 3.7%;
Local Similarity 47.8%;
les 109; Conservative
GCTCAGCGTCCCGCTGATCGCGGCCTGGCACTGGTATCGCGGCTACCAGCCGGCGCCCT
                                                        GAACTTTGCCTTGCGCGTCGCGGTGCGGGGAACAGCATCTCGCTAAACCGCTAGCGGGCGT 551
                                                                                                                   CGCCTTCACCCAGCAACTCTGGTTCAGTTGGCTGATCTACCTGCTGGTGATCCTCAGTTC
                                                                                                                                                                               AGCCATCCAGCAGCAAACCGACTACGACAAGTATTGCCTGATGGGGTTCTCACTGGGTGG
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| imtoaltflagmliffragmliffragmlifflgfliffariaflartvallas
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8776. .
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NKILEPQIGAVLGKILILALIVLFIQKRPQGLFALKGRVID"
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transporter"
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/transl_table=11
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Dodson,R.J., Haft,D.H., Gwinn,M.L., Nelson,W.C., Richardson,D.,
Moffat,K.S., Qin,H., Jiang,L., Pamphile,W., Crosby,M., Shen,M.
Vamathevan,J.J., Lam,P., McDonald,L., Utterback,T., Zalewski,C., Makarova,K.S., Aravind,L., Daly,M.J., Fraser,C.M. et,al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-NOV-1999) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers 1. .213732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             White,O., Eisen,J.A., Heidelberg,J.F., Hickey,E.K., Peterson,J.D., Dodson,R.J., Haft,D.H., Gwinn,M.L., Nelson,W.C., Richardson,D.L., Moffat,K.S., Qin,H., Jiang,L., Pamphile,W., Crosby,M., Shen,M., Vamathevan,J.J., Lam,P., McDonald,L., Utterback,T., Zalewski,C., Makarova,K.S., Aravind,L., Daly,M.J., Minton,K.W., Fleischmann,R.D., Ketchum,K.A., Nelson,K.E., Salzberg,S., Smith,H.O., Venter,J.C. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deinococcus radiodurans
Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.

1 (bases 1 to 213732)
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Deinococcus radiodurans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deinococcus radiodurans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 (5444), 1571-1577 (1999)
                                                                                                                                                                                                                                                                                                                                                       GAQGRLRRALAEVSGDYDVALIDSPPSLGQLAILAALAADQMIVPVPTRQKGLDALPG
LQGALTEYREVRPDLTVALYVPTFYDARRRHDQEVLADLKAHLSPLARPVPQREAVWL
DSTAQGAPVSEYAPGTPVHADVQRLTADIAAAIGVAYPGENA"
                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MVSAVKTLTVFNHAGGAGKTSLTLNVGYELARGGLRVLLLDLDPQANLTGWLGISGVTREMTVYPVAVDGQPLPSPVKAFGLDVIPAHYSLAVAEGQMMGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to GB:D26185 SP:P37522 PID:467381
PID:580906 GB:AL009126 percent identity: 54.96;
by sequence similarity; putative"
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/TRANSLATION="MTRRRPERRRDLIGLIGETPVDLSQANDIRALPVNELKVGSTQP
                                                                                                                                                                               by sequence similarity;
                                                                                                                                                                                                    /note="similar to GB:L34077 GB:X85964 PID:407375
PID:757761 PID:1163135 percent identity: 57.34;
                                                                                                                                                                                                                                                                                 /gene="1
1432...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAF12301.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="chromosome partitioning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="DRA0001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="2"
                                                                                                                                                                                                                                                          /gene="DRA0002"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       camily"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="DRA0001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="R1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Deinococcus
                                                                                                                                 transl_table=11/
                                                                                                                                                     codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _xref="taxon:1299"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 1435
                                                                                                                                                                                                                                                                                                    DRA0002"
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R1 section
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Zalewski,C.,
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/translation="mdrrsspQlrtmtnwnreQpaphagatgpnsspgatmQplersl TGAVGAALAAAGLrsrsglekvvltgLGAGLIAVAARGQnpLatalkIeQndegetvv

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complement(5894.
/gene="DRA0006"
                                                                                                                                                                                                                                                                                    complement (5894.
/gene="DRA0006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to GB:L33464 SP:P47734 PID:496118 percent identity: 74.23; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2418. .3881)
/gene="DRA0003"
                                                                                                                                                                                                                                                                                                                                                                                DRVPERLAMAEAAGCQTINYEKEDVLLSLREATGGRGPDHVIDAVGMEAHGHGPGSTM
DKVQQNLKLTFDRITALRWAILSCAKGGTVSMPGVYGGLVDKMPIGAAFAKGLIFRMG
QTHTHRHIPSLLGRIEAGQIDPSFVITHRASLDQAPELYKTFRDKQDCCIKVVLNPWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"alcohol dehydrogenase, zinc-containing"
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/protein_id-"AAF12293.1"
/db_xref-"G1:6460587"
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/translation-"MKAIVWQGVNKVGVETVPDPTLLLPTDAIVKITSTAICGSDLHL
LDGYLFSMETGDILGHEFMGETVEVGSEVRKLKVGDRVVVPFALVGVDPCKRGFFS
ACDNSNPNHRAMAEALYGATSGGALFGYSHMYGGYAGGAQVYEVPFALVGPFKLESGL
ACDNSNPNHRAMAEALYGATSGGALFGYSHMYGGYAGGAGFVGQFAARSAQMLGAAHVIVI
KDEQVLFLTDIFFTGYQAAEQCNIVPGRDVVAVFGAGFVGQFAARSAQMLGAAHVIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(4719.
/gene="DRA0005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALTQPFMNDSRVRKLTFTGSTEVGRLLYQQAAGTIKRVSLELGGHAPFLVFDDADLER
AASEVVASKFRNSGQTCVCTNRVYVQRGVAEEFIRLLTEKTAALQLGDPFDEATQVGP
VVEQAGLDKVQRQVQDALTKGAQATTGGQVSSGLFFQPTVLVDVAPDSLILREETFGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MTTTDLRTTYSSVTRSQAYFDGEWRNAPRNFEVRHPGNGEVIGE
VADCTPTDARQAIDAEWALBWRQVAPYERGKILRRWHDLMETHKEELAQLMTLEMG
KPISETRGEVHYAASFIEWCAEEAGRIAGERKHLRFPHKRGLTISEPVGIVYAVTPWN
FPAGMITRKAAPALAAGCVMILKPAELSPMTALYLTELWLKAGGPANTFQVLPTNDAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QAELLKLAQNGASRSQLLQALQTPSQTSAVTPEHFAKVLSSKRFLSGLDTPTREALDR
WLARMPERVRQAIDEQS"
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GDEHEQLDQVFRSMGETWRTFAKNKLRILNWPQPVLEALRAGLPLTLGSVVASAPPER
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/db_xref="GI:6460586"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mnSlsslaavllmagrstrmgqpkallplggmplcrhaaqtlve
agygevwavlppgetgdavraalqglplrwvtnpqpaqgllssfqaagealwaesaap
ayvftladmplvrrdthqalgtvfgaeqpaalitrygevaapptllrrdllprlhefp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="conserved hy
/protein_id="AAF12299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="DRA0004"
4024. .4668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="DRA0005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to GP:2924378 percent identity:
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="DRA0004"
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/db_xref="GI:6460588"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="DRA0003"
                                                                                            transl_table=11
                                                                                                                                                       dentified by sequence
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                                                                                                                                   codon_start=
                                                                                                                                                                                                  'note="similar
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                                                                                                                                                          PID:1653488 percent identity: uence similarity; putative"
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99.1"
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Query Match
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                                                                                                                                                                                                          243
363
                                                                                                      303
CGACACCTACCACTTAAACCGCGGCATATTTAACTCATCGCTGATTGACGAAGTAGTGGG 422
                                                TGGCAGCACGCTTTTCGACAATGGGTTCGACACTTTTCGCCTTAATTTTCGCGATCACGG 362
                                                                                                                                                    TCTGGTGCAGGCGACGCTCACGCCCGCCGATCTCGGCAGCTCGGCGGATGTCCGCAGCGG 58870
                                                                                                                                                                                                        109;
                                                                                                                                                                                                                                                                                   3.7%;
Similarity 47.8%;
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                               9816. 10451
/gene="DRA0010"
/note="similar to GB:AL009126 percent identity: 67.84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MTTLPNVPARRTSALPVLAQLTLGELRRLLRSPMFTVGAIGFPV
MFFALFGLPAVQEYGATDPHVGPVILTQFAAYSLLSLALFSFGAAVATERSGGWLRLL
RSSPLPVPLYFVSKTLAALAFGAVSLALLYAFAHFAGGVTLPLGLALLLAGKLLLGMI
PLVALGLCIGFLASPQAAQILANILSVVMSFASGLFVPLDQLPGFVQQIAPLLPAYHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRAAFWEAVTGLRARGRTILLTTHYLEEAERTADRVVVMNGGRILADDTPQGLRSGVG
GARVSFVSDLVQAELERLPGVSAVQVDAAGRADLRTSVPEALLAALIGSGTTFSDLEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIRLVITDTLPELPADLESTLAMVLREAVTNVVRHSGASELRLTLRGQANGFQLTLQD
DGRGGDAPEGTGLNSMRERLRAMGGTFERDGHTGTRLQAFVPLSAGTAGLKAPELLEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQIATNIVSGQTASEPAHWLALAAFTLVFGTLAVWGLKRDESREG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRATLEEAYLQLTGPQDMTAVTRSA"
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APLGVDEALALADLGPVAGRRAAQLSGGQKRRLAFALAVVGDPELLLIDEPTTGMDAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="ABC transporter, ATP-binding protein, putative"
/protein_id="AAF12291.1"
/db_xref="G1:6460585"
/translation="MITTFEQVSKTYGHVTALSDFNLTLRTGELTALLGPNGAGKSTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RMFNQEPSQQLRDDLMRFKREQELGHAPTAQGQSSGRAALTPPNKRGDLV"
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ELTADEPGKRIAWRSLPGARIENSGEVLFRPAPGARGTEVVVRLTYRPPGGSAGAVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                           9816. .10451
/gene="DRA0010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELAGKLAEKHPQRAAAEIREVERISREALSEVRAAVQGYRGSGLAAELARAKVALDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYGPSALSFLVYGGSLIGWQRRQWVALGGAAINALLMVGRLLTLPERSQGDFIFLLFI
LASAYANHATYRGLRARRRLAQVQLEKEKLAADAERERIARDLHDLLGHTLSVIVLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="DRA0008"
7861. .8652
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/gene="DRA0007"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to GB:AL009126 percent identity: 52.46;
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="DRA0008"
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identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="DRA0009"
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    dentified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                   Score 37.6; DB 1; Pred. No. 23;
                                                                                                                                                                                                                                                           Mismatches 119;
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LOCUS DEFINITION

AK023005 2264 bp mRNA PRI 29-SEP-2000 Homo sapiens cDNA FLJ12943 fis, clone NT2RP2005162, highly similar

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KEYWORDS
SOURCE
ORGANISM
RESULT
AK023005
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AUTHORS
TITLE
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MEDLINE
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Matches 82; Conserv
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                                                                                                                   CGCTAGCGGGCGTGCTCGCCGTATGCCCGGTACTCGA 575
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                                                                                                                                                          CCCCTCCTGGTCTGAACTTGAAGATGCACTTCAACCCCGAGCTACCCCCTCTCAGAAACC
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                                                                              AGCTGATCCACAGGGTCCCCCATGGGCTCTGTCATCAA 992
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L37878.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="monoamine oxidase"
/protein_id="AAA64302.1"
/protein_id="AAA64302.1"
/db_xref="Gi:728485"
/db_xref="Gi:728485"
/translation="MTAQNTFDVIVIGGGISGLSAAKLLKEKGLSPVVLEARDRVGGR
/translation="MTAQNTFDVIVIGGAISGLSAAKLLKEKGLSPVVLEARDRVGGSYPFK
TFTVQNBQTKYVDLGGAYVGPTQNRILEAKECGVKTIKVNEEERLVHYVKGKSYPFK
TFTVQNBQTKYVDLGGAYVGPTQNRILEAKECGVKTIKVNEERLYHVVKKGLFDKICTT
GSPPMMNPFALMDYNNLMRKMDEMGSEIPREAPWKAPHAEEWDKMTMKQLFDKICGSSQ
GSFPDMMNPFALMDYNNTSEPHEVSALWFLMYVKQCGTMRIFSTTMGGQEKFLGGSSQ
ISECMARELGERVKMESSYVK LDQTGDWVEVETLNKETYKAKTUTATPARATITATTA
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100. 1599
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EEYSGGCYTAYFPPGILTQYGKVLREPVGRLYFAGTETATEWSGYMEGAVQAGERAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oncorhynchus mykiss"
/db_xref="taxon:8022"
/tissue_type="liver"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPELPPLRNQLTHRVPMGSVIKCIVYYRENFWRKKGYCGTMVIEEEEAPIGLTLDDTK
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               pieces.
AC013822
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NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, institute of medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISOgai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y. Nishikawa,T., Nagai,K., Sugano,S., Takahashi,Fujii,A., Hara,H., Tanase,T., Nomura,Y., Todyya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J. Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A.
                                                                                      Homo sapiens clone RP11-22B20, WORKING DRAFT SEQUENCE, 15 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oligo capping; fis (full insert sequence).

Homo sapiens teratocarcinoma cell_line:NT2 cDNA to mRNA,
clone_lib:NT2RP2 clone:NT2RP2005162.
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Isogai,T. and Otsuki,T.
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precursor cells after 2-weeks retinoic acid (RA)
induction "
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/clone="NT2RP2005162"
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* NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
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Birren, B., Linton, L.,
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HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as soon as it is available and the accession number will be preserved.
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Center clone name: 22_B_20
Center clone name: Xtatistics
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15708 15807: gap of 100 bp
15808 16980: contig of 1173 bp in length
16981 17080: gap of 100 bp
17081 18764: contig of 1684 bp in length
18765 18864: gap of 100 bp
18865 20765: contig of 1901 bp in length
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bp in length

length length

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Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 15, 2001 this sequence version replaced gi:10440710. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome
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83589 97092: contig of 13404 bp in length
97093 97192: gap of 100 bp
97193 115404: contig of 18212 bp in length
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Pred. No. 63;
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AC011236
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                     misc_feature
                                                                 misc_feature
                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 186118 bases at least Q40 Consensus quality: 187014 bases at least Q30 Consensus quality: 187507 bases at least Q20 Insert size: 188000; agarose-fp Insert size: 188042; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemistry: Dye-primer ET; 46% of reads
Chemistry: Dye-terminator Big Dye; 24% of
Assembly program: Phrap; version 0.990319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (04-OCT-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC011236 188342 bp
Homo sapiens chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality coverage: 0.00 in Q20 bases; agarose-fp Quality coverage: 6.52 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: H_NH0312D01
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AC011236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston, R.H.
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Mammalia; Eutheria; Primates;
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                 as soon as it is available and the accession number be preserved.
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Feb 7, 2001 this sequence version replaced gi:8748874.
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5092
29325
29425
55483
55583
                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
                                                                                                                                                                                 1. .188342
/note="assembly_name:Contig7
                                          note="assembly_name:Contig6"
                                                                                      clone="RP11-312D1"
                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                      4991: contig of 4991 bp in length
5091: gap of unknown length
29324: contig of 24233 bp in length
29424: gap of unknown length
55482: contig of 26058 bp in length
55582: gap of unknown length
188342: contig of 132760 bp in length.
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2 clone
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RP11-312D1,
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WORKING DRAFT SEQUENCE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             531 CGCTAAACCGCTAGCGGGCGTGCTCGCCGTATGCCCGGTACTCGACCCCGCACACACCAT 590
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Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrx
This sequence is the entire insert of clone RP11-29107 The true left end of clone RP11-528B10 is at 143354 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is
                                                                                                                                                                                                                                                                                       During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALI39109 197536 bp DNA PRI 22-DEC-2000
Human DNA sequence from clone RP11-29107 on chromosome X. Contains ESTs, STSs, GSSs and a CpG island. Contains a 40S ribosomal protein 26 (RPS26) pseudogene, the 3 part of a novel gene and the 3' part of the DLG3 (KIAA1232) gene for discs, large Drosophila homolog 3 of the DLG3 (KIAA1232) gene for discs, large Drosophila homolog 3
                                                                                                                                                                                                         http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 requests: clonerequest@sanger.ac.uk
On Sep 9, 2000 this sequence version replaced gi:9943979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL139109.14 GI:10045311
HTG; CpG island; discs; DLG3; KIAA1232; neuroendocrine-dlg; ribosomal protein; RPS26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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Mammalia; Eutheria; Primates;
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29425. .55482
/note="assembly_name:Contig8"
55583. .188342
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                                                     /note="L1PA14 repeat: matches 5470.
25218. .25605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="match: GSS: Em: Pcomplement(2720...3059)
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complement(2676. .3182)
                                                                                          24540.
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/note="CpG island"
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8720. .10859
/note="L1MC3
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/db_xref="taxon:9606"
/chromosome="X"
/note="LIME1 repeat: matches 4683.
join(25606. .25702,26024. .26184)
/gene="bA29107.1"
                                                                                                                         'note="SVA repeat: matches 761. .1385 of consensus"
24475. .24539
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                                                                                          note="L1ME1 repeat: matches 4620.
4540. .25217
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3446. .13749
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'note="L1ME1 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                            note="L1MC5 repeat:
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note="LlMA9 repeat: matches 5762.
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1928. .11967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="LIMA9 repeat: matches 5121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="L1MA10 repeat: matches 5529.
                                                                                                                                                                                                                               note="SVA repeat: matches 3.
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                                                                                                                                                                                                                                                                                                                                        note="Ll repeat:
                                                                                                                                                                                                                                                                                                                                                                                                           note="L1PA9 repeat: matches 5557. .6163 of consensus"
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                                                                          /note="LIME repeat: 69094. .69145
                                                                                                                                          59438. .60221
/note="L1PA2 repeat: matches 4. .776 of consensus"
61189. .62208
              /note="LTR40a repeat: matches 171.
72748. .72916
                                                                                                            /note="LIPA11 repeat: matches 5152. .6158 of consensus"
68700. .68785
                                                                                                                                                                                                                                                   51696. .53871
/note="L1MA8 repeat: matches 3916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           match: ESTs: Em:D51473
match: proteins: Sw:930742 Tr:Q9Y8H0 Sw:P49206 Sw:P70394
Sw:P13008 Sw:P02383 Sw:P21772 Sw:P27085 Sw:P49171
Tr:Q45499 Tr:Q9UT56"
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 /note="MER96
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/note="L1PA9 repeat: matches 5466.
50629. .51434
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/note="L1ME2 repeat: matches 4562.
10514. .40631
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/gene="bA29107.1"
                                               /note="L1ME repeat: matches 5677.
70081. .70113
                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MER47 repeat: matches 2235.
44766. .46175
note="LINC2 repeat: matches 4892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31806. .32132
/note="MER58B repeat: matches 1. .340 of consensus"
32417. .32672
                                                                                                                                                                                     'note="L1PA2 repeat: matches 900.
                                                                                                                                                                                                                                                                                                                                                                                                         note="L1ME repeat: matches 429. .504 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="L1P repeat: matches 3. .1817 of consensus"
18371. .39276
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26310. .27309
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                                                                                                                                                                                                                                                                                                                                                                             note="AluSg/x repeat: matches 132. .289 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MER3 repeat: matches 1. .206 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="Tigger3b repeat: matches 293. .1231 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63. .43740
te="MER47 repeat: matches 12. .88 of consensus"
63. .43846
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e-"AluJ repeat: matches 1. .304 of consensus"
                                                                                                                                                                                                                                                                                                                 e-"L1MA8 repeat: matches 6170.
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                                                                                                                                                                                                                                      .54205
                                                                                                                                                                                                                    repeat: matches 3248. .3609 of consensus"
repeat: matches 9. .175 of consensus*
                                                                                          matches 5727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    matches 2237. .2323 of consensus"
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                                                                                                                                                                                       .6146 of consensus"
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                             .203
                                                            .5727 of consensus"
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AC017033/c
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                                                                                                                        MO 6310
On Feb
Center
                                                                                                                                                                                                               4 (bases 1 to 183887) Waterston, R.H.
                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (09-DEC-1999) Genome
University School of Medicine,
MO 63108, USA
3 (bases 1 to 183887)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 183887)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston, R.H.
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                             മ
                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-297J22"
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                                                                                                         Location/Qualifiers
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                             45666 c
                                                                                         .183887
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51.2%;
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                           49645 g 47409
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Pred. No.
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3973 TGTCCATACAAAGAGACACACGTGAATGCTCACAGCAGCTTTATTTGTAATGTCCTAAAA 3914
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                                              Direct Submission
Submitted (11-FEB-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                         Direct Submission
Submitted (10-FEB-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
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    2001 this sequence version replaced gi:10999016
project name: H_NH0297J22.

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/note="LlPA16 repeat: matches 5782. .6013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="13 copies 2 mer ta 100% conserved"
77889. .78844
/note="LIMC1 repeat: matches 5317. .6322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note-"20 copies 2 mer aa 82% conserved"
76135. 76444
70135. 76446 /note-"LIMC5 repeat: matches 7604. .7911
77546. .77571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                               Sequencing Center, Washington 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ta 75% conserved
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AC019078/c
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Best Local S
Matches 55
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                                                                                                                                                                                                                                          Insert size: 180000; agarose-fp
Insert size: 184927; sum-of-contigs
Quality coverage: 4.11 in Q20 bases; agarose-fp
Quality coverage: 4.12 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                       Sequencing vector: plasmid; 0% Chemistry: Dye-primer ET; 99% of reads Chemistry: Dye-terminator Big Dye; 0% of read Assembly program: Phrap; version 0.990319 Consensus quality: 171161 bases at least 030 Consensus quality: 176449 bases at least 030 Consensus quality: 179564 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (30-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Nov 30, 2000 this sequence version replaced gi:9887808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
1 (bases 1 to 187027)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Washington University Genome Sequencing Center Center code: WUGSC
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: M13; 99%
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HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence of Homo sapiens clone
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                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                          runs of \tilde{N}, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil be preserved.
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                      1120
1220
2643
2743
7459
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1119: contig of 1119 bp in length
1219: gap of unknown length
2642: contig of 1423 bp in length
2742: gap of unknown length
7458: contig of 4716 bp in length
7558: gap of unknown length
11010: contig of 3452 bp in length
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Pred. No. 73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
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19736
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   /note="assembly_name:Contig26"
87796. .98686
                                                                                             57507. .66359
                                                                                                                                                                                                                  29768. .35444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
                                            /note="assembly_name:Contig25"
                                                            /note="assembly_name:Contig24"
66460. .76814
                                                                                                                                                                                                                                                          /note="assembly_name:Contig18"
                                                                                                                                                                                                                                                                           /note="assembly_name:Contig17"
19736. .24016
                                                                                                                                                                                                                                                                                                         /note="assembly_name:Contig16"
15161. .19635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-330P9"
                                                                                                      note="assembly_name:Contig23"
                                                                                                                                   note="assembly_name:Contig22"
                                                                                                                                                                   note="assembly_name:Contig21"
                                                                                                                                                                                                                             note="assembly_name:Contig19"
                                                                                                                                                                                                                                                                                                                                                  note="assembly_name:Contig15"
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                               .87695
                                                                                                                                                                                                                                                . 29667
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of 13536 bp in
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of 10355 bp in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF096268 13186 bp DNA ROD 19-FEB-ZUU Marmota monax lymphotoxin-beta (LT-beta), tumor necrosis fac (TNF), and lymphotoxin-alpha (LT-alpha) genes, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (29-SEP-1998) Microbiology, Pathology & Parasitology, College of Veterinary Medicine, North Carolina State University, 4700 Hillsborough St., Raleigh, NC 27606, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 13186)
Li,D.H. and Cullen,J.M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li,D.H., Havell,E.A., Brown,C.L. and Cullen,J.M. Woodchuck lymphotoxin-alpha, -beta and tumor necrosis structure, characterization and biological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marmota monax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 242 (1-2), 295-305 (2000)
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/db_xref="taxon:9995"
619. .624
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126103. 139276
/note-"assembly_name:Contig30"
139377. .159274
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98787. .112322
                                                                                                                                                                                                                                               /product="lymphotoxin-beta"
650. .2549
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/note="assembly_name:Contig32"
185752, .187027
/codon_start=1
/product="lymphotoxin-beta"
/protein_id="AAF34866.1"
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46859 c 48198 g 44042 t
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/gene="LT-beta"
                                                                                  )oin(659. .820,1224.
/gene="LT-beta"
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Pred. No. 73;
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                                                                                                   /product="lymphotoxin-alpha"
/protein_id="AAF94868.1"
/protein_id="AAF94868.1"
/db_xref="G1:7001359"
/translation="mTPPGRLYLPRVRGTRLLFLLLGLLLALPPRAKGLPGVGLLPSA
/translation="mTPPGRLYLPRVRGTRLLFLLGLLLALPPRAKGLPGVGLLPSA
ARAAQQHPOKHFAHGTLKPAAHLVGDPSMQNGLRWRANTDRAFLHGFSLSNNSLLVP
TSGLYFVYSQVVFSGEGCSSKAVSTPLYLAHEVQLFSSQYPFHVPLLSAQKSVCPGPQ
GPWRSYYQGAVFLLTMRQDLSTHTDGISHLLFSPSSVFFGAFAL"
complement(10968...11073)
complement(11159.
/gene="LT-alpha"
                                                                                                                                                                                                                                                                                                                 complement(join(10312. .10724,10968. .11073,11159.
/gene="LT-alpha"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                   9693. .9698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(7236.
/gene="TNF"
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LVWLSRRANALLANGMELIDNQLVVPANGLYLVYSQVLFKGQGCPSYVLLTHTVSRFA
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/gene="LT-beta"
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complement(9678. .11687)
/gene="LT-alpha"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(7833.
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7833. .8174))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(9678.
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/protein_id="AAF34867.1"
/db_xref="G1:7001358"
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/gene="LT-beta"
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AL03447.1 GI:4007715
50S ribosomal protein L32; acy;
50S ribosomal protein L32; acy;
acylphosphatase; acyltransferase; ammonium transporter; amt;
ATP-dependent DNA helicase; chromosome associated protein;
ATP-dependent DNA helicase; ddlA; formamidopyrimidine-DNA.
D-alanine-D-alanine ligase; ddlA; formamidopyrimidine-DNA.
glycosylase; fpg; ftsy; glnB; glycerol-3-phosphate dehydrogenase;
gpdA; KDO transferase; kdtB; methylase; nitrogen regulatory protein
P-II; phosphomethylpyrimidine kinase; prokaryotic docking protein;
recG; ribonuclease III; rnc; rpmB; rpmF; SRP54; sugar transporter;
thiamine monphosphate kinase; thiD; thiL; transcriptional
                                                                                                                                                                                                                                                                                                                     Submitted (09-DEC-1998) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrellesanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
3 (bases 1 to 32039)
Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83;
(URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complement
                                                                                available on the World Wide Web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bentley, S.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murphy,L. and Harris,D.
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                                                                                                                                                    Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                            A set of ordered cosmids and a detailed genetic and for the 8 Mb Streptomyces coelicolor A3(2) chromosom Mol. Microbiol. 21 (1), 77-96 (1996)
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/gene="LT-alpha"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     overlapping sections once, or longer, because we arrange small overlap between neighbouring submissions. Cosmid 77 between 102 and 221 on the AseI-B genomic restriction fra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequenced clone. It may be shorter because we only overlapping sections once, or longer, because we are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the movement of the code of the cod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prediction is based on positional base preference in codons using specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS which show significant similarity to other CDS in the database The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in codons is given for each CDS.
Usually the highest scoring match found by fasta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMPORTANT: This sequence MAY NOT be the entire insert sequenced clone. It may be shorter because we only so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        jun/cgi-bin/frameplot.pl. CAUTION: correct initiation codon. Where po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           upstream initiation codon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="SC7Al 02, possible acyltransferase, len: 2 similar to several proposed acyltransferase eg. (EMBL:297188) acyltransferase from Mycobacterium tuberculosis (251 aa) fasta scores; opt: 266, z-s 384.5, E(): 4e-14, (29.7% identity in 229 aa over
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(97...735)
/gene="SC7A1.01c"
/note="SC7A1.01c"
/note="SC7A1.01c, unknown, len: 212aa; similar to
//note="SC7A1.01c"
//note="SC
                                                          /product"putative acyltransferase"
/protein_id="CAA22401.1"
/protein_id="CAA22401.1"
/db_xref="G1:4007717"
/translation="MPRRRIGFWYRLAAVICKPPLVVLIKRDWRGMENIPAEGGFITA
/translation="MPRRRIGFWYRFLAKSGLEKKGFVGAAMRCGQIPVYRESTDALS
VNHNSHYDDFRYAHYQYNTGRVPRFLAKSGLEKKGFVGAAMRCJTKCPUTPVACWGCU
AFRAAIDAVERGECYAFYPEGTLTRODDGWPHAXTGAARMALJTKCPUTPVACWGCU
ELLPPYAKKPSVLPRKTHQVLAGPPVDLSRFYDREMTTEVLKEATEVIMAAVTRQLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACPAVADVAVVTDDARAGRELAALGAGVVADEPGGGLNAALAHGAAVVRAARPESPVA
ALNADLPALRPAELARVLAAATQFPRAFLPDAAGIGTTLLTVAPGQELAPAFGADSRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RHRASGAVELRLDAVDSVRQDVDTGGDLRSALALGVGPRTAAVAARLLIAGQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein SC7A1.01c"
/protein_id="CAA22400.1"
/db_xref="GI:4007716"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EMBL: AL031124).
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/clone="cosmid 7A1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Streptomyces
/strain="A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SC7A1.02"
/note="SC7A1.02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SC7A1.01c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="SC7A1.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="Overlap with Streptomyces
RGEKAPETPYDPRRERIEQRRRTQQAKSQVAPPRTHGPQAEGQST*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation-"MQWTLVVPVKALARAKSRLSDTADDGLRPGLALAFAQDTVAAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .32039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coelicolor A3(2)"
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                                                                                                                                                             complement(4119. .4352)

/gene="SC7A1.05c"
/note="SC7A1.05c, conserved hypothetical protein, len
/note="SC7A1.05c, conserved hypotheticals eg.
77aa; similar to several putative /hypotheticals eg.
TR:028868 (EMBL:AE001007) proposed transcriptional
regulatory protein from Archaeoglobus fulgidus (77 ar
fasta scores; opt: 123, z-score: 217.3, E(): 8.3e-05
(31.9% identity in 69 aa overlap)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SC7A1.03"
/note="Pfam match to entry PF01210 NAD_G1y3P_dh,
NAD-dependent glycerol-3-phosphate dehydrogenase
295.10, E-value 8.8e-85"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycerol-3-phosphate dehydrogenase from Bacillus subtilis (345 aa) fasta scores; opt: 874, z-score: 1221.4, E(): 0, (41.8% identity in 330 as overlap). Contains a possible PS00017 ATP /GTP-binding site motif A (P-loop) and Pfam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"SC7A1.04, ddlA, D-alanine-D-alanine ligase, len: 389aa; similar to many eg. SW:DDLA_SALTY D-alanine-D-alanine ligase from Salmonella typhimurium (363 aa) fasta scores; opt: 742, z-score: 1018.5, E(): (39.3% identity in 377 aa overlap). Contains PS00843 D-alanine-D-alanine ligase signature 1."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="SC7A1.03"
/note="PS00017 ATP
2772. .3941
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/db_xref="GI:4007720"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="SC7A1.04"
/note="PS00843 D-alanine-D-alanine ligase signature 1."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGSSIGITKVDDLAGLDEAIEEARRHDPKILVEAALRGREIECGVLEFEDGPRASVPA
EIPPPSEHAYYDFEAKYIDSTPGIVPAPLTAEETAEVQRLAVAAFDAASCEGLVRADF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MSTENLPONPEQSPRRPPRKPRVAVVFGGRSSEHGISVVTAGAVLAAIDRTRYDVLP1GITRDGRWALTADEPERWAITERRTPDVEELAESTEGGVLLPVD
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VGQDKEYMKAVFTSYGLKVGPYAVIRPREWEQDRSGARKKIVDFAGEHGWPLFVKPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="SC7A1.04"
2772. .3941
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TRGLAETTRLGVALGADPLTFSGLAGLGDLVATCSSPLSRNHTFGTNLGKGMTLEETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="glycerol-3-phosphate dehydrogenase"
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translation="MVQAYILIQTEVGKASTVAETISKLPGVIQAEDVTGPYDVIVRA/
                                                                                                                       transl_table=11
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/protein_id="CAA22403.1"
/db_xref="GI:4007719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVTKQTAEGVKSCESVLDLARRHGVDMPITETVVAIVHEGKSPVVAVKELMSRSAKPE
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/transl_table=11
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1670. .2680
                                                                                                                                                       codon_start=
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Search completed: June Job time: 26090 sec
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Best Local
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                                                                                12693 GAGGC 12689
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                                                                                                                                                                                                                                                                                       Local Similarity nes 69; Conserv
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                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SC7A1.06"
/note="SC7A1.06,
                                                                                                                                                                                                                                                                                                                                                      /note="SC7Al.06, thiL, thiamine monphosphate kinase, len:
322aa; similar to many eg. TR:P95118 (EMBL:283018)
hypothetical protein from Mycobacterium tuberculosis (333
aa) fasta scores; opt: 959, z-score: 1227.0, E(): 0,
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/gene="SC7A1.06"
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Pred. No. 87;
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em_esthum26:*
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em_esthum25:* em_esthum21:*
em_esthum22:*

em_esthum20:

em_esthum23:*

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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gb_est6:*
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Result
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        em_gss_pln1:
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DS ALLO48326
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ANJ5592
ANJ5592
ANJ5669
ANJ5693
ANJ51747
ALGENTAL
SHORT ANJ517811
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AA343594 EST49403
AL048326 DKFZp586B
AL048326 DKFZp586B
AL048326 DKFZp586B
AL069472 DKCosophil
AZ049266 GSSBTU081
A1972528 wr38f07.x
AL073486 Drosophil
AQ384363 RPCII1-13
AW347779 32002 MAR
AW325992 16587 MAR
H12582 y112f12.s1
AQ074469 CIT-HSP-2
AW006059 wr884d06.x
AI1050839 ov12906.x
AI1050839 ov12906.x
AI158414 wc94910.x
D36725 CELK036DXF
BF035938 601457622
AW517811 xu61802.x
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9b est48: *
9b est59: *
9b est51: *
9b est51: *
9b est52: *
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9b est55: *
9b est56: *
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9b est66: *
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9b est810: *
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REFERENCE
AUTHORS
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SOURCE
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                                                                                                           JOURNAL
MEDLINE
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35.26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA343594 243 bp
EST49403 Gall bladder I
AA343594
                                                                     Other_ESTs: THC104718
Contact: Kerlavage, AR
                                                                                                                                                                                              , Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L. Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Weit, F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fanno, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
                                                   Bioinformatics
                                                                  Contact: Kerlavage,
                                                                                                                       Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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               Institute for Genomic Medical Center Drive,
3018699056
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Primates;
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                                  Research
                 Rockville,
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                 ð
                 20850
                                                                                                                                                                                                                                                   Kim, A.K., Kozak, D.L.,
                  USA
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N51572 yy86d05.s1
AQ254230 CpG0716A
B26675 T15G3TF TAM
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AI246358 qil3b09.x
AI263453 qi07b02.x
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AA677757 zi12f01.s
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N75389 za80h08.s1
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N33165 yy35a10.s1
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AI783986 tn91c05.x
BF353680 QV2-HT069
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D35295 CELK019E2F
D36401 CELK032G1F
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H86954 ys72h12.s1
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DKF2p586B2324_s1 586 (synonyn
DKF2p586B2324, mRNA sequence.
AL048326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: M13 Reverse.
                                                                            Please contact the RZPD: Ressourcenzentrum, Berlin- Charlottenburg, GERMANY; Email: clo
                                                                                                                   No r1 sequence available.
This clone (DKFZp586B2324) is available at the RZPD in
                                                                                                                                                           sequenced by Qiagen (Hilden/Germany) within the consortium of the German Genome Project.
                                                                                                                                                                                                  Clone from S. Wiemann, Molecular Genome Analysis, Research Center (DKFZ); Email s.wiemann@dkfz- heid
                                                                                                                                                                                                                                          Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 3' sequence of the clone insert
                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
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                                                                                                                                                                                                                                                                                                             Contact: Duesterhoeft A
                                                                                                                                                                                                                                                                                                                                                                                            Duesterhoeft,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
1 (bases 1 to 790)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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/note="Organ: gall bladder; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI"
a 37 c 54 g 88 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="ATCC (inhost):145105"
/db_xref="taxon:9606"
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                       location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Gall bladder I"
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Pred. No. 0.1;
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clone@rzpd.de.
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/clone="DKFZp586B2324"

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                                                                                                                                                                                                                                                                                                                           Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC ilbrary was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 190genic strain y2; cn bw sp. the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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BACR29H14 of RPC1-98 library from Drosophila melanogaster (frui
fly), genomic survey sequence.
AL069472
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                                                                           /note="end :
                                                                                                           /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-88"
/clone="BACR29H14"
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/lab_host="DH10B"
/lab_host="DH10B"
/note="Vector: pSport1; Site_1: Not1; Site_2:
Not2; Site_2: N
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                                                                  TTCATATAAGCGATGGTGATTTACGCTCGGCCATAGCTGCGTCCTGCGCCCATTCCACCCG 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 5411-4621-3316/1683 Fax: 5411-4481-1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Zandomeni,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: zandomeni@inta.gov.ar
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                                                                                                                                                                                                                                                                                                       /clone_lib="Sheared genomic library"
/note="Vector: pBluescript SK(-) (STRATAGENE); Genomic was mechanically sheared, blunt ended, and size-fractionated by agarose gel electrophoresis.
Fragments between 1.5-3 Kb were recovered and ligated the EcoRV site of the pBluescript SK (-) vector."
112 c 97 g 63 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                    with a modified polylinker; plasmid DNA from the normalized library NCI_CGAP_Pr22 was prepared, and scircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from a pool of 5,000 clones made from the same library (cloneIDs 98508-986759, l101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. "a subtraction by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NCI_CGAP_Pr28"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:2489989"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'lab_host="DH10B"
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Pred. No. 1.6;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                              832 CGTARTARCGRCAGCGCARARGAGAGAGTTTGGAGAGAMAGARTCTGTAAAGAGGAGGTT
                                                                                                                                                                                                                                                                                                                                                                         261 CTTAATGGGGTGGGAGAGGCTGCAGAGTTTTTTGGAAAAAGAGCTCGGAGTTAAGAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    892 AAWGCAGATATMAAMKGCGAARRAGGGCYWCCTGWTGCCCATTAAASCAGMRAATAAGAG
                                                                                                                                                                                                                                       772 SGAAGAAATGTAWTCTGTYCCCCACACTAAGTCAAARGAACAGATCATGGAGAAAGAGAT 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 AAAACTCCTGAAAGAGGTAAACTGGCTCAAACTTTTTAAGTTCAAAACACCGAAAATGGG 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the 150genic Strain y2; cn bw sp. the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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  AQ384363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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32002 MARC 2PIG :
AW347779
AW347779.1 GI:61
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1 Similarity 55.4%;
72; Conservation
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Zhao, S., Adams, M.D., Nierman, W., Malek, J.,
   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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Other_GSSs: RPCI11-138B19.TJ
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                    scrofa
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/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/RPCI1 Human Male BAC Library"
RPCI1 Human Male BAC Library"
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/clone="RPCI-11-138B19"
/clone_11b="RPCI-11"
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/db_xref="GDB:7552650"
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162 GGCGGAGAGCGGCATCCCCGTGGACATGGTCGGAGGGACGTCCATCGGGGCCTTCATGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 CGTCTTTTACGCTTCGGGCTACACTCCCGACGAGATG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 GGAAGAGCTCGGTATAAAGGTAAAGAGGCTCAGCGGGGTAAGTGCTGGAGCTATCGTTTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCCCTGTACGCCGAGGAGCGGAACTACAGCCAGATG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTAGTTCTTTCGGGAGGGGCTGCCAAGGGTATCGCCCATATAGGTGTTTTAAAAGCTCT 101
                                    1 (bases 1 to 365)
Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M.,
Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Laegreid, W.W. and Keele, J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle 
Unpublished (2000)
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                           Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                 AW325992
                                                                                                                                                                                                                                                                                                                                                                                    AW325992 365 bp
16587 MARC 3BOV Bos t
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Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4366
Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 353) Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T. Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A.,
                                                                                                                                                                               Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Design and use of two pooled tissue normalized cDNA libraries for
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Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
107 c 130 g 57 t
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107 c
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/db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="pooled"
/lab_host="DH10B"
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Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
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                                                                                                                                                                                                                                                                                                                                                                                      5', mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laegreid, W.W.
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                                                                                                                                                                                                         Bovoidea;
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RESULT 1
H12582/c
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AUTHORS
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCCAAGGGTATCGCCCATATAGGTGTTTTAAAAGCTCTGGAAGAGCTCGGTATAAAGGT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATTGGCAATTTGAAATTGAAGAGGTTTGAAGAGGTTAACTTAGTTCTTTCGGGAGGGGG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGCCAAAGTGGTACCATGAAAGGTGAGGGGAGGAGGAGTGCAGAGGCCTCAGTGGAAAAGT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACTTCCAACTTGGGAAGGAAGAGGTGAAAGTATTTCAACTCAGTCCTAGGGTAAGAAGT 228
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PO Box 166, Clay Co
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76;
                                                                               Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H12582 448 bp mRNA EST 27-JUN
yj12f12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone
IMAGE:148559 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mins
and -minmatch 12 options.
Insert Size: 429
High quality sequence stops: 265
Source: IMAGE Consortium, LLNL
                                                                                                                                                                      Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                           ,R., Williamson,A., Wohldman The WashU-Merck EST Project
                                                                                                                                                                                                                           ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons, Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterst,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                         Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
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Seq primer: ATTTAGGTGACACTATAG.
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                                                              Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                 (bases 1 to 448)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
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/clone_lib="MARC 3BOV"
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/lab_host="DH10B"
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Pred. No. 2.5;
0; Mismatches
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2.5;
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                                                                                                                            St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            512 CTTTGGAAAAGTTCAAAGAACCCATAATCGGGGTAGATGTGCTTCCCATAACTCAAGAAA 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
             Contact: Mark Adams

Department of Eukaryotic Genomics,
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACAATATTGAAATTTTGCTCTATTTTCTGATCATGAAACTGATTGTAAAGCTTTTTGACA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTAATAAATGCAANGGTAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76;
                                                                                                                 Unpublished (1998)
Other_GSSs: CIT-HSP-2362F18.TR
                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 458)
                                                                                                                                                                                                                                                                                                                                                        AQ074669 458 bp
CIT-HSP-2362F18.TF C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 429 Std Error: 0.00
                                                                                                                                               Map Building
                                                                                                                                                                                                                                                                                                                                         sequence
                                                                                                                                                              Use of a random human BAC
                                                                                                                                                                          Venter, J.C
                                                                                                                                                                                          Berry, K., Granger, D.,
                                                                                                                                                                                                        Adams, M.D., Rounsley, S.D.,
                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                               AQ074669.1
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/clone="IMAGE:148559"
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                                                                                                                                                                                          Suh, E.,
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                                                                                                                                                                                          Zhao, S.,
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,C., Shizuya,H., Simon,M. and
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Clones are available

Research Genetics (info@resgen.com). BAC

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RESULT 12
AW006059/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wz81d06.x1
similar to
                                                                                                                                                                                                                             www-bio.llnl.gov/bbrp/image/image.html
Seg primer: -40UP from Gibco
High quality sequence stop: 349.
                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: Christopher Moskaluk, M.D., Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Robert_Strausberg@nih.gov
                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2565227"
/clone_11b="NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
/lab_host="DH10B"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: saSite_2: NotI; Cloned unidirectionally. Primer: Oligo
                                                                                                                                                                                                        Location/Qualifiers
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/note="Yector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
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Pred. No. 3.
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                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LINL www-bio.ilni.gov/bbrp/image/image.html
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 327.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
AI050839
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                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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Unpublished (1997)
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National Cancer Institute, Cancer Genome Ana
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                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Gred Lenon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
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                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1637146"
/clone_lib="NCI_CGAP_Kid3"
Fatima Bonaldo.
65 c 57 g
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'512 CTTTGGAAAAGTTCAAAGAACCCATAATCGGGGTAGATGTGCTTCCCATAACTCAAGAAA 571
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similar to
                                                                                                                                                                                                                                                                                                                                                                                    Possible reversed clone: polyT not found Seq primer: -40UP from Gibco High quality sequence stop: 383.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Christopher Moskaluk, M.D., Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                           193
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                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Robert_Strausberg@nih.gov
                                                                                                                                                                          /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"
                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:2633262"
/clone_lib="NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
signet ring_cell_features"
                                                                                                                                                                                                                                                                                                                                                                          1. .616
                                                                                                                                                                                                                                              /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
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TR:076084 076084 ALPHA-CATENIN-LIKE PROTEIN. ;, mRNA
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                                                   Score 36.6; DB Pred. No. 3.9; 0; Mismatches
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CATTTTTAAAAATCAAATGATCCTTTATCTTTTCAGAAATTCATCAATTTTATAAAGAAA 87

Matches Query Match Best Local

76; Conser

Conservative

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Indels Length

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Gaps

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4.9%;

Score 36.4; D Pred. No. 4.8; Mismatches

DB 23; 66;

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                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -40UP from Gibco
High quality sequence stop: 459.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arraying: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-GAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Ana
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1 (bases 1 to 779)
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Insert Length: 230 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                   Ω
                                         /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI; list strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. "
               normalization. "
149 c 136 g
                                                                                                                                                                                                        /tissue_type="colon"
/lab_host="DH10B"
                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Co3"
/sex="pooled"
                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="IMAGE:2326338"
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                   4 others
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                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

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US-09-813-206-832
US-60-281-593-182
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QY 336 ACCAACCTATCTTTGCTCGGCGGATCTGTACACGGGAAAGGCTCTTTACTTCGGCAGAGG 395
Qy 276 GAAGGCTGCAGAGTTTTTGGAAAAAGAGCTCGGAGTTAAGAGGCTGGAAGACCTGAACAT 335
Qy 222 CTGCCTCAAACTTTTTAAGTTCAAAACACCGAAAATGGGCTTAATGGGGTGGGA 275
Qy 162 CGTCTTTTACGCTTCGGGCTACACTCCCGACGAGATGTTAAAACTCCTGAAAGAGGTAAA 221
Qy 102 GGAAGAGCTCGGTATAAAGGTAAAGAGGCTCAGCGGGGTAAGTGCTGGAGCTATCGTTTC 161
Qy 42 CTTAGTTCTTTCGGGAGGGGCTGCCAAGGGTATCGCCCATATAGGTGTTTTAAAAGCTCT 101
Ouery Match 7.0%; Score 52.8; DB 5; Length 4411529; Best Local Similarity 46.2%; Pred. No. 0.0001; Matches 217; Conservative 0; Mismatches 247; Indels 6; Gaps 1;
; TYPE: DNA ; ORGANISM: Mycobacterium tuberculosis ; OTHER INFORMATION: H37Rv US-09-103-840A-1
SOFTWARE: PATENTIN Ver. 2.1 SEQ ID NO 1 LENGTH: 4411529
FITTE OF INVENTION: TUBERCULOSAS FITE REFERENCE: 24366-2007.00 CURRENT APPLICATION NUMBER: US/09/103,840A CURRENT FILING DATE: 1998-06-24 NUMBER OF SEO ID NOS: 2
H40
; Sequence 1, Application US/09103840A ; GENERAL INFORMATION: ; APPLICANT: FLEISCHMAN, Robert D. ; APPLICANT: WHITE, Owen R.

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PRIOR APPLICATION NUMBER: 2000-12-19;
PRIOR APPLICATION NUMBER: US 09/514,000;
PRIOR FILING DATE: 2000-02-23;
NUMBER OF SEQ ID NOS: 13351;
SEQ ID NO 4665;
LENGTH: 858
TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
US-09-739-449-4665
                                    US-09-739-449-213; Sequence 213, Application US/09739449; GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
APPLICANT: Hinkle, Gregory J. APPLICANT: Slater, Steven C.
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APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGCTGCAGAGTTTTTGGAAAAAGAGCTCGGAGTTAAGAGGCTTGGAAGACCTGAACATAC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gccgcattgccggcctgctcgacctgacgatcggcggcggcggcctcttcggcggcatgc 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAACTGGCTCAAACTTTTTAAGTTCAAAACACCGAAAATGGGCTTAATGGGGTGGGAGA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gttgttatctcgccggcaagctcgacgágctggaggaattcgcacgatcgctgacgatgc 205
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45.0%;
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Pred. No. 0.0037;
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Sequence 197, Application US/09668337 GENERAL INFORMATION:

APPLICANT: Hodgson, David M. APPLICANT: Lincoln, Stephen APPLICANT: Russo, Frank D.

Stephen

Spiro, Peter A.

APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:

> Dufour, Gerard E. Banville, Steve C. Bratcher, Shawn R. Russo, Frank

APPLICANT: APPLICANT: APPLICANT:

> Shah, Purvi Rosen, Bruce H. Cohen, Howard J.

APPLICANT: APPLICANT: APPLICANT:

Chalup, Michael S. Hillman, Jennifer Jones, Anissa L.

Jimmy Y.

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US-09-668-337-197
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PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 213
LENGTH: 300663
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Best Local Similarity
Matches 211; Conserv
                                                                                        111909 gcaatggccgcaccctgatcgacggcgctcgtcaatcccgtgcccgt 111957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111609 gttgttatctcgccggcaagctcgacgagctggaggaattcgcacgatcgctgacgatgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111669 gccgcattgccggcctgctcgacctgacgatcggcggcggcggcctcttcggcggcatgc 111728
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NAME/KEY: unsure
LOCATION: (1)..(300663)
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                                                                                                                                                                                                                                                                                                                                 338
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                                                                                                                                                                                                                                                                                                         CAACCTATCTTTGCTCGGCGGATCTGTACACGGGAAAGGCTCTTTACTTCGGCAGAGGTG
                                                                                                                                       ACGAGAATTTTCTACTTGTTGACGGAGGTATAGTGAACAACCTGCCCGT
                                                                                                                                                                                   atctcgtcaccgcgctgcgctcctcctacgcgctgcccggcatcttcgagcccgtgcaat 111908
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                                                                                                                                                                                                                                                                              ccttcatcgctgtcgccacggaactgcgaaccggccacgaggtctggatccatcaaggtg
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45.0%;
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Best Local Similarity 50...
93; Conservative
                                                                         SEQ ID NO 832
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LENGTH: 1098
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OTHER INFORMATION: Incyte ID No: 246400.6.dec
-09-668-337-197
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/1
PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 474
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TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT FILE REFERENCE: PT-0086 US
                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/813,206
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/090,181
                                                                                                                                                                                                                                             APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NUCLEIC AGIN MOLECULES DERIVED FROM A
TITLE OF INVENTION: HUMAN CORONARY ARTERY SMOOTH MUSCLE LIBRARY
FILE REFERENCE: 1600.1023-002
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CURRENT FILING DATE: 2000-09-22
                                                                                           NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 1999-09-28
                                                                                                                                 PRIOR FILING DATE:
                                                                                                                                                  PRIOR FILING DATE: 1998-06-22 PRIOR APPLICATION NUMBER: 09/
                                                                                                                                                                                                                                                                                                            APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Dougla
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                                    TYPE: DNA
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FEATURE:
                ORGANISM: Homo sapiens
                                                    ENGTH: 2268
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Stockdreher, Theresa K.
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Wright, Rachel J.
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PCT-US01-01339-6834/c
; Sequence 6834, Application PC/TUS0101339
; GENERAL INFORMATION:
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Best Local Similarity
Thes 71; Conserve
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; LOCATION: (1)...(2268)
; OTHER INFORMATION: n = A,T,C or G
US-09-813-206-832
                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; NAME/KBY: misc_feature
; OTHER INFORMATION: Incyte ID No: 399300.18
US-60-281-593-182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Amy Lasek
TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
FILE REFERENCE: PA-0045 P
CURRENT FILLING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PERL Program
SEQ ID NO 182
LENGTH: 2478
TYPE: DNA
SOFTWARE: PatentIn Ver. SEQ ID NO 6834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                               APPLICANT: Human Genome Sciences, Inc., et al TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PC006PCT CURRENT APPLICATION NUMBER: PCT/US01/01339 CURRENT FILING DATE: 2001-03-17 NUMBER OF SEQ ID NOS: 10231
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                                                                                                                                                                                                                                                  2443 actaataaatg 2453
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                                                                                                                                                                                                                                                                                   632 ATTCGGAAAAG 642
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54.2%;
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                                                                                                                        Inc., et al.
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; OTHER INFORMATION: Description US-09-270-849B-23466
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US-09-270-849B-23466
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                                                                                                                                                             SEQ ID NO 23466
LENGTH: 897
TYPE: DNA
                                                                                                                                                                                                                                                                                           Sequence 23466, Application US/09270849B
GENERAL INFORMATION:
APPLICANT: Swimmer et al.
TITLE OF INVENTION: Insect genome survey devices
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CURRENT FILING DATE: 2001-03-17
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 6835
LENGTH: 639
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GENERAL INFORMATION:
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Best Local Similarity 57.48;
                   Query Match
Best Local
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Best Local Similarity 57.4%;
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CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                        FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: PC006PCT
                                                                                                                          FEATURE:
                                                                                                                                           ORGANISM: Artificial Sequence
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   1 Similarity
69; Conserv
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     Conservative
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                   54.3%;
Score 34.2; D
Pred. No. 2.2;
0; Mismatches
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Pred. No. 1.7;
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                                                                                                       of Artificial Sequence: Synthetic
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RESULT 11
US-09-739-449-77/c
Sequence 77, Application US/09739449;
GENERAL INFORMATION:
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APPLICANT: Human Genome Sciences, Inc., et al.; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies; FILE REFERENCE: PC006PCT
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Best Local Similarity
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CURRENT FILING DATE: 2001-03-17
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 749
SEQ ID NO 749
                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: SITE LOCATION: (618) OTHER INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                NAME/KEY: SITE LOCATION: (643
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                                                                                             GTATTAMAATTGTAGAMAGTGTGATAGCCAACTT 484
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Pred. No. 3.8;
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23

Genome

Sequences

Uses

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RESULT 13
US-09-270-849B-128449
; Sequence 128449, Application US/09270849B
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 4015
SEQ ID NO 4015
LENGTH: 936
TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
US-09-739-449-4015
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NAME/KEY: unsure

LOCATION: (1)..(711)

OTHER INFORMATION: unsure
US-09-739-449-77
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Matches
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SEQ ID NO 77
LENGTH: 711
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Best Local Similarity 47.5%;
Matches 96; Conservative
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APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
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nes 62; Conservative
                                                                                                                                                                      TTGTTGACGGAGGTATAGTGAACAACCTGCCGTAGAACCTTTGGAAAAGTTCAAAGAAC 532
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                                                                                                                     CCATAATCGGGGTAGATGTGCT 554
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mismatches
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Pred. No. 7.2;
0; Mismatches 106;
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APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: Characterization of the Ye
TITLE OF INVENTION: Transcriptome
FILE REFERENCE: 01107.78572
CURRENT APPLICATION NUMBER: US/09/335,032
CURRENT FILING DATE: 1999-06-16
PRIOR APPLICATION NUMBER: US 60/035,917
PRIOR APPLICATION NUMBER: US 60/035,917
PRIOR APPLICATION NUMBER: US 09/012,031
PRIOR FILING DATE: 1997-01-23
PRIOR FILING DATE: 1998-01-22
NUMBER OF SEO ID NOS: 12219
CONTENTAL DESCRIPTION OF TRANSCRIPTION OF TRANSCRIPT
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 128449
LENGTH: 873
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SEQ ID NO 12217
LENGTH: 784328
TYPE: DNA
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Best Local Similarity
Matches 77; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Insect genome survey devices FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Velculescu, Victor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Swimmer et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Saccharomyces cerevisiae
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                          483 AGGTATAGTGAACCAACCTGCCCGTAGAACCTTTGGAAAAGTTCAAAGAACCCATAATCGG 542
                                                                                                                                                                 543
603 AAGGAGCTTCT 613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        680 TTGAAGAGTTCTCTCTCTGGACGTAAATAAG 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 tggttaaagtgactgcgcagatctgaagcgccatctacagggtagagctagatggcttca 129
                                                                                                                                                          GGTAGATGTGCTTCCCATAACTCAAGAAAGAAAGATTAAAAATATACTCCACATCCTTAT 602
                                                                                                                                                                                                                                                                                                                                                                  69;
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52.7%;
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                                                                                                                                                                                                                                                                                                                                                                                              Score 31.8;
Pred. No. 66;
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Db 476895 ATGTATATGCT 476885

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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June 2, 2001, 20:50:58; Search time 10284.9 Seconds (without alignments) 1075.447 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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,	58.2	63.2	66.4	66.4	66.4	68	83	72.4	73.4	739	Score
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DA100710D	AE004756	A96530	AX044035	AE002562	A96526	NMA122491	A96528	AP001516	AB025342	AE000737	ID
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/protein_id="NADH dehydrogenase I chain L"
/protein_id="NACO7352.1"
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/translation="MEGLEVLETPLIAFLIILAFGRKIGDLGSGLLASYLLIGYYHEOKK
MTDERGKWVERKFYAYLSLEFFAMLLIVLSDHLLGIFGREGVGLGASYLLIGYYHEOKK
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MTRADERGKWVERKFYAYLSHAMAGDTPVSALLHAATMYAAGYYMYARLYPMEEATPOTIK
ATKASFEAEVMNRIGDWLFIFFIFFTVSALLHAATMYAAGYGDKGGAMFHLTTHA
FGAVURKGGGFLTWAMAGDTPVSALLHAATMYAAGYGDKGGAMFHLTTHA
FFKALLFLAAGAVITAFHHHLYDIFKMGLKKYMPVTYVAFMIGALSLAGVPFSGGW
SKDRIVASMYEWSGULGVLGTUTVAFITAYYAFREGFLYBHGRESMREIYDKVHEVEG
VMTVPMGLLGFLTVLTGLFGLWLEHWYVGLIGGEEKGIHLSVALVSLGVALAGIWLAW
AVYVKEVIDVNKAYESLKFIHTTFKEDFFTEKLYHNVAKGYLVVSRVAXKVGDRTVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                elcosapentaenoic acid biosynthesis gene cluster from the docosahexaenoic acid-producing bacterium Vibrio marinus strain MP-1 Biotechnol. Lett. 21, 939-945 (1999)

2 (bases 1 to 41587)
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Isolation of clustered genes that are notably homologous to the
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Direct Submission
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1. .41587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transl_table=11/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes, complete cds, similar to eicosapentaenoic
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Query Match
Best Local :
                                                                                                                                                                                                    Local Similarity hes 252; Conserv
TTGGCTTAGTCCTTTCTGGCGGTGGTGCGAAAGGTATTGCTCATCTTGGTGTATTAAAAT 7495
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                                                                                                                                                                                                         Conservative
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Takami, H.,
Sasaki, R.,
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AP001516 BA000004
AP001516.1 GI:10175192
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/transl_table=11 /transl_table=11 /product="stage V sporulation protein (soprulation /product="stage V sporulation protein) (spore cortex)" /protein_id="stage V sporulation" /protein_id="stage V sporulation" /protein_id="stage V sporulation" /translation="mrvsurvrrrlifvLvgLafflimLrLgvvpfaLgDwLrgq AQDSWSEDVPFEAKRGEITDRNDVVLATMVSAPSILVVPRQVKDPAETAEKLANVLQM AQDSWSEDVPFEAKRGEIVRLNPEGRKISKDKANEVRKLRLPGVYIAEDSKRHYPFGSYLS HVLGFAGIDNQGLTGLELYYDEQLKGEKGHVSFFSDAKGGRLPNLADEYTAPINGLKL RLTIDSRRVQTILERLDIAETYSPDGALAIAMNPNTGEILGMSSRHYNPERFREVP PEVYNQNKPIMMQYEPGSTFKIITLAAALEENEVDLINDRFHDPGFIEVAGHRLRCWK KGGHGSQTFLEVVENSCNPFQVVAGERLGKDRLFDYIEAFGFGQKTGIDLGGEAKGII FNNDRIGPLEAMTAFGGQUSVTPPIQQVAAVSAAVNGGTLYEPTYAKDWVDPYTGEVV ESSAPKMKRQIISETSKEVRYALESVVARGTGQGAFVDGYRVGGKTGTAQKAKDGRY LENNHIYSFIGFAPADDPQIVVVVAIDNPKDTVQFGGVVAAPIVGKIIGDSLQALGIE KRENQIEXEKKWNDEPLVEPDLVGRTKRDLHESYYELKIDADGKGDVVVAQAPEPGT KVANGSTIRLYMDDDTEPTD"	complement(1792113) /gene="spovD" /note="BH2572"	. 11		Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and Technology Center, Deep-sea Microorganisms Research Group; 2-15 Natsushima, Yokosuka, Kanagawa 237-0061, Japan (F-mail-takamih@lamatec on in	11 (bases 1 to 300950) Takami, H. and Takaki, Y. Direct Submission		ki,Y., Sasaki,R., Maeno,G., Sal mi,H.	Analysis of the genome of an alkaliphilic Bacillus strain from an industrial point of view Extremophiles 4 (2), 99-108 (2000) 20263314	-4331 (2000)	Ogasawara, N., Kuhara, S. alkaliphilic bacterium E comparison with Bacillus	943-945 (199 ., Maeno,G.,	49-284; Springer-Verlag (1999) (51tes) ant,H. and Horikoshi,K. dentification of facultatively alkaliphilic Bacillus sp. C-125	123 n) Extremophiles in deep-sea environments (Ed.); HORIKOSHI, K. TSUJII;	tes) .H. analysis of facultatively alkalihilic Bacillus halodurans	Extremophiles 3 (3), 227-233 (1999) 99411980	Genetic analysis of the chromosome of alkaliphilic Bacillus
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Patent: WO 9924578-A 561 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAF
CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA
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                                    /organism="unidentified"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis
segment 1/7.
Details of N. meningitidis sequencing at available on the World Wide Web.
                                                sequencing team, Sanger Hinxton, Cambridge CB10
                                                                             Direct Submission
Submitted (30-MAR-2000) Submitted on behalf of the Neisseria
                                                                                                                                                                                Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth, Davies,R.M., Davis,P., Deviln,K., Feltwell,T., Hamlin,N., Holroyd,S., Jagels,K., Leather,S., Moule,S., Mungall,K., Quail,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M., Skelton,J., Whitehead,S., Spratt,B.G. and Barrell,B.G. Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491
                                                                                                                                                                                                                                                                                                                                                                                                                      AL162752 AL157959
AL162752.2 GI:7378778
                                Notes:
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                                                                                                                     Parkhill,J
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                                                Centre, Wellcome Trust Genome Cam
1SA E-mail: parkhill@sanger.ac.uk
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Location/Qualifiers
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                                                                                                                                                                                                                                                    NADH-Ubiquinone oxidoreductase (complex I), chain N-terminus, score 77.20, E-value 3.5e-19" complement (2487. .2828)
/gene="NMA0003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPMLYGDFFKDVIFVNADAHPTMHIMKEEFHGALAMVSHSLHSPVLYLAIAGVLSAWL
LYVKLPHLPAKIAQAFRPVYVLFENKYYLDALYFNVFAKGTRALGTFFWKVGDTAIID
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/gene="nuoL"
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/gene="NMA0001"
                                                                                                                                                                                                                  complement(2487. .2828)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NADH-Ubiquinone/plastoquinone (complex I), various chains, score 351.80, E-value 7.3e-102"
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/translation="mSNTQTIRSADFTTSRAWGALDIANMNGTTVRLHWTDQPYKWHV
NDGEEVFAVMDGEVDMHYRENGEEHIVRLKSGDIFYAGIGTEHVAHPRGETRILVIEK
/product="hypothetical protein NMA0003"
/protein_id="CAB83323.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="nuoL"
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/protein_id="CAB83322.1"
/db_xref="G1:7378780"
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/protein_id="CAB83321.:
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complement(38. .358)
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                                                                                                         codon_start-
                                                                                                                                                                                    /gene="NMA0003"
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                                                                           transl_table=11/
                                                                                                                                       note-"NMA0003, unknown,
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/gene="nuoK"
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/gene="nuoK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              score 141.50, E-value 1 complement(3863. .4534)
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/gene="NMA0004"
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/gene="NMA0004"
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/note="NMA0004, unknown, len: 191 aa; similar to hypothetical proteins e.g. Y977, HAEIN H10977 (191 aa), fasta scores; E(): 0; 80.5% identity in 190 aa overlap, and to proteins involved in cell cycle e.g. TR:054679 (EMBL:AF036487) Lactococcus lactis Plasmid pNZ4000 putative mobilization protein (200 aa), fasta scores; E(): 0, 55.1% identity in 167 aa overlap, and FIC_ECOLI cell filamentation protein FIC (200 aa), fasta scores; E(): 0.093, 29.4% identity in 126 aa overlap"
                                                                                                                                                                                                 /note="NMA0006, nuoJ, NADH dehydrogenase I chain J, len: 223 aa; similar to many e.g. NUOJ_RHOCA NADH dehydrogenase I chain J (EC 1.6.5.3) (202 aa), fatsa scores; E(): 9.7e-21; 41.3% identity in 201 aa overlap. Contains Pfam match to entry PF00499 oxidored_q3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NADH-ubiquinone/plastoquinone oxidoreductase chain score 141.50, E-value 1.5e-38"
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IHRYLFGGLYDFAGQIREDNISKGGFRFANAMYLKEALVKIEQMPERTFEEIIAKYVE
MNIAHPFLEGNGRSTRIWLDLVLKKNLKKVVMWQNVSKTLYLQAMERSPVNDLELRFL
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/translation="mmdKnQLEQEFHKAMLNIYQEALNLPQPYKATRFLQIVNEFGGK
EAADKLLSTGEKKTQTGFTELILSGGGVHALKYSMEYLVLQKPWCDLFTEEQLAVARK
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/protein_id="CAB83325.1"
/db_xref="GI:7378783"
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/product="NADH dehydrogenase I chain
/protein_id="CAB83326.1"
                                                                                                                                                           NADH-ubiquinone/plastoquinone
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/protein_id="CAB83324.1"
/db_xref="GI:7378782"
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/trans1ation="MTFQLIEVIFAVIILYGAIKTVTAKNPVHAALHLVLTFCVSAM
/trans1ation="MTFQLIEVIFAVIILYGAIKTVTAKNPVHAALHLVLTFCVSAM
LMMLMQAEFLGVTLVVVYVGAVMLFLEVVMMLNIDIEEMRAGFWRHAPVAGVVGTLL
AVALILILVNPKTDLAAFGLMKDIPADYNNIRDLGSRIYTDYLLPFELAAVLLLLGMV
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/gene="NMA0007"
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/protein_id="CAB83327.1"
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/gene="nuoJ"
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                                                                                                                                                                                                                                                                                                                                          Neisseria;
Bacteria;
                                                                 Tettelin,H., Saunders,N.J., Heidelberg,J., Jeffries,A.C.,
Nelson,K.E., Eisen,J.A., Ketchum,K.A., Hood,D.W., Peden,J.F.,
Dodson,R.J., Nelson,W.C., Gwinn,M.L., DeBoy,R., Pereson,J.D.,
Hickey,E.K., Haft,D.H., Salzberg,S.L., White,O., Fleischmann,R.D.,
Dougherty,B.A., Mason,T., Ciecko,A., Parksey,D.S., Blair,E.,
Cittone,H., Clark,E.B., Cotton,M.D., Utterback,T.R., Khouri,H.,
Qin,H., Vamathevan,J., Gill,J., Scarlato,V., Masignani,V.O.,
Qin,H., Vamathevan,J., Gill,J., Scarlato,V., Masignani,V.O.,
Citton, V., Vamathevan,J., Gill,J., Control                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisserial antigens
Patent: WO 9924578-A 559 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAP
CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA
                       Pizza, M., Grandi, G., Sun, L., Rappuoli, R. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pizza, M.,
                                                                                                                                                                                                                                                                                                               Neisseria.
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meningitidis MC58
Proteobacteria; beta subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scarlato, V., Rappuoli, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.9<del>8</del>;
46.2<del>8</del>;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _xref="taxon:32644"
230 c 255 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
Neisseria meningitidis serogroup
                                                     Smith, H.O., Fraser, C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B strain MC58
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                                                                                                                                                                                                                                                                                                                                                Neisseriaceae;
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'EGA (IT)
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                                                        Moxon, E.R.,
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CDS

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REFERENCE
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MEDLINE
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Science 287
20175755
10710307
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2 (bases 1 to 9831)

Tettelin, H., Saunders N.J., Heidelberg, J., Jeffries, A.C.,

Tettelin, H., Saunders N.J., Ketchum, K.A., Hood, D.W., Peden, J.F.,

Nelson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.D.,

Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D.,

Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D.,

Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, E.,

Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H.,

Qin, H., Vanathevan, J., Gill, J., Scarlato, V., Masignani, V.,

Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R.,

Rappuoli, R. and Venter, J.C.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (17-MAR-2000) The Institute for Genomic Medical Center Dr. Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287 (5459), 1809-1815 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MSRHPAPTGEKTFFGHPFQLSTLFHIELWERFSFYGMQGILLIY
LYYTADKGGLGIDKTLAGGIVGAYSGSVYLST ILGAWFADRWGAEKTLFLSGIVVML
GHIVLAAAPGLYGLLIGLIFIALGSGGVKSTASSMVGALYEQDEMPFLRGFJFYI
AINIGGFLGPLLTGLLGENIGFHYGFGAAAVGMAFGLWRYSLGRKNLPHPTVPHPLSK
GQGKTAAAVGIALIAALATAIKTGLVNLDNFSGILLSTVILAVIAYFARLLTNPRVSS
DNKRHIIAYIPLFLTICMFWAYWFQIYTVATVYFDETYNRTIGSFTYPYAWKDSMQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="NMB2137"
2752. .2964
                                                  /translation="meaevinglnntlndlekrsedirvymdygkkdrleeviglse
DPELWNDPKRAQEIGKERKILEGIVLTLDNIASGIEDNRMLIEMTVEENDEEGFAAVQ
EDVAGLEKQMADLEFKRMFNGPADPNNCFIDITAGAGGTEAEDWAGMLFRMYSRYAER
                                                                                                                                                                                                                                                                                                      /note="similar to GB:M38590 SP:P28353 PID:154276 percent
identity: 80.11; identified by sequence similarity;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                 complement(3122. .4225)
/gene="NMB2138"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVLAITIGELMISPIALSISTKIAPPLFKTQMVALNFLAFSLGFTLGGVLFEKGYQAG
DEIGFYRLLFYIGAATGFLLLLLVPKLNKMLEGTD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WVILFSGLMAAMWTKMGRKQPKTPLKFAMAVFVTGASFLGFVPFISSGTPMPIAVFAL
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772. .2229
FASVFVYPEIDDSIEIEINPADLRIDTYRASGAGGQHINKTDSAVRITHEPTGIVVQC
                               KGFRIEILEEDDGEIAGINRATIRVEGEYAYGLLRTETGVHRLVRYSPFDSNNKRHTS
                                                                                                                                                      /product="peptide chain release factor
/protein_id="AAF42446.1"
/db_xref="GI:7227395"
                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="MB2138"
complement(3122. .4225)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MLKQPTRTLGGQRHCVLFGLAPNGVWPAAYCYQMRGAPLPHLFT
LTCAAKAAIGGFAFCSTFRRVTAPGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
/product="hypothetical protein"
/protein_id="AAF42445.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="peptide transporter"
/protein_id="AAF42444.1"
/db_xref="GI:7227393"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Neisseria meningitidis MC58"
/strain="MC58"
/strain="MC58"
/note="serogroup: B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to GB:AL009126 percent identity:
ldentified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="NMB2136"
                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'db_xref="GI:7227394"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="NMB2137"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="hypothetical protein; identified by Glimmer2;
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/note="conserved hypothetical protein; identified by
Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                     LKMGGWARKQFDRVAERLPLALHGLSMSLGGQAPLDTDLIDGIKEMMRRYDCTFFSDH
LSYCHDGGHLYDLLPLPFTEEMVHHTARRIREVQDRLGCRIAVENTSYYLHSPLAEMN
EVEFLNAVAREADCGIHLDVNNIYVNAVNHGLLSPEAFLENVDAERVCYIHIAGHDVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAHGSCGASKSAEGSCGAAGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MKIGTTWQTASAMLVLRLFAAYEFLESGLQKWNGENWFSEINDQ
FPFPFNLLPDALNWNLAMYAELLLPVLLLLGLATRLSALGLMVVTAVAWAAVHAGSGY
NVCDNGYKMALIYIVVLIPLLFQGAGGWSLDTLLKKRFCPRCRLKQD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="NMB2140"
5566. .6015
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LGKTDLVDLTLSTSGFIKGEKLQNYINRKVGGRQIQQFPIKFAAVATDFETGKAVAFN
QGNAGQAVRASAAIPNVFQPVIIGRHTYVDGGLSQPVPVSAARRQGANFVIAVDISAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="conserved hypothetical
Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(4328. .5221)
/gene="NMB2139"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEEAARAALPEIKRKLAAYRY"
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IKDLRTGYEVGNTKAVLDGDLDGFIEASLKQGV"
                                                                                                                                                                                                                                                               QTRAGKECRRAA"
                                                                                                                                                                                                                                                                                             TPELLIDTHGAAVLPTVWDLLELAYAKLPTIPPTLLERDFNFPPFSELEAEVAKIADY
                                                                                                                                                                                                                                                                                                                                                                                                      /product="conserved hypothetical protein"
/protein_id="AAF42450.1"
/db_xref="GI:727399"
/translation="MPSEPGKNMIQHAGLGYRRDLAEDFLSLSENSPICFIEAAPENW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          putative"
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/db_xref="GI:7227396"
/product="conserved hypothetical protein"
                           transt,
                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="NMB2142"
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/protein_id="AAF42449.1"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="NMB2141"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="conserved hypothetical protein"
/protein_id="AAF42448.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGKNISQGFFSYLDQTLNVMSVSALQNELGQADVVIKPQVLDLGAVGGFDQKKRAIRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="NMB2139"
                                                                                                                                                'gene="NMB2143"
                                                                                                                                                                                                gene-"NMB2143"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transl_table=11/
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GTTATCATCGGCAGGCATACATATGTTGACGGCGGTCTGTCGCAGCCCGTGCCCGT 4626
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                                              GTTGAGTACGAGAATTTTCTACTTGTTGACGGAGGTATAGTGAACAACCTGCCCGT 506
                                                                                                 CAGGGGAATGCCGGGCAGGCTGTGCGCGCCTTCCGCCGAATGTGTTCCAACCC
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                                                                                                                                                                                              CCCATCAAATTTGCCGCCGTTGCTACTGATTTTGAAACCGGCAAGGCCGTCGCTTTCAAT 4742
                                                                                                                                                                                                                                               AACATACCAACCTATCTTTGCTCGGCGGATCTGTACACGGGAAAGGCTCTTTACTTCGGC 390
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8705. .8884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
/product="hypothetical protein"
/protein_id="AAF42453.1"
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putative"
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GHWTQEGQPQHWNTPEKSLNNNEFQKILQSCLYNLPENTARVFTLKEILGFSSDEIQQ
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/protein_id="AAF42452.1"
/db_xref="GI:7227401"
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/db_xref="GI:7227400"
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Best Local Similarity 46.2%;
Matches 220; Conservative
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                                                                                                                                                                 GTTGAGTACGAGAATTTTCTACTTGTTGACGGAGGTATAGTGAACAACCTGCCCGT
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                                                                                                                                                                                                                                                                                                      CCCATCAAATTTGCCGCCGTTGCTACTGATTTTGAAACCGGCAAGGCCGTCGCTTTCAAT 153441
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                                                                                                                                          GTTATCATCGGCAGGCATACATATGTTGACGGCGGTCTGTCGCAGCCCGTGCCCGT 153325
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Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AX044035 172325 bp I
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Scarselli, M.,
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Stover, C.K., Pham, X.Q., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.,
                                                                                                                                                                                                                              genome.
AE004756
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Pizza, M., Scarlato, V., Rappuoli, R., Grandi, G. and Masignani, V. Neisserial antigens
Patent: WO 9924578-A 563 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOLI RINO CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
                                                          1 (bases 1 to 11039)
Stover, C.K., Pham, X.Q
                                                                                                                                               Pseudomonas aeruginosa
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5.1 GI:994
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228 c 257 g 21
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Pred. No. 3.1e-07;
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2 (bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Westbrook-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lin,R.M., Smith,K.A., S Wong,G.K.-S., Wu.Z., Paulsen,I.T., Reizer,J., Saier,M.H Hancock,R.E.W., Lory,S. and Olson,M.V.
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Complete genome sequence
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_406 (6799), 959-964 (2000)
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GLTVVRSASNLFAHCVTVLPEGADQGFGSSAA"
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Kowalik,D.
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ARDMGVDVVIVVDIGNPLRDRKDLSTVLDVMNQSITLMTRKNSEAQLATLKPGDVLIQ
PPLSGYGTTDFGRVPQLIDAGYRATTVLAARLAELRKPKDLNSEALDVARTPNQRKPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NPEAIDELRGRYPALLQMPATETPAATTKDDDWSDLPLAESPVLQQPDATSGADGFGD
LNLDLDLDWGALENPLDNPDLPRRAAAGKAEPAEEPLAFESNLHELPDVAEYEHLELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPLRRAPRPPAAAPABAKVEEQARPPVAAPSSPPPSPPPAPAAAPRAAMAAADKLDGA
DIYIAYGRYGQARDLLRQVLAEQPQRLSARMKLLLVLAELGDAAGFDALAEETLASGG
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        Genetique, FRANCE
                                          Submitted (18-AUG-1997) P. Glaser, Regulation de l'Expression Genetique, Institut Pasteur, 28 Rue du Dr Roux, Paris, 75724,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ctaA gene; ctaB gene; ctaC gene; ctaD gene; ctaE gene; ctaF gene; ctaG gene; ctaG gene; ctaG gene; ctaC gene; ctaC gene; ctaC gene; carboxylaSe; ribosomal protein L32; rpmF gene; subunit I; subunit II; subunit III; subunit IV; ylaP gene; ylbA gene; ylbB gene; ylbC gene; ylbD gene; ylbE gene; ylbF gene; ylbG gene; ylbH gene; ylbI gene; ylbK gene; ylbD gene; ylbM gene; ylbM gene; ylbM gene; ylbM gene; ylbA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z98682
Z98682.1 GI:2339988
                                                                                                                           Direct Submission
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2 (bases 1
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Bacillus subtilis chromosomal
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Institut Pasteur, 28

Bacillus/Clostridium group;

Bacillus.

Glaser,P., Richou,A. and Dawsonal region downstream nprE

and Danchin, A.

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Query Match Best Local Similarity - 44 TAGTTCTTTCGGGAGGGGCTGCCAAGGGTATCGCCCATATAGGTGTTTTTAAAAGCTCTGG 103 164 TCTTTTACGCTTCGGGCTACACTCCCGACGAGATGTTAAAACTCCTGAAAGAGGTAAACT 223 ACGAACAGGGCATCCAGATCGACGCCATCGCCGGCACCAGCATGGGCGCGGTGGTCGGCG AAGAGCTCGGTATAAAGGTAAAGAGGCTCAGCGGGGTAAGTGCTGGAGCTATCGTTTCCG TGGTCCTCTCCGGCGGTGCCGCCCGCGGCCTGGCCCATATCGGCGTGCTCAAGGCCCTCG 3696 GCCTGTACGCCTCCGGCTACACCCCCCGCGAACTGGAGCGCATCGCCCTGGAGATGGACT 3816 Bacillus subtilis genomic DNA 23.9kB fragment. Conservative 23897 bp 7.8%; 57.4%; 0; Score Pred. Mismatches e 58.2; DB 1; | No. 1.3e-05; | Smatches 78; Length 11039; Indels 19-AUG-1997 0, Gaps 3756 163 0

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FEATURES
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LEIEKA"
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                                                                                                                                                                                                                                                                                                                                                                                       4441. .5358
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                                                                                                                                                                                                                                                                                                                                                              codon_start=1
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9195. .9527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLPGQGLETGNLISTIGAFFMAAAVILLLVNVIWTSVKGEYVGADPWHDGRTLEWTVS
SPPPEYNFKQLPFVRGLDPLWIEKQAGHKSMTPAEPVDDIHMPNGSILPLIISFGLFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVIPVVLYTIELADTSPMDKKGRKAEDALVVNVRANILWWEEFEYPDYGIITSGELIVP
TDQRVYFNIKASDVKHSFWIPSYGGKLDTNTDMENKFFIFDSKRSKEAGDMFFGKCA
ELCGPSHALMDFKVYTMSAKEFOGFWTKEMKNYKSTAESDLAKOGEELFKEKNCLISCHA
VEPNDKRAEAARTAPNLATFGERTKVAGVKEANKENVKAWLKDPDSIKPGNKMTGTYP
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                                                                                                                                                               9195. .9527
/gene="ctaf"
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'gene="ctaD"
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transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58
                                                                                                                                                                                       ATCATCGCTTCGGATGTTTCCAGGGTTCGAAAAA 17660
                                                                                                                                                                                                                                                                                                                                              GACGCCCCCCTCCATCCAATTCCCCCTTTCTCTTGTGAAAGACATGCGAGCTGATATT 17626
                                                                                                                                                                                                                                                                                                                                                                                                                       GACGGAGGTATAGTGAACAACCTGCCCGTAGAACCTTTGGAAAAGTTCAAAGAACCCATA 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAAGTTGTTCCATACCCGGGATTTTTGAACCAGTTGAGTACGAGAATTTTCTACTTGTT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATCTACAGACGGGAGAAAAGATTGTGTTCCGAAAAGGATCAGTGTCAGATGCAGTGAGG 17506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATCTGTACACGGGAAAGGCTCTTTACTTCGGCAGAGGTGACTTAATTCCCGTGCTTCTC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTTATACATTCGGAAAACCGATTGAAGAGCTCCAAATCCCGCTGGGCATTGTTGCGTGT 17446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAGAGCTCGGAGTTAAGAGGCTGGAAGACCTGAACATACCAACCTATCTTTGCTCGGCG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATTATACGGTGCCGAAACTCGGTTTTTTAAAAGGTGACCGCGTCAGACAGCTTGTGCAT 17386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGTTCAAAACACCGAAAATGGGCTTAATGGGGTGGGAGAAGGCTGCAGAGTTTTTGGAA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGACATGACGTGGCAACGATGAAAAAAGTAGCCAAAGCCTTTAAACGAAGGCTTTATGCT 17326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTACACTCCCGACGAGATGTTAAAACTCCTGAAAGAGGTAAACTGGCTCAAACTTTTT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGGTAAAGAGGCTCAGCGGGGTAAGTGCTGGAGCTATCGTTTTCCGTCTTTTACGCTTCG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGGGCCCAGAGGGCTTGCTCATCTCGGTGTGCTTTCCAGTTTACATAAGCACCAAATT 17206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGGCTGCCAAGGGTATCGCCCATATAGGTGTTTTAAAAGCTCTGGAAGAGCTCGGTATA 117
                                                                                                                                                                                                                                                                    ATCGGGGTAGATGTGCTTCCCATAACTCAAGAAA 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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EAMRLCVPADMMGQVPLTGPEMLNTLPLLEDQQLGAVMMKIIQEIVYGTFLAVIFFQW
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/gene="ctaG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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MEDLINE
REFERENCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Borriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Bron, S., Brouillet, S., Bruschi, C.V., Caldwell, B., Capuano, V., Carter, N. M., Choi, S. K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Emmerson, P.T., Entian, K.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Galiger, D., Fitz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Galiger, D., Fitz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Gandi, G., Guiseppi, G., Guy, B.J., Haga, K., Haiech, J., Harwood, C.R., Henaut, A., Hibbert, H., Holsappel, S., Hosono, S., Hullo, M.F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y., Klaerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Frandins, A., Frandin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur, Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75 Paris Cedex 15, FRANCE B. F.mail: moszer@pasteur.fr panadanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus subtilis
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The complete genome sequence of the gram-positive bacterium Bacillus subtilis
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Bacillus subtilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus/Staphylococcus group;
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                                                                                                                                                                                                                                                                                                                                                                          /gene="ykzD"
/function="unknown"
/note="similar to hypothetical proteins from B. subtilis"
                                                                                                                                          /db_xref="SPTREMBL:034405"
/translation="MEKKEEQYINQAEYVPHPTKEGEYALFLHETYHLLSEDDETQTT
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/db_xref="GI:2633700"
                                                                                                                                                                                                                                                                                                 /transl_table=11
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/strain="168"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="ykzD"
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                                                                 .2044
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2857. 3039
/gene="ykoL"
/db_xref="STTREMBL:034949"
/db_xref="STTREMBL:034949"
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EFAVLELLYTRGPQKLQQIGSRLLLVSGNVTYVIDKLERNGFLVREQDPKDKRSVYAH
LTDKGNEYLDKIYPIHALRIARAFSGLSPDEQDQLIVLLKKAGIHSQHLLFR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MYQNMTYDELILRIIILLRDGKIRDFRSVIDALQPYDMAFIFKE MPEKHARYLSYLTVDDITDMIGELEREFQLVVLNKVGKTKATLAMNKHUNDDLAQLL EEMDEELKEQLLSSMEASESKAVQLLMNYPADSAGRMMTNRYWHIPQHYTYKDAVYKL KSFAEIAESINYLYVLNESKOLYGYLSYRDLIIGEPEEKVQDLMFTRVISADALQDQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation-"MTTEDHSYKDKKVISIGIVSELTGLSVRQIRYYEERKLIYPQRS
SRGTRKYSFADVERLMDIANKREDGVQTAEIIKDMRKKÉQMLKNDPQVRKKMLEGQLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of nrgAB, nasB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(2087. .2419)
/gene="tnrA"
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KAYVAAYRRLPWLILLLFIGLISGSIISYFEDALKQVVALAFFMPMVSGMTGNTGTQS
                                                                                           /codon_start=1
/transl_table=11
/protein_id="CAB13207.1"
/db_xref="GI:2633705"
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2614. .2769
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/db_xref="GI:2633701"
                                                                                                                                                                                                        /gene-"ykoM"
/function-"unknown"
                                                                                                                                                                                 /note="similar to transcriptional regulator
                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAB13206.1"
/db_xref="GI:2633704"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAB13205.1"
/db_xref="GI:2633703"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAB13204
/db_xref="GI:2633702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         'codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation-"MEEEKAVSLAKEIIELDIKRDEMLETFMQLAGEQAFQLLRSVQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transl_table=11
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                                                                                                                                                                                                                                                                                                                           FFRSITNHKNYPYTR"
                                                                                                                                                                                                                                                                                                                                                                     'db_xref="SPTREMBL:034763"
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                                                                                                                                                                                                                                                                                                                                                lation-"MSNLLKSALEKERRHYSEKLYQIGVYNKEVMNKMTISELRKEYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 3039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al nitrogen regulation (positive regulation gabP, ureABC; negative regulation of
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                      238 AAGTTCAAAACACCGAAAATGGGCTTAATGGGGTGGGAGAAGGCTGCAGAGTTTTTGGAA 297
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                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                    GGACATGACGTGGCAACGATGAAAAAAGTAGCCAAAGCCTTTAAACGAAGGCTTTATGCT
                                                                                                                                                                 GAAGTGGATATGATTGCAGGAAGCAGCATGGGCGCTTTGGTGGGCAGTTTTTACGCCGCC 176749
                                                                                                                                                                                                             AAGGTAAAGAGGCTCAGCGGGGTAAGTGCTGGAGCTATCGTTTCCGTCTTTTACGCTTCG 177
                                                                                                                                                                                                                                                           GGAGGGGCCAGAGGGCTTGCTCATCTCGGTGTGCTTTCCAGTTTACATAAGCACCAAATT 176689
                                                                                                                GGCTACACTCCCGACGAGATGTTAAAACTCCTGAAAGAGGTAAACTGGCTCAAACTTTTT
                                                                                                                                                                                                                                                                                                       GGGGCTGCCAAGGGTATCGCCCATATAGGTGTTTTAAAAAGCTCTGGAAGAGCTCGGTATA 117
                                                                                                                                                                                                                                                                                                                                                           227;
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RLEKLSSVaylkwiqyfpkrysgiyellacceefqhdkryfmyecvfyoqmhilqek
QPDIAFCTHALPSYLLNRLKPEYPNLTVNVVTDFVNQLMGRNIDYHFVPSTEVKK
QLISEGIDQNNIYLTGIPVHQNFEMESADTLQHHPPYTIITTGSSMGVGGILKMVQEL
SPGGKILYKILCGRNEKLYSYVKSLHHPLIEAIPYLHSKAEMNRLYEQATGIMTKPGG
VTISECLQKRLPVFIYHALPGQEEMNLNLLHERKLYTDMRNMDMQKAEEYIAAFFQSN
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KLKPAYGMYAVFGNHDYVLKBEDFQRLKRVLBENGCITLQNEHVRIETAAGPVNIIGI
DDYSTNRSNITGSYQSLENGYHLVLTHDPNIILDMKDVHYDYLLSGHFHGGQIHWPKP
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VVLSDGTHIRKNDVLVKIHLHNIKLIRELQSIESAVRKGIIIYQKVYPSMPLLLDYIN
NHKKSEKIKGNHWITMLDKGVERLGFDVITPVNPFYRCFKKVSHVPILXLTSKPVSLR
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/db_xref="G1:2633707"
/db_xref="SPTREMBL:034495"
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/protein_id="CAB13208.1"
/db_xref="GI:2633706"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YHLVKMGKLVRMNMIKGLHYHHDKPFYISEGLGQTGVNIRVGSRPEVTFHQI"
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1864. .5415
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note="similar to hypothetical proteins
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7.3%;
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Pred. No. 0.0002;
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                                                                        available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E., Tekaia, F., Badcock, K., Basham, D., Chillingworth, T., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A., Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
                                                                                                                                                                                                                                                                                                                                         Trust denome compus, minor, community 28 rue du Docteur Roux, Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk on Jun 27, 1998 this sequence version replaced gi:1460072.
                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA Unite de Genetique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tu
Z77250 AL123456
Z77250.1 GI:326
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                              CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation code
                                                                                                                                                                                                                                                                                                     Details of M.
                                                                                                                                                                                                                                                                                                                              Notes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parkhill,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barrell,B.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence
5), 537-544 (1998)
Where possible we choose an initiation codon which is preceded by an upstream ribosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   initiation codon.
                              complement(2038.
/gene="Rv2559c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Rv2557, (MTCY9C4.11c), similar to MTCY9C4.10c (69.2%)
                                                                                                                                     /translation="mpgSagwrkvfggTggaTgalprhgrgSivyarsTTIEAQPLSV
DIGIAHVRDVVMPALQEIDGCVGVSLLVDRQSGRCIATSAWETLEAMRASVERVAPIR
DRAALMFAGSARVEEWDIALLHRDHPSHEGACVRATWLKVVPDQLGRSLEFYRTSVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SWISS-PROT:050741"
/translation="MTGGATGALPRTMKEGWIVYARSTTIQAQSECIDTGIAHVRDVV
MPALQGMDGCIGVSLLVDRQSGRCIATSAWETAEAMHASREQVTPIRDRCAEMFGGTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTWQSIVLVDLNQDNPRRSVRLSFVEG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mlDvDTarrrIvDLtDavrafCTaHDDGLCNvfvPHaTaGVaII
ETGAGSDEDLVDTLVRLLPRDDRYRHAHGSYGHGADHLLPAFVAPSVTVPVSGGQPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           overlap"
                                                                                     DVAEFELAIAHLRVPELV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Rv2556c, (MTCY09C4.12), len: 129. Conserved
/note="Rv2556c, (MTCY09C4.12), len: 129. Conserved
hypothetical protein similar to AE000961|AE000961,
Archaeoglobus fulgidus (126 aa) fasta scores: opi
z-score: 312.5 E(): 7e-10; 35.8% identity in:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="H37Rv"
/db_xref="taxon:1773"
/clone="Y9C4"
                                                                                                      ELESLDGFCSASLMVDHPACRRAVSCSTFDSMDAMARNRDRASELRSRRVRELGAEVL
                                                                                                                                                                                                                                        /transl_table=11
/product="hypothetical protein
/protein_id="CABD1046.1"
/db_xref="GI:1460082"
                                                                                                                                                                                                                                                                                                                                                                           /note="Rv2558, (MTCY9C4.10c), toMTCY9C4.11c (69.2% identity
                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="Rv2558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Rv2558"
1298. .2008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVEEWE IAAMHRDHRSAEGACVRATWVKVPADQVDQGIEYYKSSVLPQIEGLDGFCSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical
/protein_id="CAB01047.
/db_xref="GI:1460083"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical
/protein_id="CAB01048...
/db_xref="GI:1460084"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Rv2556c"
/note="b-^~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Rv2556c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mycobacterium
/strain="H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLLVDRTSGRAVSSATFDSFDAMERNRDQSNALKATSLREAGGEELDECEFELALAHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="YW318"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:1773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mycobacterium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:1773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mycobacterium"
                                                                                                                                                                                                                     'db_xref="SWISS-PROT:Q50740"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="Rv2557"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'db_xref="SWISS-PROT:Q50742"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
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                                                       3396)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aı protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tuberculosis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tuberculosis'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown,
identity
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                                                                                                                                                                                                                                                                                                   Rv2558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rv2557*
                                                                                                                                                                                                                                                                                                                                                                           len: 236, highly similar
in 224 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rv2556c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        len:
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misc_feature
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VKEVRAVIENSRKALLHGEQTYLFIDEVHRESKTQQDALLSAVEHRVVLLVAATTENP
SFSVVAPLLSRSLILQLFREDTRAVQVARIDDPRGLGRAVAVAPEAVDLLVQDAG
GDARRALTALEVAAEAQAAGELVSVQTIERSVDKAAVRYDDDGDQHYDVYSAFIKSV
RGSDVDAALHYLARMLVAGEDPRFIARRLMILASEDIGMAGPSALQVAVAAAQTYALI
GMPEAQLTLAHATIHLATAPKSNAVTTALAAAMNDIKAGKAGLVPAHLRDGHYSGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              egYCAJ_HAEIN P45262 hypothetical protein hi1590. (446 aa FASTA scores, opt: 1140, z-score: 1193.7, E(): 0, (42.5% identity in 428 aa overlap); contains PS00017 ATP/GTP-binding site motif A; also to MTCY227.09, (30.1% identit in 296 aa overlapy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLPPGYNAPPPPPGYGPPPGPPPPGYPTHLQSSGFSVGDAISWSWNRFTQNAVTLVVP
VLAYAVALAAVIGATAGLVVALSDRATTAYTNTSGVSSESVDITMTPAAGIVMFLGYI
ALFALVLYMHAGILTGCLDIADGKPVTIATFFRPRNLGLVLVTGLLIVAVTFIGGLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RG.
                                                                        /translation="maeqkvkrnvelagvdvilvhrmiknevpvseylfmtdvvaqcl
DESVRKLATPLTHDFEGIGETSTHYIDLATSDMPPAVPDHSFFGLLWADVKFEWHALP
                                                                                                                                                                                                                                                                /gene="Rv2562"
5225. .5614
                                                                                                                                                                                                                                                                                                                   /db_xref="SWISS-PROT:Q50737"
/translation="MGIQRAVLLIADIGGYTNYMHWNRKHLAHAQWTVAQLLESVIDA
AKCMKLAKLEGDAAFFWAPGGQHQCPGMRPAPADAPEVPHAARADQKRPSLRL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(3160. .3183)
                                                      YLLGFKKACAGFRSLGRGATEEPAEMG'
                                                                                                                           /product="hypothetical protein
/protein_id="CAB01042.1"
/db_xref="GI:1460078"
                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein
/protein_id="CAB01043.1"
/db_xref="GT:1460079"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLCFVGMLIGIPVAALIHVYTYRKLSGGQVVEAVRPAPPVGWPPGPQLA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIPGLIFGFVAQFAVAFAVDRSTSPIDSVKASIETVGSNIGGSVLSWLAQLTAVLVGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"hypothetical protein
/protein_id-"CAB01044.1"
/db_xref-"GI:1460080"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3542. .4519
/gene="Rv2560"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGNAQGYKYSHDDPDGVVAQQYPPDELVDVDYYRPTGRGGEREIAGRLDRLRAIIRKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="SWISS-PROT:Q50739"
/translation="MPEAVSDGLFDVPGVPMTSGHDLGASAGAPLAVRMRPASLDEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein
/protein_id="CAB01045.1"
/db_xref="GI:1460081"
/gene="Rv2563"
5757. .6806
                                                                                                                                                                                                                             /note="Rv2562,
                                                                                                                                                                                                                                            /gene="Rv2562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="Rv2561"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Rv2560,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Rv2560"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="PS00017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Rv2559c"
                                                                                                             'db_xref="SWISS-PROT:Q50736"
                                                                                                                                                                                    transl_table=11
                                                                                                                                                                                                       codon_start-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="Rv2561,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Rv2561"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MSQPPEHPGNPADPQGGNQGAGSYPPPGYGAPPPPPGYGPPPGT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="SWISS-PROT:Q50738"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="Rv2559c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'codon_start-]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP/GTP-binding
                                                                                                                                                                                                                         (MTCY9C4.06c),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MTCY9C4.07c),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MTCY9C4.08c),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MTCY9C4.09),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          len:
                                                                                                                                                                                                                           len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 len:
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                                                                                                                                                                    Rv2562"
                                                                                                                                                                                                                                                                                                                                                                                                                   Rv2561"
                                                                                                                                                                                                                             129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97. Unknown"
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                                                                                                                                                                                                                         Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unknown
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, (42.5%
                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                          SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rocas
                                                                                                                                                  MEDLINE
                                                                                                                                                                                                                           TITLE
                                                                                                             AUTHORS
                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9421
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CDS

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Query Match
Best Local Sim
Matches 217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTACGAGAATTTTCTACTTGTTGACGGAGGTATAGTGAACAACCTGCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Silvesti, M.L., Siqueira, W.J., de Souza, A.A., de S
Terenzi, M.F., Truffl, D., Tsai, S.M., Tsuhako, M.H.,
Sluys, M.A., Verjovski-Almeida, S., Vettore, A.L., Za-
Meidanis, J. and Setubai, J.C.
The genome sequence of the plant pathogen Xylella
Tylella fastidiosa Consortium of the Organization
Sequencing and Analysis, Sao Paulo, Brazil
Nature, 406 (6792), 151-157 (2000)
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Xylella fastidiosa, sec
AE003860 AE003849
AE003860.1 GI:9104830
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Xylella fastidiosa
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349 aa overlap"
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46.2%;
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Martins, E.M. F., Matsukuma, A.Y., Menck, C.F.M., Miracca, E.C.,
Miyaki, C.Y., Monteiro-Vitorello, C.B., Moon, D.H., Nagai, M.A.,
Nascimento, A.L.T.O., Netto, L.E.S., Nhani Jr. A., Nobrega, F.G.,
Nunes, L.R., Oliveira, M.A., de Oliveira, M.C., de Oliveira, R.C.,
Palmieri, D.A., Paris, A., Peixoto, B.R., Pereira, G.A.G., Pereira
Jr., H.A., Pesquero, J.B., Quagqio, R.B., Roberto, P.G., Rodriques, V.,
de M. Rosa, A.J., de Rosa Jr., V.E., de Sa, R.G., Santelli, R.V.,
de M. Rosa, A.J., de Rosa Jr., V.E., da Silva, F.R., da Silva, A.M., Silva
Jr., W.A., da Silva, A.C.R., da Silva, F.R., da Silva, A.M., Silva
Jr., W.A., da Silveira, J.F., Silvestri, M.L.Z., Siqueira, W.J., de
Souza, A.A., de Souza, A.P., Terenzi, M.F., Truffi, D., Tsai, S.M.,
Tsuhako, M.H., Vallada, H., Van Sluys, M.A., Verjovski-Almeida, S.,
Vettore, A.L., Zago, M.A., Zatz, M., Meidanis, J. and Setubal, J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lopes, C.R., Machado, J.A., Machado, M.A., Madeira, A.M.B.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Frohme, M., Furlan, L.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ferreira, V.C.A., Ferro, J.A., Fraga, J.S.,
                                                                                                /note-"similar to GI|5921548 (percent identity: 37 %/query alignment coverage: 93.4 %/subject alignment coverage: 95.7 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERRWLACKAVDIKLKAVIRELIDDQVRRVQRAENIQRENLIQLEIAVALRDDKERLGT
LEKVAAEWNKGINWYSERINFLEVVETWSLISQAVSEGITADITAINDLYRLEKVNQT
AAKTIIDQAKVDPGINMRKIVREKLQNAKPITNEKNATIDSRMQESKTDFQEGETHLQ
NISNOEKPAYVASAFLPDAAQLYALAAKQMETLCTEVSALSKILHQRQDVISALGDV
LQNVYQAQAALFRIRHVLASLANSK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment coverage: 64.9 %/subject alignment coverage: 65.1 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                  complement(2427. .3152)
/gene="XF0063"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity; putative; ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(277. .1356)
/gene="XF0061"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(277. .1356)
/gene="XF0061"
                                                                                                                                                                                                                                                                                     complement(2427. .3152)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
/protein_id="AAF82875.1"
/db_xref="GI:9104832"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="hypothetical protein; identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1331. .1657)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(1331. .1657)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MLLLQTLFELDRATAMSLEGNRIKPTQEQNQLATVAFSGEHIEE
IDPELIDLEKQMRSKDNPGETIESLMELGNDMKRDGQHEPVILRKNSKKPGRYLMVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="transcriptional repressor"
/protein_id="AAF82874.1"
/db_xref="GI:9104831"
                                                                                                                                                                                                                                                                                                                                                                                                                              LEWDQNFKNTNEICAENTSPIQSIYRPRPPEQHVNIFPILIPHLMPVQHLKMYQARHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="xF0062"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to SP|P07674 (percent identity: 28 %/query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Xylella fastidiosa"
/dh vref="taxon:2371"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
/product="competence protein F"
                                                                                                                                                                                                                                                /gene="XF0063"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MYHRSIFQRSNSIHNETVKHKCWSDLQNHDIDTTYPLPNSTNNI/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="XF0062"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:2371
                                                                  codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brazil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .10593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goldman, G.H., Goldman, M.H.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Franca, S.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Franco, M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laigret, F.,
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/gene="XF0067"
6138. .6377
/gene="XF0067"
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4281. .4382
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CQLLLPRMENACLRCAAPLKELEGIHPTCGPCLYDPPPLETAHAAFLYHWPINKLISR
FKFHQDLACGHLLADNNAMAAQHWPRFQALVPVSLHHGRLRTRGYDQALELARHYGNR
LQLPCLPALRRVRATLPQSQLNANKRRSNLHNAFIPIHPLPAHVALVDDVMTTGTTLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MSLINHKNGVSCNCGSTCSRDILNRLLMRRVVSGCNRYPVHLSY LALSSMCFTFRCSFLATIVVALLTACSSAPRSASRLSSVSQLSDISLPPLRIGIALGG GAAKGFAHIGVLKMLEANGLAPSVVAGTSAGSVVGALYASGMDSFKIGTKAVAMDESN IRDLRFFSGGLYQGQKLQNYVBELVGKRPIEKLNKPFGAIATRLEDGQFRMFVRGNVG EAVRASCSIPGVFEPVTIGAYHYVDGGITSPVPVDAVRQLGADFVIAVDISSKATGKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to SP|034731 (percent identity: 33 %/query alignment coverage: 63.3 %/subject alignment coverage: 96.2 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MSSIIRYDWTAEELHALFDLSLPELLYRAASVHRQHFDDAEIQV
STLLSVKTGGCPEDCSYCPQAQRYDTGVTAQKLMDVDAVVAKARQAKLAGASRFCMGA
AWRSPKDRDIPKIAAMIREVKALGLETCATLGMLNTCQAQALKDAGLDYNHNVDTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment coverage: 94.4 %/subject alignment coverage: 93.1 %); identified by sequence similarity; putative; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFYDSVIHTRQYQDRLDTLAHVRDVGLKTCCGGIVGMGETRQHRVGLLLTLATLPAHP
DSVPVNLLVQVAGTPLHGTQTLDPFEFVRMIAVARITMPRSMVRLSAGRESMSDELQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="
3202. .
                                                       /transl_table=11
/product="hypothetical protein"
/protein_id="AsP82880.1"
/db_xref="GI:9104837"
                                                                                                                                                                                                                       similarity; putative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="conserved hypothetical protein"
/protein_id="AAF82879.1"
/db_xref="GI:9104836"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein"
/protein_id="AAF82878.1"
/db_xref="GI:9104835"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="biotin synthase"
/protein_id="AAF82877.1"
/db_xref="GI:9104834"
/translation="MSCKEIFEYIVIKQCWLPMFFAQMGMVMGAIWCADRYPPIVLIS
RCVLSYYVGWGYRVRFSVILWPMCYWLGVMIVLAF"
                                                                                                                                                                                                                                                                                                                                                                                                                                              AVIPEIREKLAQLQQQRIQAARKTANQSAIEAVESYRRCQNSRTRWEKLRGKEKDCTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGGLVGTVNQSISIMGQHLGEAELKRANIVIHPKVLDIGSTDFDQRNAAILEGERATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="XF0064"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAARALRHTGVTRIDAWICARVP"
                                                                                                                                                                                                                       /note="hypothetical protein; identified by sequence
similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="XF0066"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MATLVDVVSFMYDGVNLDSWSDGGERRKVVEFS"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACKHVV
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                                                                                                                                                                                      'codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="hypothetical protein; identified
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Glimmer/RBSfinder"
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RESULT 15
AE004145
            KEYWORDS
                                      VERSION
                                                                                                          DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGGGGCTGCCAAGGGTATCGCCCATATAGGTGTTTTAAAAGCTCTGGAAGAGCTCGGT 114
                                                                                                                                                                                                                                                      GTGGATGGTATCACTAGTCCGGTACCAGTGGATGCGGTGCGTCAATT
                                                                                                                                                                                                                                                                                                       GTTGACGGAGGTATAGTGAACAACCTGCCCGTAGAACCTTTGGAAAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                        CTCGGAAGTTGTTCCATACCCGGGATTTTTGAACCAGTTGAGTACGAGAATTTTCTACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGCGGTTAGAGGATGGGCAACGTACGATGTTTGTACGCGGGAATGTCGGTGAGGCAGTG 5148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGGATCTGTACACGGGAAAGGCTCTTTACTTCGGCAGAGGTGACTTAATTCCCGTGCTT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATGAACTAGTAGGTAAACGTCCAATCGAAAAGCTGAACAAGCCATTCGGGGCGATCGCC 5088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAAAAGAGCTCGGAGTTAAGAGGCTGGAAGACCTGAACATACCAACCTATCTTTGCTCG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTGACTTGCGTTTTTTCTCGGGTGGCTTGGTACAGGGGCCAGAAACTTCAAAACTATGTC 5028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCGGCATGGACTCGTTCAAGATACAGACAAAAGCGGTTGCTATGGATGAGAGTAATATT 4968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTAGCTCCGAGTGTGCGGGTACCAGTGCTGGTAGTGTGGTGGCGCGCTATACGCC 4908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAAAGGTAAAGAGGCTCAGCGGGGTAAGTGCTGGAGCTATCGTTTTCCGTCTTTACGCT 174
                                                                                                                                                                                                                                                                                                                                                     CGTGCTTCCTGTAGCATCCCAGGTGTATTTGAGCCTGTCACTATTGGGGCCCTACCACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTAAGTTCAAAACACCGAAAATGGGCTTAATGGGGTGGGAGAAGGCTGCAGAGTTTTTG 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGGGCTACACTCCCGACGAGATGTTAAAACTCCTGAAAGAGGTAAACTGGCTCAAACTT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208;
                                                                                                     Vibrio cholerae chromosome
                              chromosome.
AE004145 AE003852
AE004145.1 GI:96
                                                                                                                                 AE004145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="milngehehiqvy.hhlnsfofplnpssdnspysmayerftsai
Tllmhwrnrldpymklargdrygfllllwpymwalwilaggvpmwtlcvyfygiwl
Traggvindytdrwildphuertrireplytgavsprnallmeatlmllirefilvitmo
Traggvindytdrwildphuertrireplytgavsprnallmeatlmligkvptqawllyv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment coverage: 86.8 %/subject alignment coverage: 99.7 %); identified by sequence similarity; putative; ORF located using Glimmer/RBSfinder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(7517. .7909)
/gene="xr0069"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANILWTTAYDTWCAMVDRDDDIKMGAKSTAILFADLDLTVQGVLYTLMLFTLCLVGLR
ATLSHTYWISLIAAVALIGYQFIIARRREPTACFRAFMHNNWVGMTIFAGIALATTH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hydroxybenzoate octaprenyltransferase"
/protein_id="AARB2881.1"
/db_xref="GI:9104838"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(6494. .7495)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="tRNA-Arg-1"
/note="found by tRNAscan"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="tRNA-Arg"
7506. .7582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="XF0068"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="tRNA-Arg-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transl_table=11
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                                 GI:9655032
                                                                                                                               10372 bp
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                                                                                                     Ŧ,
                                                                                                        section 53
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AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                      CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.

1 (bases 1 to 10372)

Heidelberg,J.F., Eisen,J.A., Nelson,W.C., Clayton,R.A., Gwinn,M.L.,

Dodson,R.J., Haft,D.H., Hickey,E.K., Peterson,J.D., Umayam,L.,

Gill,S.R., Nelson,K.E., Read,T.D., Tettelin,H., Richardson,D.,

Ermolaeva,M.D., Vamathevan,J., Bass,S., Tolin,H., Dragoi,I.,

Sellers,P., McDonald,L., Utterback,T., Fleishmann,R.D.,

Nierman,W.C. and White,O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (14-JUN-2000) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 10372)
Heidelberg, J.F., Eise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 406 (6795), 477-483 (2000) 20406833
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Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                       LPGAASINOLTEOLSDLASEWBICPLYGOMEERAQORAIAPTAAGRRKVVLAGYINIAET
SLTIIEGIRIVLDSGLERSARFDLKTGIITRLEOVRIAGRAGRAGRAGRLEFGICVRL
YSEAOLKOOPHVPEPEHHITDLAPLALELAQNGAQPSOLAMLMLPPSSARLAGAQOLLO
RIGLLDARTOITAAGKEAHLLGVEPRIAAMLLSADRLGESALQSALALITVLLEEPERO
VIDVOHSLHRHOQGRHPKQKLLIQRAGSIAHKLDTAFSLSSVDSAWLPLVACLAFPDR
IAQORGOQTOGPELLANHGAWLAVEDBLSAADYLVALDLMRGOTQASOLFFSALEDIN
ALERVLPALISRVEQVDWDEKAGRLSAEAQMRIDQLVLRREKLPEPDKQKMTQALLSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similar to GB:D:
PID:145948; identified
                                                                                                                                                                                                                                                                                                                                                                         VRRKGLTVLQWSEDASEWLARARCAAEWLPEEAWPALDDETLLARLELWLEPYLAGVT
SVKGLQSVSVLQALKHYLGWELSQQLDEWLPTHHLLPTGNHKKIRYQLGMEPTLSVRM
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                                             /product="penicillin-binding protein 1B"
/protein_id="AAF93769.1"
/db_xref="GI:9655034"
                                                                                                                                                                                                                                                 /gene="VC0602"
2539. .4872
                                                                                                                                                                                                                                                                                                                      HVWPDDPANHVATSKTKRQLNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB:U00096 PID:1488196; identified by sequence similarity;
                                                                                                                                                                                                                        /gene="VC0602"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="VC0601"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Vibrio cholerae"
/strain="N16961"
                                                                                                                          transl_table=11/
                                                                                                                                                 codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene-"VC0601"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /serotype="01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note-"biotype:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:666"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eisen, J.A., Nelson, W.C.,
                                                                                                                                                                     GB:D26562 SP:P02919 GB:M12486 GB:X02163 Lfied by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SP:P37024 PID:473807 PID:473806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clayton, R.A.,
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ORIGIN
                                                                                             Matches 100;
                                                                                                       Query Match 6.7%;
Best Local Similarity 54.6%;
Matches 100.
43 TTAGTTCTTTCGGGAGGGGCTGCCAAGGGTATCGCCCATATAGGTGTTTTAAAAGCTCTG 102
                                                                                                                                                                                                                                                                       2457
                                                                                             Conservative
                                                                                                                                                                                                                                                                 DSVIFQEPA"
a 2488 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MLEAYRKHVAERAAEGVVPKPLDAEQVAGLVELLKNPPQGEEAF ILDLLENRIPGVDEAAYVKAGFLTAVARGEVASPLVSREKAAELLGTMQGGVNIEPL IELLDDSALAPIAAKALSHTLLAMENDEYDVEEKAKAGNPEAKQVLQSWADAEWFLSKP ALPEKVTLTVFKVTGETUTDDLSPAPDAWSREDIPVHALAMLKNARDGIEPDVPGKVG PIKQIEALKAKGHQLVYVGDVVGTGSSRKSATNSVLWFMGDDIPNPNKRTGGYVLGG KIAPIFFNTWEDAGALPIEVDVSKLNWGDVIDVYPFEGKVCNHATGEVLATFKLKTDV
                                                                                                                                                                                                                                                                                                                                                                                                                                     LYDEVRAGGRIPLIVGRGLTDKARHALGLEASKEFRRPVAVADSGKGYTLAQKMVGKA
GGVQGLTRGTTCEPKWTTVGSQDTTGEWTRDELKDLACLGFSADLVMQSFCHTSAYPK
PVDVQTHHTLPDFINNRGGVSLRPGDGVIHSWLURWLLPDTVGTGGDSHTRFPLGISF
PAGSGLVAFAAATGVMPLDMPESVLVRFKGKMQPGITLRDLVHAIPYCIKQGLLTVE
KAGKINEFSGRILEIEGVEHLTVEQAFELSDASAERSAAGCTVKLSQASIEEYLNSNI
                                                                                                                                                                                                                                                                                                                           TKMDRDQLIEEGYYGIFGRAGVRIETPGCSLCMGNQARVADKATVMSTSTRNFPNRLG
TGANVYLSSAELAAVGAILGRIPSVAEYMDYAKQIDAAAADTYRYLNFHRMGQYTSKA
                                                                                                                                                                                                                                                                                                                                                                                    CAPNDPDDARLLSECAGETINEVFIGSCMTNIGHFRAAGKLLEKFNGQLNTRLWVAPP
                                                                                                                                                                                                                                                                                                                                                                                                                VMLKWMTAEGYGDRRTIERRIQAMEAWLANPTLMEADKDAQYAHVIEIDLAEIKEPIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="aconitate hydratase 2"
/protein_id="AAF93771.1"
/db_xref="GI:9655036"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to SP:P36683 GB:U00096 PID:2367097;
identified by sequence similarity; putative"
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/gene="VC0604"
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                                                                                          0;
                                                                                                                                                                                                                                                              2872 g
                                                                                    Score 50.2; DB 1; Length 1 Pred. No. 0.0025; 0; Mismatches 83; Indels
                                                                                                                                                                                                                                                                 2555 t
                                                                                                                                              Length 10372;
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                                                                                    Gaps
                                                                                       0;
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'gene="VC0604"

VYRYRWEDNDEGMETSPVYLGASIEYGGVWSDEDLRLQDAELYGAGSIEAGVNSEIGE IMFCYGRTEQNYDSIYEIIGTTEK" RGVFFDYRHDTLDDFSLPQQGIYFDLEYLISKDSFDGSNPLSGDALSSDTVSELSGRL IAAHTFSRHTLVANLDMGVVKSKHSSTPIDPKSIGGFLNLSGIPRNSLIGQNKLYGNL SLAATENYLPVTYSEWVAELALGYQIELWREMKLGARYSKGNGEASSLPVFGDFSFQR EERRKTLRYGDNVQVDEIVLQNNTHYSDLLLLINRLNLEPAQKLSTEEIEASIEDLYAL DRFELVRYQYEQRDDQQQLVVDVREKSWGPNYVNFRFFLEDDFDTESQYALGVSTNFT DINSHGAELALNMDMGTDKLIEAELYSPLLSGQKTFTTALLHFSNERRNAPLAGFDDT DRVDRSQRRVRDKEYEDRYQITTDLGLHWGEVRAPKGVVQGQNMLRMLRETTGNLPAF DSFDQLVIPYRAVATDIIHLQEVVLDKGFLVDAMMASMSVPGALPPYEIDGLWLVDGG

KGAAHMGVLRALEEMHVPVDIITGTSMGAYVGGLYATGMSAEEIEALIYSVDWNRGYR

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transl_table=11 /codon_start=1

'note="identified by Glimmer2; putative"

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VAQPREPGEYASSSSRIELIRRPFEFADGPEPDRRVMLTFDGSGLNKIESLEQKRELG
YLRLEFKLMGHLEKDSPEQRLFLRRDQFPEYLVDALLVTEDRDFYQHDGYSFLAIGRA
MYVNUKAGRTYVQGGSTLTQQLAKNIFLSSDRTLWRKLKEAYMALIIDYRYSKDRILEA
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RARERRDLVLKLMMEHDILTAPEYQQAVTRPLDVQKTAQIASRQPAYFQQVSIELKEK
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IRPVPSMLLGSFSLTPYQVAQMYQTLTNSGKKAPLSALRSVLDLEGNVLYESLPRVSQ
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                                                                                                                                                                                                                      LGDKFKADSGLRVFTSLDPVSQSKLEQAIHDQIPQLAKTAGKDLEAAAIAVDRHSGEI
RAMVGGKRTGYDGFNRVLNASRQIGSLVKPAVYLTALAHPDQYNLATTLEDKPLTLKG
                                                                        TTIWLGRDDNQPTKLTGASGALRVYAQYLKYRIPEKLQLPWPEGITTFGFAKQTQGGL
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5397 TGG 5399
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                                                                                                                                                                                                                      163
                                                                                                                                                                                                                  GTCTTTTACGCTTCGGGCTACACTCCCGACGAGATGTTAAAACTCCTGAAAGAGGTAAAC 222
                                                                                                                                                                                                                                                                                               GAAGAGATGCACGTCCCCGTCGATATCATCACAGGTACCAGTATGGGTGCTTATGTGGGT 5336
                                                                                                                                                                                                                                                                                                                                                            GAAGAGCTCGGTATAAAGGTAAAGAGGCTCAGCGGGGTAAGTGCTGGAGCTATCGTTTCC 162
                                                                    TGG 225
                                                                                                                                             GGGTTATACGCAACAGGAATGAGCGCAGAGGAGATTGAAGCGCTGATTTATAGCGTTGGAT 5396
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Search completed: June Job time: 25640 sec 2 2001, 20:55:42 gene

SdC

/gene="VC0603" 5109. .7403

/gene="VC0603"

5109.

KLDCDNAFKLPIWDNQQQLKQQCENRPTEWIKKLFEW"

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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                           000
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YSIS INC. S, Maffia AM, Murphy D; on RV, Warren PV;		<pre>vF5-34LC. ; ester; chiral compound sugar; lignocellulose; ; ss. lifiers t= (pos: 295297, aa:Gl</pre>	ALIGNMENTS	2.44514 2.24514 C.65853 X13009 X14030 X03030 A15011 Z00822 Z00849	C47253 C47253 X04401 X04344 C91316 A01250	A26697 X13381 A02178 X61534 X61534 X61533 X61533	A81390 X20681 T79332 X20520 X21106 X11108 X11110 X11113 T413482 X11107 X11119 X111111
·		; cheese;		Pinus radiata cell Human lung tumor a Human lung cancer Enterococcus faeca H. pylori GHPO 881 Human IL-lra BAC c Nucleotide sequenc Human secreted pro Human secreted pro	Arabidopsis thalia Human secreted pro Human secreted pro Human secreted coro Human polynucleoti Human colon cancer	Candida albicans p Enterococcus faeca Human colon cancer B. burgdorferi ant B. burgdorferi ant Borrelia burgdorfe	N. meningitidis Me Polynucleotide seq DNA encoding whale Polynucleotide seq Human biallelic po Human biallelic po Human biallelic po ATM gene exons 48-Human biallelic po Human biallelic po

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Best Local
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                                     ggaggtatagtgaacaacctgcccgtagaacctttggaaaagttcaaagaacccataatc
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of Aquifex pyrophilus, a Gram-negative, chemolithoautotrophic knall gas marine bacterium which grows optimally at 85 deg C and pH 6.8. It can be amplified from a pBluescript vector by PCR (see T79306-07). Claimed, newly identified polynucleotides (T79321-30) encoding esterases (W23069-77, W23088) were recovered from genomic gene libraries. They can be used for recombinant production of the enzymes in host cells, and as probes to identify related sequences. The esterases are stable at high temperature and in organic solvents, making them superior for use in production of pure chiral compounds used in pharmaceutical, agricultural and other chemical industries. A method is claimed for transferring an amino group from an amino acid to an alpha-keto acid using a claimed esterase making
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Matches 516
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                               V. marinus PKS-like cluster comprising ORFs 6,7,8 and
                                                                                                                               V81946
Polyketide-like synthesis; PKS; PKS-like gene; PUFA; DHA;
                                                                19-0CT-1999
                                                                                                V81946;
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                                                                                                                                                                                                                          CCTCCCTTGAAGAGTTCTCTCCTCTGGACGTAAATAAGGCGGACGAGATATT 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGATGTTAAAACTCCTGAAAGAGGGTAAACTGGCTCAAACTTTTTAAGTTCAAAACACCG 252
                                                                                                                                                                                                        cctgagcttgaggagttcacaccccttgatgttagaaaagcggaccaaataat 713
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                                                                                                                                                                                                                                                                                        TTTCTGGCGGTTCGTTCCAATTCGGAAAAGAGAAAAGGTTCTGCAACGTAGTTATAGAA 672
                                                                                                                                                                                                                                                                                                                                      cttcccatagagccggaaaaggatataaagaacattcttcacatccttttgaggagcttc
                                                                                                                                                                                                                                                                                                                                                     CTTCCCATAACTCAAGAAAGAAAGATTAAAAAATATACTCCACATCCTTATAAAGGAGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                      AACAACCTGCCCGTAGAACCTTTGGAAAAAGTTCAAAGAACCCATAATCGGGGTAGATGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGCTCTTTACTTCGGCAGAGGTGACTTAATTCCCGTGCTTCTCGGAAGTTGTTCCATA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aggagaatagaaaaacttgagataccgacgtatatatgcgcgacggatttatactcggga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ctgaagggattgatagggtgggagaaggctataagattccttgaggaagttctcccttac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAATGGGCTTAATGGGGTGGGAGAAAGGCTGCAGAGTTTTTTGGAAAAAGAGCTCGGAGTT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gggatgttcagccttctgaagagggtaaactggctgaagctgtttaagttcaagccacct 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agcggggtgagcgccggggcaatcgtttcggtcttttatgcctcaggctactcccctgaa 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCGGGGTAAGTGCTGGAGCTATCGTTTTCCGTCTTTTTACGCTTTCGGGCTACACTCCCGAC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atagcccacataggtgttttgaaagctataaacgagctcggtataagggtgagggcttta 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCGCCCATATAGGTGTTTTAAAAGCTCTGGAAGAGCTCGGTATAAAGGTAAAGAGGCTC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttgagattgaggaaatttgaagagataaacctcgttctttcgggaggagctgcaaagggc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGAAATTGAAGAGGTTTGAAGAGGTTAACTTAGTTCTTTCGGGAGGGGGCTGCCAAGGGT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       516;
                                                                                                                               standard;
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72.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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poly-unsaturated fatty acid; elcosapentenoic acid; docosahexanoic acid; EPA; oil; dietary supplement; infant feeeding formulation; malnutrition intravenous feeding formulation; cooking oil; fat; anti-inflammatory; cholesterol; open reading frame; ORF; ss.
                                                                                                                                                                                                                                              Vibrio marinus
                                                                                                                                                                                                                                                             malnutrition;
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CDS /*tag= a /product= "ORF 25509..28160 Location/Qualifiers 17394..25352 34454..36118 /product= "ORF 9" /product= "ORF 28209..34265 /*tag= /*tag= 'product= "ORF ъ O ω, 9 7 ,

98WO-US11639

04-JUN-1997; 97US-0048650

(CALJ) CALGENE LLC

Facciotti D, Lassner Z, Metz JG.

WPI; 1999-070271/06

New nucleic acid encoding polyketide-like synthesis enzymes Vibrio marinus - and transformed plants and microbes that propyrnsaturated fatty acids, useful as pharmaceuticals and f of.

Example 1; Fig 5; 153pp; English.

generate transgenic plants that can express transgeness encoding PRS-like genes associated with PUFA production. The PRS-like genes are used to transform plants and microbial cells to give recombinants having altered contents of PUFA (specifically DHA and EPA). Oils from these plants are useful as dietary supplements (in infant feeeding formulations, to give a PUFA profile closer to that of human milk; for treating malnutrition; in intravenous feeding formulations; in cooking oils, fats etc.), also as anti-inflammatory agents and for reducing cholesterol levels. Fragments from the genes are useful as probes to isolate related molecules or to detect organisms that express PKS-like genes. The method facilitates synthesis or suppressing interfering pathways. Expression of PUFA in seeds allows simple recovery, as oil which can be engineered to have a particular PUFA profile. Expression in microbes also allows simple recovery and control of PUFA profile and is not subject to external variables such as weather or food supply. The present sequence represents an approximately 40 kb PKS-like cluster DNA fragment from v. marinus comprising open reading frames (ORFs) 6, 7, 8 and 9. production of docosahexanoic acid (DHA) in Vibrio marinus are used to The invention provides polyketide-like synthesis (PKS)-like genes that are used for the production of long chain poly-unsaturated fatty acid (PUFA) productions. Genes responsible for eicosapentenoic acid (EPA) production in Shewanella putrefaciens and novel genes associated with the

Sequence 40138 BP; 11845 A; 7635 C; 8758 G; 11900 T; 0 other;

Query Match Best Local Similarity Matches 252; Conservative 9.8%; 0 Score 73.4; Pred. No. 3. Mismatches 3.5e-1 В 20; Length 40138; Indels ω,. Gaps

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                                                                 New DNA sequences encoding for polyketide (PK)-like synthesis pathway genes from Shewanella, Vibrio and Schizochtrium, useful for creating transgenic plants that express poly-unsaturated long chain fatty acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKS pathway; polyunsaturated long chain fatty acid; plant; transgenic; polyketide-like synthesis; PUFA; dietary supplement; intravenous feedimalnutrition; cooking oil; cooking fat; margarine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JAN-2000; 2000WO-US00956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V. marinus PKS-like gene cluster encoding ORF6 to ORF9.
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                                                                                                                                                                                                                                                                                                Facciotti D,
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                                                                                                                                                                                                                                                                                                    Metz JG,
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                                                                                                                                                                                                                                                                                                    Lassner
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genes. They are also useful for creating transgenic plants that express poly-unsaturated long chain fatty acids. The poly-unsaturated long chain fatty acids of the poly-unsaturated long chain fatty acids produced recombinantly are useful as dietary supplements for patients undergoing intravenous feeding or for preventing or treating malnutrition. The poly-unsaturated long chain fatty acids can also be incorporated into cooking oils, fats or margarine formulated so that in normal use the recipient receives a desired amount of poly-unsaturated long chain fatty acids. The nucleic acids are also useful in large scale production of docosahexenoic acid and elicosapentenoic acid, and for the modification of the fatty acid profile of host cells and edible plant tissues and/or plant parts. Transgenic production of polyunsaturated fatty acids in particular host cells allows quicker purification from natural sources such as fish or plants. This sequence represents a vibrio marinus DNA fragment encoding the PKS gene cluster incorporating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel DNA sequences encoding for polyketide (PK)-like synthesis (PKS-like) pathway genes from Shewanella, Vibrio and Schizochtrium. The nucleic acids are useful for isolatting related molecules or in methods to detect organisms expressing the PKS-like
                                                           ORF6 to ORF9.
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Sequence 40138 BP; 11845 A; 7634 C;

8759 G; 11900 T; 0 other;

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15297 aagatgattgcgataaaataatcggcgtatacgtgtcgcccattcgtcagg
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                          AAAAGTTCAAAGAACCCATAATCGGGGTAGATGTGCTTCCCCATAACTCAAG
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                                                                              ttgacgatcaagtgtattcagatggcggtattgttaatcatttccccgtgagtgtcattg
                                                                                                                       ACGAGAATTTTCTACTTGTTGACGGAGGTATAGTGAACAACCTGCCCGTAGAACCTTTGG
                                                                                                                                                                                                   ACTTAATTCCCGTGCTTCTCGGAAGTTGTTCCATACCCGGGATTTTTGAACCAGTTGAGT
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Pred. No. 3.5e-12;
0; Mismatches 276;
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RESULT 212214 ID Z1 XX AC Z1 XX DT 08

Z12214 standard; DNA; 903 BP.

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08-OCT-1999 212214;

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequences z11972-z12358 represent open reading frames (ORFs) of Neisserla meningitidis and N. gonorrhoeae which encode antigenic proteins (see x38499-y38944). The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-NOV-1997;
27-NOV-1997;
10-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteins from Neisseria meningitidis and diagnosis, treatment and prevention of ir
                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                          as hybridisation probes and antisense reagents.
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06-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment;
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 430
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                                                                                                                                                                                                                                                                                       31 GAAGAGGTTAACTTAGTTCTTTCGGGAGGGGCTGCCAAGGGTATCGCCCATATAGGTGTT
                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                          TTAAAAGCTCTGGAAGAGCTCGGTATAAAGGTAAAGAGGCTCAGCGGGGTAAGTGCTGGA 150
cccatcaaatttgccgccgttgctactgattttgaaaccggcaaggccgtcgctttcaat
            AACATACCAACCTATCTTTGCTCGGCGGATCTGTACACGGGAAAGGCTCTTTACTTCGGC
                                                 ggcgaaaagctgcaaaattacatcaaccgaaaagtcggcggcaggcggattcagcagttt
                                                                                                      gaaattttaggtaaaaccgatttggtcgatttaaccttgtccaccagtggttttatcaaa
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                                                                            TGGGAGAAGGCTGCAGAGTTTTTGGAAAAAGAGCTCGGAGTTAAGAGGCTGGAAGACCTG
                                                                                                                                                        tcgatagtcggcagcctttttgcatcgggtatgtcgcccgaccgcctcgaattggaagcc
                                                                                                                                                                                                                                                                                                                 221;
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                                                                                                                                                                                                                                                                                                                                                                                 903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   meningitidis; Neisseria gonorrhoeae; antigen;
; Neisseria infection; meningitis; septicaemia
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                                                                                                                                                                                                                                                                                                                  Conservative
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97GB-0023516.
97GB-0024190.
97GB-0024386.
97GB-0025158.
97GB-0026147.
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                                                                                                                                                                                                                                                                                                                                                                                231 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prevention
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                                                                                                                                                                                                                                                                                                                            Score 68; DB 20;
Pred. No. 2.9e-11;
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                                                                                                                                                                                                                                                                                                                                                                                 210 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection
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                                                                                                                                                                                                                                                                                                                                        Length 903;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine;
; gonorrhea;
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TTAAAAGCTCTGGAAGAGCTCGGTATAAAGGTAAAAGGCTCAGCGGGGTAAGTGCTGGA

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gcagtggtcggtttggcactcggtggcggcatctaaaaggatttgcccatgtaggtatt 189

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Best Local :
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14-NOV-1997;
18-NOV-1997;
                                                                                                     prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
                                                                                                                                              Nucleotide sequences Z11972-Z12358 represent open reading frames (ORFs) of Neisseria meningitidis and N. gonorrhoeae which encode antigenic proteins (see Y38499-Y38944). The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis,
                                                                                 Sequence
                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                          Proteins from Neisseria meningitidis and N. gonorrhoeae useful for diagnosis, treatment and prevention of infection
                                                                                                                                                                                                                                                                                          Grandi G,
                                                                                                                                                                                                                                                                                                                                              27-NOV-1997
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                                                                                                                                                                                                                                                                                                              (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                                                                     14-JAN-1998;
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GAAGAGGTTAACTTAGTTCTTTCGGGAGGGGCTGCCAAGGGGTATCGCCCATATAGGTGTT
                                                                                                                                                                                                                                                                     1999-327407/27
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                              220;
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                                        Similarity
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                                                                                                                                                                                                    Page 323; 524pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             meningitidis
                                                                                                                                                                                                                                                                                        Masignani
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                             Conservative
                                                                                 BP;
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97GB-0026147
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97GB-0024190
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                                                                                 230
                                                                                                                                                                                                                                                                                          Pizza
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                       Score 66.4; pred. No. 9.1e-0; Mismatches
                            0;
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                                       No. 9.1e-1
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences, A81433 to A82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; A81 to A81303 and B25620 to B25663 represent Neisseria DNA sequences and their corresponding proteins; A81254 to A81259 and A81304 to A81321 represent PCR primers used in the isolation of Neisseria meningitidis sequences; and A81322 to A81452 represent Neisseria meningitidis MenB
                                                                                                                             Isolated nucleotide sequences of Neisseria meningitidis which used in the diagnosis and treatment of N. meningitidis infectiother Neisserial infections, for example, N.gonorrhoea
                                                                                                       Claim 7; Page 471-498; 1760pp;
                                                                                                                                                                                                                           Frazer CM, I
                                                                                                                                                                                                                                                                                                          09-OCT-1998;
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antigen; vaccine; diagnosis; infec
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ction; antibacterial; identification;
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Ratti G, Scarselli
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RESULT F21613/c

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standard;

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172325

ВP

Neisseria meningitidis B nucleotide sequence SEQ ID

F21613 stan F21613; F3-MAR-2001

(first entry)

Neisseria r diagnosis;

meningitidis; ; antigen; dete

detection;

infection;

gene

therapy;

antibacterial;

Neisseria

gonorrheae;

immunogenic;

NO:114

Neisseria meningitidis

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, cand antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against consequences from the bacterium will also facilitate production of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none chare successfully overcome antigenic variability. The provision of conserved them, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
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GTTATCATCGGCAGGCATACATATGTTGACGGCGGTCTGTCGCAGCCCGTGCCCGT
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                                                                               CAGGGGAATGCCGGGCAGGCTGTGCGCGCCTTCCGCCGCCATTCCCAATGTGTTCCAACCC
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Pred. No. 7.9e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes the full length genome of CC Neisseria meningitidis B (NMB). The sequences in F21544 and F21607 to CC F21613 represent fragments of the NMB genomic sequence, as the sequences cC was too long to go in a record on its own it was split into 8 sequences CC which overlap each other at the beginning and end of each sequence by 4980 bp (i.e. the last 49980 bp of F21544 is repeated at the beginning CC of F21607, the last 49980 bp of F21547 are repeated at the beginning of F21508, and so on). F21545 to F21588 encode the Neisseria proteins given in B5550 to B5593, and F21589 to F21607 are repeated at the beginning CC are used in the exemplification of the present invention. The NMB genome CC and fragments from it have antibacterial activity, and can be used in CC vaccines and gene therapy. Neisseria nucleic acids, proteins and/or antibodies which binds to the proteins can be used in compositions for CC treating or preventing infection due to Neisserial bacteria or as a CC diagnostic reagent for detecting the presence of Neisserial bacteria or conjuter storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Sequence 172325 BP; 43072 A; 47583 C; 41465 G; 40205 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Appendix A; 692pp; English
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08-OCT-1999;
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                                                                            GAAATTTTAGGCAAAACCGATTTGGTCGATTTAACCTTGTCCACCAGTGGTTTTATCAAA 153561
                                                                                                                                                        TCGATTGTCGGCAGCCTTTTTGCATCGGGTATGTCGCCCGACCGCCTCGAATTGGAAGCC 153621
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                                  TGGGAGAAGGCTGCAGAGTTTTTGGAAAAAGAGCTCGGAGTTAAGAGGCTGGAAGACCTG
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INST GENOMIC
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C, Mora M,
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46.2%;
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Scarlato V,
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Rappuoli R;
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The present invention describes methods of obtaining immunogenic C proteins from Neisseria genomic sequences. A81453 to A82414 represent C specifically claimed Neisseria meningitidis genomic DNA sequences; A81260 C to A81303 and B25620 to B25663 represent Neisseria DNA sequences and C their corresponding proteins; A81254 to A81259 and A81304 to A81321 C represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and A81322 to A81452 represent Neisseria meningitidis DNA cequences; and A81322 to A81452 represent Neisseria meningitidis DNA sequences, and A81322 to A81452 represent Neisseria meningitidis DNA composition. The composition of the present invention. The nucleic acid sequences, protein sequences, of the present invention can be used in the exemplification of composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against C all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have falled mainly due to antigen tolerance. Multivalent vaccines have also been tried but none can be used as a medicament of the new successfully overcome antigenic variability. The provision of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 629-865; 1760pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        other Neisserial infections, for example, N.gonorrhoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleotide sequences of Neisseria meningitidis which can used in the diagnosis and treatment of N. meningitidis infection \boldsymbol{a}
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30-APR-1999;
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Meningococcus B; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 GTTGAGTACGAGAATTTTCTACTTGTTGACGGAGGTATAGTGAACAACCTGCCCGT 506
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99US-0132068
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Ratti G, Scarselli
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Best Local Similarity
Matches 220; Conserv
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18-NOV-1997;
27-NOV-1997;
10-DEC-1997;
14-JAN-1998;
                                                                          01-SEP-1998;
06-NOV-1997;
                                                                                                                       09-OCT-1998;
                                                                                                                                                    20-MAY-1999
                                                                                                                                                                                WO9924578-A2
                                                                                                                                                                                                            Neisseria
                                                                                                                                                                                                                                        treatment;
                                                                                                                                                                                                                                                                                     Neisseria
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                                                                                                                                                                                                                                                                                                                                                                           Z12215 standard; DNA; 903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 further, complete sequences may provide an opportunity to secreted or surface exposed proteins that may be presumed immune system and which are not antigenically variable or conserved than other more variable regions.
                                                                                                                                                                                                                                                       Neisseria
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                                                                                                                                                                                                                                     meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
; Neisseria infection; meningitis; septicaemia; gonorrh
                                                                                                                                                                                                                                                                                 gonorrhoeae complete ORF137 sequence
                                                                                                                                                                                                          gonorrhoeae
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97GB-0024190.
97GB-0024386.
97GB-0025158.
97GB-0026147.
98GB-0000759.
                                                                           98GB-0019016.
97GB-0023516.
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Pred. No. 2.2e-09;
0; Mismatches 256;
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                                                                                                                     Z12212 standard;
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08-OCT-1999

(first entry)

Neisseria meningitidis; Neisseria gonorrhoeae; antigen;

vaccine;

Neisseria meningitidis partial ORF137 sequence

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06-NOV-1997;
14-NOV-1997;
         Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds.
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14-JAN-1998;
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                                                                                                                A81390,
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 447
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prevention (as vaccines) or treatment of Neisseria infections,
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97GB-0024386.
97GB-0025158.
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56.8%;
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The present invention describes methods of obtaining immunogenic CC proteins from Neisseria genomic sequences. A81453 to A82414 represent CC specifically claimed Neisseria meningitidis genomic DNA sequences; A81260 CC to A81303 and B25620 to B25663 represent Neisseria MDA sequences and CC their corresponding proteins; A81254 to A81259 and A81304 to A81321 CC represent PCR primers used in the isolation of Neisseria meningitidis DNA Sequences; and A81322 to A81452 represent Neisseria meningitidis MenB CC sequences; and A81322 to A81452 represent Neisseria meningitidis MenB CC polynuclectide ORF sequences, which are all used in the exemplification CC of the present invention. The nucleic acid sequences, protein sequences, CC and antibodies against them, can be used as a medicament (or in the CC manufacture of a medicament) for treating, preventing or diagnosing CC infection due to Neisserial bacteria. For example, some of the identified CC proteins could be components of vaccines against Meningococcus B; against CC all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of Diological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have failed mainly due to the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleotide sequences of Neisseria meningitidis which can used in the diagnosis and treatment of N. meningitidis infection other Neisserial infections, for example, N.gonorrhoea -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Frazer CM, Hickey
Masignani V, Galec
Rappuoli R, Pizza
Sequence
                                                                     further, complete sequences may provide an opportunity to secreted or surface exposed proteins that may be presumed immune system and which are not antigenically variable or
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30-APR-1999;
                                                  conserved than other more variable regions.
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110 A; 115 C;
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114 G; 107
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Scarselli M,
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                               GCTATCGTTTTCCGTCTTTTACGCTTCGGGCTACACTCCCGAC
                                                           attaaggttttgaaagaaaacggtattcctgtgaaggtggttaccggcacctccgcaggt 249
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Pred. No. 8.4e-06;
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               T79332;
                                     T79332 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1299 BP; 298 A; 508 C; 301 G; 186 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      production of biosynthetic products such as enzymes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevenand therapy of T. pallidum infections, particularly syphilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enzyme production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treponema pallidum infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide sequence from the genome of Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X20681;
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                                                                                                                                                                                                                                                                    786
                                                                                                                                                                                                                                                                                                                                                257 TGGGCTTAATGGGGTGGGAGAAGGCTGCAGAGTTTTTGGAAAAAGAGCTCGGAGTTAAGA 316
                                                                                                                                                                                                                                                                                                                                                                             Local Sin
                                                                                                          ACACGCCGGT
                                                                                                                                   ACCIGCCCGT 506
                                                                                                                                                             GTGTTTTTGCGCCGGTGCGGCAGGAGGGGGTGTATTTGGCGGACGGCTGTATATTGAACA
                                                                                                                                                                                     GGATTTTTGAACCAGTTGAGTACGAGAATTTTCTACTTGTTGACGGAGGTATAGTGAACA 496
                                                                                                                                                                                                               AGGTTGTGCTCCAGTGGGGTGCTTGCCCGTGCATTGCGCGCCCTCGTGTGCGTACCCGG
                                                                                                                                                                                                                                       CTCTTTACTTCGGCAGAGGTGACTTAATTCCCGTGCTTCTCGGAAGTTGTTCCATACCCG 436
                                                                                                                                                                                                                                                                   CCTTTCACGATTGTAAAATTCCGTTTTTGTGCAATGCGGTCAATCTGTGTACGGGCGCGG
                                                                                                                                                                                                                                                                                 GGCTGGAAGACCTGAACCTATCTTTGCTCGGCGGATCTGTACACGGGAAAGG 376
                                                                                                                                                                                                                                                                                                                       TGGGGCTTGATTCGGGAGAAAAGTTTGCCACGCTSCTGACGCGGGTGACGGGGGGGAAAT 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1999-081273/07
                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97us-0050667.
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                                                                                                        597
                                       DNA;
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47.68;
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                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     DB 20;
                                                                                                                                                                                                                                                                                                                                                                            131;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                           temperature and in organic solvents, making them superior for use in production of pure chiral compounds used in pharmaceutical, agricultural and other chemical industries. A method is claimed for transferring an amino group from an amino acid to an alpha-keto acid using a claimed esterase. The enzymes may also be useful as ripening starters in cheese making, in lignin removal in paper and pulp manufacture, in carbohydrate derivative synthesis, in fermentable sugar production from lignocellulosic waste, in the study of plant wall structure, plant resistance to disease and organic matter decomposition and to select plants bred for production of highly degradable animal feeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This DNA sequence codes for whale mat sample 11.801 esterase es9 (W23079). Newly identified polynucleotides (T79321-40) encoding esterases (W23069-88), some of which are claimed, can be used for recombinant production of the enzymes in host cells, and as probes to identify related sequences. The esterases are stable at high
                                                                                                                                                                                                                                                                                                                 Sequence 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in cheese paper manufacture, and to study plant resistance to disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 64-65; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Callen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-AUG-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease resistance; feedstuff; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pulp; paper;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Esterase; thermostable enzyme; ester; chiral compound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding whale mat sample 11.801 esterase
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   211 AAAGA 215
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                                                                                                                                                                                    GAAGAGGTTAACTTAGTTCTTTCGGGAGGGGCTGCCAAGGGGTATCGCCCCATATAGGTGTT
                                  GCTATCGTTTTCCGTCTTTTACGCTTCGGGCTACACTCCCGACGAGATGTTAAAACTCCTG
                                                                                                  ctgcatgaccttgaaaaacaaaatattgtaccaaatgaaattgttggtacaagtatgggt
                                                                                                                                   TTAAAAGCTCTGGAAGAGCTCGGTATAAAGGTAAAGAGGCTCAGCGGGGTAAGTGCTGGA 150
                                                                                                                                                                  gaaaattctagcttagtactgtccggtggtggtgctctgggtattgctcacttgggtgta
                                                                                                                                                                                                                                  94;
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                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                   ВP;
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                                                                                                                                                                                                                                                                                                                 269 A; 123 C; 149 G; 238
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Swanson RV, Warren
                                                                                                                                                                                                                                 0;
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Pred. No. 0.022;
0; Mismatches 91;
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Best Local Similarity 70.1
Matches 47; Conservative
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||| |||
11332 aagcgct 11338
                                                                                                                                                                                                                                                                                X20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of biosynthetic products such as enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; \ensuremath{\mathrm{ds.}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        x20520;
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                                                                                                                                                                                                                                                          Sequence 11628 BP; 2692 A; 2716 C; 3308 G; 2890 T; 22 other;
                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 302-309; 1150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-081273/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotide sequence from the genome of Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
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             ν,
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                                                                                                                                                                                  Score 35; DB 20; Length 11628; Pred. No. 1.8; 0; Mismatches 20; Indels 0
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Title:
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2: /cgn2_6/ptodata/2,

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ALIGNMENTS

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RESULT 1
US-08-602-359A-29
                              TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 29
SEQUENCE CHARACTERISTICS:
LENGTH: 750 NUCLEOTIDES
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 29
Patent No.
                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
ANAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION:
TELEFAX: 619-678-5070
TELEFAX: 619-678-5099
                                                                                                                                                                                                                                                                           COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/60:
PILING DATE: February 16, 19;
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 4225 EXECUCITY: LA JOLLA STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                    TOPOLOGY:
                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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o. 5942430
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4225 EXECUTIVE SQUARE, STE 1400
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REID, John
MAFFIA, Anthony
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SWANSON, Ronald V.
WARREN, Patrick V.
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                    LINEAR
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 GENOMIC DNA
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RESULT 2
US-08-602-359A-26
                             GENERAL INFORMATION:
APPLICANT: ROBERTSC
APPLICANT: MURPHY,
APPLICANT: REID, JC
APPLICANT: MAFFIA,
APPLICANT: LINK, St
APPLICANT: WARREN,
APPLICANT: WARREN,
APPLICANT: WORNCON,
APPLICANT: KOSMOTKE
                                                                                                                                                                                Sequence 26, Application Patent No. 5942430
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Best Local Similarity
Matches 750; Conserv
               APPLICANT: KOSMOTKA, Anna TITLE OF INVENTION: ESTERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGTACACGGGAAAGGCTCTTTACTTCGGCAGAGGTGACTTAATTCCCGTGCTTCTCGGA 420
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                                     LINK, Steven
SWANSON, Ronald V.
WARREN, Patrick V.
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                                                                                                               REID, John
                                                                                               MAFFIA, Anthony
                                                                                                                              MURPHY, Dennis
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Best Local Similarity
Matches 516; Conser
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SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,359A
FILING DATE: February 16, 1996
CLASSIFICATION: 435
PRIOR APPLICATOR: 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEPAX: 619-678-5099
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LENGTH: 756 NUCLEOTIDES
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MEDIUM TYPE: 3.5 INC
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS
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TENGTH: /50 ...
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CITY: LA JOLLA
STATE: CALIFORI
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                                                                                                                AAGGCTCTTTACTTCGGCAGAGGTGACTTAATTCCCGTGCTTCTCTGGAAGTTGTTCCATA
                                                                                                                                                                                 AAGAGGCTGGAAGACCTGAACCAACCTATCTTTGCTCGGCGGATCTGTACACGGGA
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                                                                                               AGGGCTCTATACCTCTCGGAAGGGAGTTTAATCCCCGCACTTCTCGGCAGCTGTGCAATT
                                                                                                                                                                                                                                 CTGAAGGGATTGATAGGGTGGGAGAAGGCTATAAGATTCCTTGAGGAAGTTCTCCCTTAC
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                                CCCGGCATATTTGAACCCGTTGAGTATAAGAATTACTTGCTCGTTGACGGAGGTATAGTT
                                                                                                                                                                AGGAGAATAGAAAAACTTGAGATACCGACGTATATATGCGCGACGGATTTATACTCGGGA
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72.4%;
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Pred. No. 4.4e-132;
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Best Local Similarity
Matches 252; Conserv
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Patent No. 6140486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Production of polyunsaturated fatty acids by TITLE OF INVENTION: of polyketide-like synthesis genes in plants FILE REFERENCE: COUNE.131 01US CURRENT APPLICATION NUMBER: US/09/090,793 CURRENT FILING DATE: 1998-06-04 EARLIER FILING DATE: 1998-06-04 EARLIER APPLICATION NUMBER: 60/048,650 EARLIER FILING DATE: 1997-06-04 NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Vibrio marinus -09-090-793-12
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15237 ttgacgatcaagtgtattcagatggcggtattgttaatcatttccccgtgagtgtcattg
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                        ACGAGAATTTTCTACTTGATGAACGGAGGTATAGTGAACAACCTGCCCGTAGAACCTTTGG
                                                                              ccgtgattaatgccttattagcatcagccagctaccctttagtttttctccgatgatca
                                                                                                                                                        aattgcgcattgttgccaccaacatgttactcggtaaagagcatatatttaaagatggct 15176
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                                                                                                                   ACTTAATTCCCGTGCTTCTCGGAAGTTGTTCCATACCCGGGATTTTTGAACCAGTTGAGT
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47.5%;
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Best Local
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
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NUMBER OF SEQUENCES:
                                 APPLICANT:
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 195
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 22313-0299
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CITY: Alexandria
                                                                                                                                                                                                                                                         Local
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GATGTTAAAACTCCTGAAAGAGGTAAACTGGCTCAAACTTTTTAAGTTCAAAACACCGAA 254
                                                                                                                                                                                                         GAAATTGAAGAGGTTTGAAGAGGTTAACTTAGTTCTTTCGGGAGGGGCTGCCAAGGGTAT 74
                                                                   CGGGGTAAGTGCTGGAGCTATCGTTTCCGTCTTTTACGCTTCCGGGCTACACTCCCGACGA 194
                                                                                                     CGCCCATATAGGTGTTTTAAAAGCTCTGGAAGAGCTCGGTATAAAGGTAAAGAGGCTCAG 134
                                                                                                                                                                                                                                         Similarity
9; Conserv
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1800 Diagonal Road,
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i; Pred. No. 0.0031;
187; Mismatches 1
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; OTHER INFORMATION: Description of Artificial Sequence: genomic
US-08-642-274D-49
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US-08-642-274D-49/c
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                                                                                                                                GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: MOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER APPLICATION NUMBER: US 60/054,646
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                                                                 SEQ ID NO 17
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Best Local Similarity 53.7%;
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Patent No. 6117654
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APPLICANT: Shiloh, Yosef
TITLE OF INVENTION: MUTATED FORMS OF THE ATAXIA-TELANGIECTASIA GENE AND
TITLE OF INVENTION: SCREEN FOR A PARTIAL A-T PHENOTYPE
FILE REFERENCE: 229000033
CURRENT APPLICATION NUMBER: US/08/642,274D
CURRENT FILING DATE: 1996-05-03
                                                                               EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows V
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                                  TYPE: DNA
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TYPE: DNA
                  ORGANISM: Homo sapiens
 FEATURE:
                                                  ENGTH:
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                                                                                     Windows Version 3.0
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Pred. No. 0.029;
Pred. No. 0.029;
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; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C
US-09-128-155-17
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,670
FILING DATE: 12-OCT-1994
                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: MILLS, DEMETRA J.
REGISTRATION NUMBER: 34,506
REFERENCE/DOCKET NUMBER: 434
                                               MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                                ANTI-SENSE:
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                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: ALEXANDRIA
STATE: VIRGINIA
NAME/KEY:
                                                                                                                                                                                                       TELEPHONE: (703)684-1111
TELEFAX: (703)684-1124
                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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ACID AT THE
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46.78;
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Pred. No. 13;
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SN2 POSITION OF ACYLGLYCEROL LIPIDS
                                                                                                                                                                                                                                                                                                                                                                                                     Version
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; CLONE: AMT-2
US-08-268-072-2
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US-08-321-670-1
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Best Local Similarity 50.0%;
Matches 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                    TELEFAX: 612-332-9081
NFORMATION FOR SEQ ID NO:
                        IMMEDIATE SOURCE
                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/932,334
FILING DATE: 19-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2335 AGAATTAAAAAAAAAAAAAAAAAAAAAAATATGCACAAGATCGTATTATTTGTTGTTCCTCGT 2276
                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 609 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   619 GCGGTTCGTTCCAATTCGGAAAAGAGAAAGGAGTTCTGCAACGTAGTTATAGAACCTCCC 678
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0
FILING DATE: 27-JUN-1994
                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                  NAME: Nelson, Albin J
REGISTRATION NUMBER:
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                                                                                                   ropology:
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3100 No. 5563328west Center
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                                                Chlorella virus XZ-6E
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                                                                                                 linear
                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOVEL PROMOTERS FROM CHLORELLA VIRUS GENES PROVIDING FOR EXPRESSION OF GENES PROKARYOTIC AND EUKARYOTIC HOSTS
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Pred. No. 1.5;
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Query Match

4.1%;

Score 30.4;

DB 1;

Length 609;

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US-09-087-232A-14
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/09087232P Patent No. 6153431
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 765-25
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 30 MAY 1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                   630 TGTCATGGTCATCTGCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAA 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 GACGAGATGTTAAAACTCCTGAAAGAGGTAAACTGGCTCAAACTTTTTAAGTTCAAAACA 249
                                  690 GAAGAGGCACAGGGCTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTG 749
                                                                  123 AAAGAGGCTCAGCGGGGTAAGTGCTGGAGCTATCGTTTTCCGTCTTTTACGCTTCGGGCTA 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 CCGAAAATGGGCTTAATGGGGTGGGAGAAGGCTGCAGAGTTTTTGGAAAAAGAGCTCGGA 309
183 CACTCCCGACGAGATGTTAAAACTCCTGAA 212
                                                                                                                                    63 TGCCAAGGGTATCGCCCATATAGGTGTTTTAAAAGCTCTGGAAGAGCTCGGTATAAAGGT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: KOLE, LISA B.
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/048,057 FILING DATE: 30 MAY 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                 NAME/KEY:
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30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                   1071 base pairs
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                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                 7..309
                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                    single
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0; Mismatches
                                                                                                                                                                                          Score 30; DB Pred. No. 1.4;
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RESULT 10
US-09-087-232A-16
; Sequence 16, App
; Patent No. 61534
                                RESULT 11
US-09-087-232A-12
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; LOCATION:
US-09-087-232A-16
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Sequence 12, Application US/09087232A Patent No. 6153431
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Best Local
                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/087,23
FILING DATE: 28 MAY 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTORNEY/AGENT INFORMATION:
NAME: KOLE, LISA B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Quille
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: KOLE, LISA B.
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: APTELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: JUIN STREET: New York
CITY: New York
TATE: New York
TSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                                          951 GGCTCCCTACAACATTGTCCTTCTCCTGAA 980
                                                                                                                                          183 CACTCCCGACGAGATGTTAAAACTCCTGAA 212
                                                                                                                                                                              891 GAAGAGGCACAGGGCTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTG 950
                                                                                                                                                                                                                  123 AAAGAGGCTCAGCGGGGTAAGTGCTGGAGCTATCGTTTTCCGTCTTTTACGCTTCGGGCTA 182
                                                                                                                                                                                                                                                      831 TGTCATGGTCATCTGCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAA 890
                                                                                                                                                                                                                                                                           63 TGCCAAGGGTATCGCCCATATAGGTGTTTTAAAAGCTCTGGAAGAGCTCGGTATAAAAGGT 122
                                                                                                                                                                                                                                                                                                                                Local Similarity hes 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (212) 408-2628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
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                                                                                                                                                                                                                                                                                                                              Mismatches
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ADDRESSEE:

1100 NEW YORK AVE.,

NW, SUITE 600

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US-08-466-343D-1
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                                                                                                                                                                                                                                        Sequence 1, Application US/08466343D Patent No. 6025154
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                         GENERAL INFORMATION:
APPLICANT: LI, Y1
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICATION NUMBER: 60/048,057

FILING DATE: 30 MAY 1997

ATTORNEY/AGENT INFORMATION:

NAME: KOLE, LISA B.

REGISTRATION NUMBER: 35,225

REFERENCE/DOCKET NUMBER: AP 3111

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 408-2628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Quillent et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 765-251
INFORMATION FOR SEQ ID NO:
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ONE OF THE PROPERTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10112
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION
                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
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nes 75; Conserv
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New York
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28 MAY 1998
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                                                                             POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)
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COUNTRY: UZIP: 20005

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US-08-466-343D-1
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Best Local Similarity 50.0
Matches 75; Conservative
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Patent No. 6033859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1002 GGCTCCCTACAACATTGTCCTTCTCCTGAA 1031
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REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                 APPLICANT: MORIKAWA, Masaaki
TITLE OF INVENTION: A Thermostable DNA Polymerase and Kits for
TITLE OF INVENTION: Amplifying Nucleic Acids
                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       882 TGTCATGGTCATCTGCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAA 941
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                          CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                STREET:
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               COUNTRY:
                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                            INFORMATION:
20036
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                                                                  1025 Connecticut Avenue, N.W., Suite 600
                                                                                                                                                                                        KAWAMURA, Yoshihisa
IMANAKA, Tadayuki
TAKAGI, Masahiro
                                                                                                                                                                                                                                                KAWAKAMI, Bunsei
                                                                                                                                                                                                                                                                                    ARAKAWA, Taku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                       INOUE, Hiroaki
                                                                                                                                                                                                                                                                                                       KITABAYASHI, Masao
                                                                                     Kenyon & Kenyon
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; ORIGINAL SOURCE: Hyperthermophilic archaeon
US-09-073-354-6
                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08656005A Patent No. 6054301
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/656,005
FILING DATE: 24 MAY 1996
APPLICATION NUMBER: JP 134096/95
FILING DATE: 31 MAY 1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                  APPLICANT: MORIKAWA TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 ATACCAACCTATCTTTGCTCGGCGGATCTGTACACGGGAAAGGCTCT 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 GAGAAGGCTGCAGAGTTTTTGGAAAAAGAGCTCGGAGTTAAGAGGCTGGAAGACCTGAAC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 GAGGTAAACTGGCTCAAACTTTTTAAGTTCAAAACACCGAAAATGGGCTTAATGGGGTGG 273
                                  STREET: 1025 Con.
CITY: Washington
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SOFTWARE: WordPerfect 6.1 Windows
COUNTRY:
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                                                                                 ADDRESSEE:
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                       D.C
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                                                            1025 Connecticut Avenue, N.W., Suite 600
                                                                                                                                                                       MORIKAWA, Masaaki
                                                                                                                                                                                        IMANAKA, Tadayuki
TAKAGI, Masahiro
                                                                                                                                                                                                                         KAWAKAMI, Bunsei
KAWAMURA, Yoshih
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                  INOUE, Hiroaki
                                                                                                                                                                                                                                                                                     ARAKAWA,
                                                                                                                                                                                                                                                                                                       KITABAYASHI, Masao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                             Kenyon & Kenyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.5" Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.9%;
                                                                                                                                  A Method of Amplifying Nucleic Acid and A Reagent Therefor
                                                                                                                                                                                                                                                                                     Taku
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 5339;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Gaps

0

COMPUTER READABLE FORM:

CURRENT APPLICATION DATA:

OPERATING SYSTEM: PC-DOS/1 SOFTWARE: WordPerfect 5.1

IBM PC compatibl

PC-DOS/MS-DOS

3.5" Floppy disk

MEDIUM TYPE:

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US-09-073-259-6
US-09-073-259-6
US-09-073-259-6

Sequence 6, Application US/09073259

Patent No. 6143536

GENERAL INFORMATION:
APPLICANT: IMANAKA, Tadayuki
APPLICANT: TAKAGI, Masahiro
APPLICANT: MORIKAWA, Masaaki
TITLE OF INVENTION: DNA Encoding A Thermostable DNA Polymerase
NUMBER OF SEQUENCES: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.9
Best Local Similarity 48.9
Matches (81; Conservative
                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,259
FILING DATE: Concurrent Herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-429-0796
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 134096/95

FILING DATE: 31 MAY 1995

ATTORNEY/AGENT INFORMATION:

NAME: TOffenettl, Judith L.

REGISTRATION NUMBER: 39,048

REFERENCE/DOCKET NUMBER: 2418/3
PRIOR APPLICATION DATA:
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2868 TTTAACAGGAGAACTAACAAGGCCGAGCTCAAGAGAGTAAAGGCCCT 2914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2808 AAAGTAAAGAGAGAGGGCGAGACGGAAGTGCTTGAGGTCAGTGGGCTTGAAGTCCCGTCC 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2748 GAGGTTCACTTCGTCAGGATTGGAGAGCTCATAGACCGGATGATGGAGGAAAATGCTGGG 2807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 202-429-1776
TELEFAX: 202-429-0796
                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 ATACCAACCTATCTTTGCTCGGCGGATCTGTACACGGGAAAGGCTCT 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 GAGAAGGCTGCAGAGTTTTTGGAAAAAAGAGCTCGGAGTTAAGAGGCTGGAAGACCTGAAC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 GAGGTAAACTGGCTCAAACTTTTTAAGTTCAAAACACCGAAAATGGGCTTAATGGGGTGG 273
                                                                                                                                                                                                                                           STREET: 1025 Cont
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2. CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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1025 Connecticut Avenue, N.W.,
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24 MAY 1996
ON: 435
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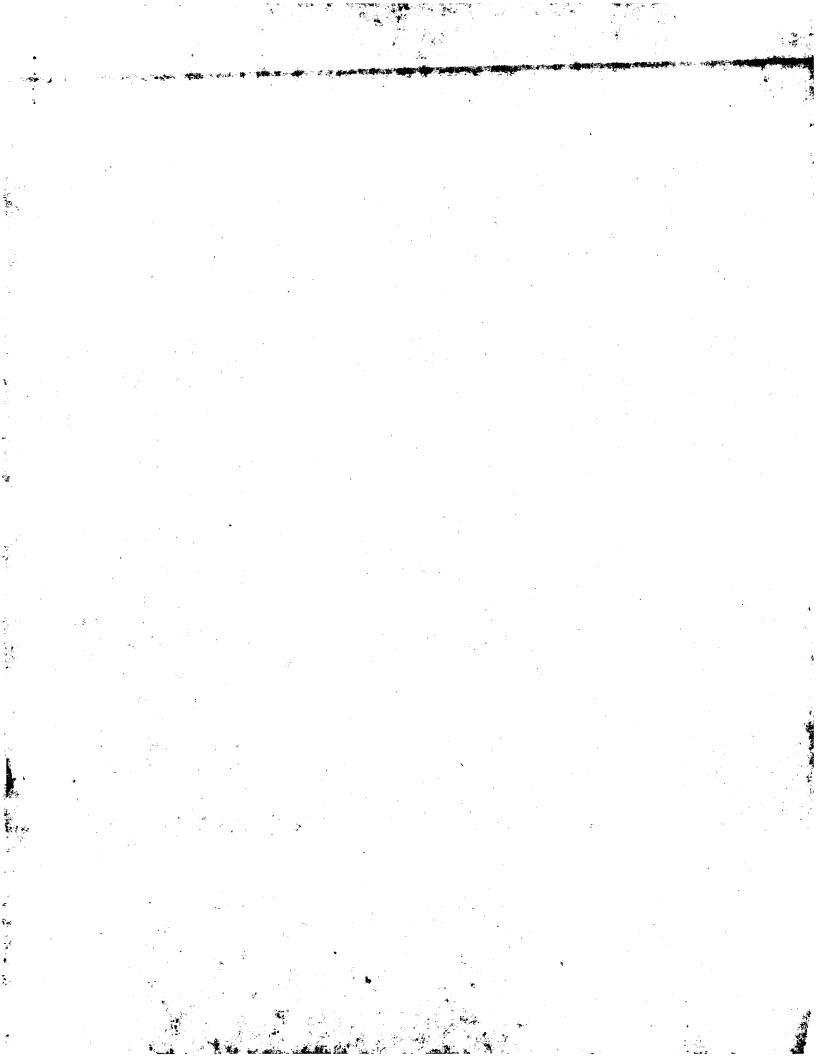
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Best Local Similarity
Conservations 81; Conservation
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 31 MAY 1995
ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti Toffenetti
                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: cDNA ORIGINAL SOURCE: Hyperthermophilic archaeon
                                                                                                                                           2748 GAGGTTCACTTCGTCAGGATTGGAGAGCTCATAGACCGGATGATGGAGGAAAATGCTGGG 2807
2868 TTTAACAGGAGAACTAACAAGGCCGAGCTCAAGAGAGTAAAGGCCCT 2914
                                                                     2808 AAAGTAAAGAGAGAGGGCGAGACGGAAGTGCTTGAGGTCAGTGGGCTTGAAGTCCCGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 202-429-1776
                    334 ATACCAACCTATCTTTGCTCGGGGGATCTGTACACGGGAAAGGCTCT 380
                                                                                                                                                                           214 GAGGTAAACTGGCTCAAACTTTTTAAGTTCAAAACACCGAAAATGGGCTTAATGGGGTGG 273
                                                                                                       274 GAGAAGGCTGCAGAGTTTTTGGAAAAAGAGCTCGGAGTTAAGAGGCTGGAAGACCTGAAC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 24 MAY APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Toffenetti, Judith L. REGISTRATION NUMBER: 39,048
                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                5339 base pairs
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                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                              double
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Search completed: June Job time: 23193 sec 2, 2001, 20:14:55



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Database :
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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                             cgn2_6/ptodata/2/pna/US082_COMB.seq: *
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/2/pna/US06_COMB.seq:*
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                   /cgn2_6/ptodata/2/pna/US6009_COMB
/cgn2_6/ptodata/2/pna/US6010_COMB
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44: /cgn2_6/ptodata/2/pna/US6012_COMB.seq:*
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57: /cgn2_6/ptodata/2/pna/US6020_COMB.seq:*
59: /cgn2_6/ptodata/2/pna/US6020_COMB.seq:*
59: /cgn2_6/ptodata/2/pna/US6025_COMB.seq:*
59: /cgn2_6/ptodata/2/pna/US6025_COMB.seq:*
59: /cgn2_6/ptodata/2/pna/US6025_COMB.seq:*
59: /cgn2_6/ptodata/2/pna/US6027_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Query . Score Match Length DB

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Description

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	221 221 221 221 220 220		1000000		ı
-60-140-121 -09-620-392- -09-620-392- -09-620-392- -09-620-392-	-09-540-229-13000 -60-168-197-675 -60-250-80-2508 -09-540-229-13747 -09-328-352-129 -09-306-350A-223 -09-726-788-1459 -09-540-236-1027 -60-128-476-2183 -60-128-476-2183 -60-082-116-208 -09-596-002-41	566-3 566-3 566-3	S-09-10 -09-663 -09-514 -09-739 -60-168	-09-252 -60-082 -09-221 -09-703 -60-164 -60-183	-09-38 -09-38 -09-33 -09-33 -60-06 -09-25 -09-25
41, 2381 5360 5449 1838	130000 675, Ap 2588, Ap 137477, 129, Ap 12333, A 1459, A 1027, Ap 2183, A 2183, A 2183, A 2183, A 2183, A 2183, A	_ 555	Sequence 1, 2 equence 578, equence 3835, equence 4665, equence 2142, equence 311,	1336 692, 305, 772, 772, 772,	29, Ap 26, Ap 12, Ap 1258, 281, 4 1180, 1225, 1225,

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                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 619-678-5070
TELEPAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 750 NUCLECTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: HATLE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KOSMOTKA, Anna
TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
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                             181 TACACTCCCGACGAGATGTTAAAACTCCTGAAAGAGGTAAACTGGCTCAAACTTTTTAAG
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CITY: I
STATE:
                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                       LENGTH: 750 NUCLEOTIE
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
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OPERATING SYSTEM:
SOFTWARE: WORD PI
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                                                                                                                                                                                                                                                      Local Similarity
nes 750; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                      TACACTCCCGACGAGATGTTAAAACTCCTGAAAGAGGTAAACTGGCTCAAACTTTTTAAG
                                                                                                                                                                                          TTGATTGGCAATTTGAAATTGAAGAGGTTTGAAGAGGTTAACTTAGTTCTTTCGGGAGGG '60
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CALIFORNIA
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REID, John
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                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FISH & RICHARDSON P.C.
                                                                                                                                                                                                                                                                                                                                           GENOMIC DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dennis
                                                                                                                                                                                                                                                 100.0%; Score 750; DB 17; 100.0%; Pred. No. 7.3e-220; O. Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INCH DISKETTE
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                         NUMBER OF SEVEL...
CORRESPONDENCE ADDRESS:
ANDRESSEE: FISH & RICHARDSON P.C.
ANDRESSEE: FISH & RICHARDSON P.C.
            ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
                                                                                                                              OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        TITLE OF
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661 GTAGTTATAGAACCTCCCCTTGAAGAGTTCTCTCCTCTGGACGTAAATAAGGCGGACGAG
                                                                                                                                                        COMPUTER: IBM PS/2
OPERATING SYSTEM:
                                          FILING DATE:
                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 92037
                                                                                                                                                                                                                                                 CITY: LA JOLLA
STATE: CALIFORNIA
                                                          APPLICATION NUMBER:
                                                                                                   FILING DATE
                                                                                                                    APPLICATION NUMBER:
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGCTCGGAGTTAAGAGGCTGGAAGACCTGAACATACCCAACCTATCTTTGCTCGGCGGAT 360
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                                                                                                                                                                                                                                                                                                                                        T: KOSMOTKA, Anna
INVENTION: ESTERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09382242
                                                                                                                                                                                                                                                                                                                                                                  WARREN, Patrick V.
                                                                                                                                                                                                                                                                                                                                                                                                             MAFFIA,
                                                                                                                                                                                                                                                                                                                                                                                                  LINK,
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                                                          08/602,359
38,347
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720 660 660 600 600 540 540 480 480 420

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RESULT 3
US-09-21-899-12
; Sequence 12, Application US/09231899
; GENERAL INFORMATION:
; APPLICANT: Lassner, Michael
; APPLICANT: Metz, James G
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INFORMATION FOR SEQ ID NO:
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LENGTH: 756 NUCLEOTIDES
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                                                                                                                                                                                                                                                                                                              CTTCCCATAACTCAAGAAAGAAAGATTAAAAATATACTCCACATCCTTATAAGGAGCTTC 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCGGGATTTTTGAACCAGTTGAGTACGAGAATTTTCTACTTGTTGACGGAGGTATAGTG 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGGCTCTTTACTTCGGCAGAGGTGACTTAATTCCCGTGCTTCTCGGAAGTTGTTCCATA 432
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                                                                                                                                                  CCTGAGCTTGAGGAGTTCACACCCCTTGATGTTAGAAAAAGCGGACCAAATAAT 713
                                                                                                                                                                                CCTCCCCTTGAAGAGTTCTCCTCCTCTGGACGTAAATAAGGCCGGACGAGATATT 725
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619-678-5099
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RESULT 4
US-09-328-352-1258
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Sequence 1258, Application US/09328352
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AN
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/048,650
EARLIER FILING DATE: 1997-06-04
EARLIER APPLICATION NUMBER: 09/090,793
EARLIER FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 86
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                                                                                                                                                                                                                              aagatgattgcgataaaataatcggcgtatacgtgtcgcccattcgtcagg 15347
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                                                                                                                                                                                                                                                                                                                        ttgacgatcaagtgtattcagatggcggtattgttaatcatttccccgtgagtgtcattg
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NUMBER OF SEQ ID NOS: SEQ ID NO 1258 LENGTH: 1014

TYPE: DNA

CURRENT APPLICATION NUMBER: US/09/328,352 CURRENT FILING DATE: 1999-06-04

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EQUENCES RELATING THERAPEUTICS

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RESULT 5
US-60-068-138-281/c
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// ORGANISM: Acinetobacter baumannii
US-09-328-352-1258

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Best Local Similarity 45.4%;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/068,138
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                        APPLICANT: CORLEY, NEIL C.
APPLICANT: RUSSO, FRANK D.
APPLICANT: HANN, AMY L.
APPLICANT: HEATH, JOE D.
APPLICANT: FINNEY, GREGGRY L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF NEISSERIA MENINGITIDIS
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LAGACE, ROBERT E.
APPLICANT: CORLEY, MEIL C.
APPLICANT: RUSSO, FRANK D.
APPLICANT: HANN, AMY L.
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                       CITY: PALO ALTO
STATE: CALIFORNIA
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                                                                                                                                                                                                                           Sequence 1180, Application US/09252991A GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 222; Conserv
                                     CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (650) 845-416
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                    FILE REFERENCE:
                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: genomic IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
                                                                                                                                                                                                                                                                                                                                                                                 3310 CGTTATCATCGGCAGGCATACATATGTTGACGGCGGTCTGTCGCAGCCCGTGCCCCGT 3254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3370 TCAAGGGAATGCCGGGCAGGCTGTGCGCGCCTTCCGCCGCCATTCCCAATGTGTTCCAACC 3311
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                                                                                                                                                                                                                                                                                                                                                                                                                           450 AGTTGAGTACGAGAATTTTCTACTTGTTGACGGAGGTATAGTGAACAACCTGCCCGT 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 GAAGAGGTTAACTTAGTTCTTTCGGGAGGGGCTGCCAAGGGTATCGCCCCATATAGGTGTT
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NO 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGAGGTGACTTAATTCCCGTGCTTCTCGGAAGTTGTTCCATACCCGGGATTTTTTGAACC 449
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ilarity 46.5%;
Conservative
                                                                                                                                                                    107196.136
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NO: 281:
                                                                                                                                                                                      Rubenfield et al.

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 2.
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RESULT 8
US-09-252-991A-1270
; Sequence 1270, Application US/09252991A
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US-09-252-991A-1225
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SEQ ID NO 1225
LENGTH: 1257
TYPE: DNA
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APPLICANT: Marc J. Rubenfield et al.
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Best Local Similarity
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Best Local Similarity 57.4%;
Matches 105; Conservative
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS.
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                  231
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                                                                                                                                                                                                                                                                                 104 AAGAGCTCGGTATAAAGGTAAAGAGGCTCAGCGGGGTAAGTGCTGGAGCTATCGTTTCCG 163
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                                                                                                   4 GGC 226
|||
1 ggc 293
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57.4%;
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Pred. No. 1e-06;
"" matches 78;
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Pred. No. 1.3e-06;
0; Mismatches 78;
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CURRENT APPLICATION NUMBER: U$/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: U$ 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: U$ 60/094,190
PRIOR APPLICATION NUMBER: U$ 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 1336
LENGTH: 2616
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US-09-252-991A-1336/c
; Sequence 1336, Application US/09252991A
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1270
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                                                                                                                                                      Query Match
Best Local Similarity
Matches 105; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                          173
                                   104 AAGAGCTCGGTATAAAGGTAAAGAGGCTCAGCGGGGTAAGTGCTGGAGCTATCGTTTCCG 163
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ACGAACAGGGCATCCAGATCGACGCCATCGCCGGCACCAGCATGGGCGCGGTGGTCGGCG
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57.4%;
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Pred. No. 1.7e-06;
Pred. No. 1.7e-06;
                                                                                                                                                      Score 58.2; DB 16;
Pred. No. 1.8e-06;
0; Mismatches 78;
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                                                                                                                                                                                         Matches 105;
                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                      25605
                                                                                                                        25545
                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (650) 845-4166
NFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PM-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1943 GGC 1941
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                    164
                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF
                                                                                  104 AAGAGCTCGGTATAAAGGTAAAGAGGCTCAGCGGGGTAAGTGCTGGAGCTATCGTTTCCG 163
                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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CITY: PALO ALTO
CONTY: PALO ALTO
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                                                                                                                                      44 TAGTTCTTTCGGGAGGGGCTGCCAAGGGTATCGCCCCATATAGGTGTTTTAAAAGCTCTGG 103
                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: doub.
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
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TCTTTTACGCTTCGGGCTACACTCCCGACGAGATGTTAAAACTCCCTGAAAGAGGGTAAACT 223
                                                  ACGAACAGGGCATCCAGATCGACGCCATCGCCGGCACCAGCATGGGCGCGGTGGTCGGCG
                                                                                                                    TGGTCCTCTCCGGCGGTGCCGCCCGCGCCTGGCCCATATCGGCGTGCTCAAGGCCCTCG
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                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T: FINNEY, GREGORY L.
T: BROOKS, JACQUELINE
INVENTION: NUCLEOFIDE SEQUENCES OF PSEUDOMONAS AERUGINOSA
INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CERRONE, MICHAEL C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CALIFORNIA
                                                                                                                                                                                                                                                                                            PAE1c696
                                                                                                                                                                                                                                                                                                                                                                                          26737 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/60082302
                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (650)
                                                                                                                                                                                                                                                                                                                          genomic DNA
                                                                                                                                                                                                                                                                                                                                                             double
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57.4%;
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                                                                                                                                                                                  Score 58.2; DB 4v,
Pred. No. 5.3e-06;
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                                                                                                                                                                                     Indels
                                                                                                                                                                                                                    Length 26737;
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                                                  25664
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                                                                                                                      US-09-221-017B-305
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                                            Matches 209;
                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 305, Applica GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2108 base pair
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APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                            ORIGINAL
                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                          ANTI-SENSE:
                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 10-DEC-1998 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                               TELEFAX: VI
TELEFAX: 706141
STREET: 755 PAGE
CITY: Palo Alto
                                                           Local Similarity
                                                                                                                                  NAME/KEY: misc_feature LOCATION: 1...2108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                                                                                                                                                                                                                                                     FOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Monroy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                            SOURCE
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                                                                                                                                                                                                                                                                                           2108 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROSS, Bruce C.
VENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
LEQUERCES: 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                     650-494-0792
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSTEM: Windows FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                        UNKNOWN
                                                                                                                                                                            PORYPHYROMONAS GINGIVALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM Compatible
                                                                                                                                                                                                                                                    circular
                                                                                                                                                                                                                                                                                                                                                                    650-813-5600
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10-DEC-1998
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30-JAN-1998
                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-DEC-1997
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                                                        7.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                           32,430
                                                                                                                                                                                                                                                                                                                          305:
                                            0;
                                           Score 56; DB 16; I
Pred. No. 7.7e-06;
0; Mismatches 255;
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                                                                    Length 2108;
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US-09-703-708-772/c
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; LOCATION: (1)..(50769)
; OTHER INFORMATION: uns
US-09-703-708-772
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NUMBER OF SEQ ID NOS:
SEQ ID NO 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 772, Application US/09703708 GENERAL INFORMATION:
                                                                                                                                                                                                                                                Query Match 7.1%;
Best Local Similarity 43.8%;
Matches 230; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/703,708
CURRENT FILING DATE: 2000-11-02
PRIOR APPLICATION TO NUMBER: US/09/703,708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hinkle, Gregory J. TITLE OF INVENTION: Xant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
  44004
                                                                                  44064
                                                                                                                                                                44124 AGATCGGCGTCGCCGCCGGCGGCGGCGGTGCGCCCAAGGGCTTTGCACATATCGGCGTGATCA 44065
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Xanthomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 50769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1433 TTTCAGATTCCTAACAGAGTGGCAAATACCACAAAGAGGTGTATTCAGCATCCAACGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1313 TGAGGACAATGGGATTCGTCCCGACATCATAGCAGGTACGAGTGCAGGAGCGTTGGTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1253 CTTGGCTCTTAGCGGCGGAGCGGCCAAAGGCTTTGCACATTCGGGAGTACTCCATGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1673 TGGAACCACCTATGTCGATGGAGGACTGTTCAAAGACCTTCCGG 1716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1553 CAGAATAGTGGCAACGGACCTTGACCGTGGAGTTGTCAAAGTTTTTTCACAAGGCTCTCT
                                         155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 CGTCTTTTACGCTTCCGGCTACACTCCCGACGAGGTTAAAACTCCCTGAAAGAGGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        462 GAATTTTCTACTTGTTGACGGAGGTATAGTGAACAACCTGCCCG 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            402 AATTCCCGTGCTTCTCGGAAGTTGTTCCATACCCGGGATTTTTTGAACCAGTTGAGTACGA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282
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                                                                                                                                                                                                       35 AGGTTAACTTAGTTCTTTCGGGAGGGGCTGCCAAGGGTATCGCCCATATAGGTGTTTTAA 94
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                                  TCGTTTCCGTCTTTTACGCTTCGGGCTACACTCCCGACGACGAGTGTTAAAACTCCTGAAAG 214
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APPLICANT: BOWEY, Stanley G.
APPLICANT: HINKLE, Gregory J.
APPLICANT: HINKLE, Gregory J.
FILE OF INVENTION: Xanthomonas campestris
FILE REFERENCE: 38-10(15804)A
CURRENT APPLICATION NUMBER: US/60/164,320
CURRENT FILING DATE: 1999-11-10
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SEQ ID NO 772
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TYPE: DNA
ORGANISM: Xanthomonas campestris
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APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Kanthemonas campestris Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15804)B
CURRENT FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 18992
SEQ ID NO 772
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                                                                                                                                                                                                                                                                             GCAATGCCGGCCAGGCGGTGCGCGCCTCCAGCAGCATTCCCGGCGTGTTCGAGCCGGTGA 43705
                                                                                                                                                                                                                                                                                                                                              GTGACTTAATTCCCGTGCTTCTCGGAAGTTGTTCCATACCCGGGATTTTTGAACCAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                   AGAAGCTGCAGGACTACGTCAACGAACAGCTCGGCGGCAAGCCGATCGACAAACTGCGCA 43825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGTTTCCGTCTTTTACGCTTCGGGCTACACTCCCGACGAGATGTTAAAACTCCTGAAAG
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                                                                                                                                                                                                       AGTACGAGAATTTTCTACTTGTTGACGGAGGTATAGTGAACAACCTGCCCGTAGAACCTT 514
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nilarity 43.8%;
Conservative
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Pred. No. 0.00029;
0; Mismatches 295;
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; GENERAL INFORMATION:
; APPLICANT: FLEISCHM
; APPLICANT: WHITE, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FRASER, C
APPLICANT: VENTER, J
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 217; Conserv
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TITLE OF INVENTION: DNA SEQUENCES FOR STRITITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
2885952 caatggcgagcagctgctcgtcgacggtgggctgttgaacaatctgccgg 288600:
                                                                                                                                                                                                                                                                                                       2885772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4411529
                            456 GTACGAGAATTTTCTACTTGTTGACGGAGGTATAGTGAACAACCTGCCCG 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 GGAAGAGCTCGGTATAAAGGTAAAGAGGCTCAGCGGGGTAAGTGCTGGAGCTATCGTTTC 161
                                                                                                                                             396 TGACTTAATTCCCGTGCTTCTCGGAAGTTGTTCCATACCCGGGATTTTTGAACCAGTTGA 455
                                                                                                                                                                                                                                                 336 ACCAACCTATCTTTGCTCGGCGGATCTGTACACGGGAAAGGCTCTTTACTTCGGCAGAGG 395
                                                                                                                                                                                                                                                                                                                                                   276 GAAGGCTGCAGAGTTTTTGGAAAAAGAGCTCGGAGTTAAGAGGCTGGAAGACCTGAACAT 335
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Pred. No. 0.0027;
0; Mismatches 247;
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Match Length DB ID
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1: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/US00_NEW_COMB.seq:*
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5 US-09-724-866A-7154
5 US-09-724-866A-18661
5 US-09-739-449-5912
5 US-09-739-449-216
5 US-09-739-449-218
5 US-09-739-449-218
5 US-09-739-449-218
5 US-09-739-449-207
5 US-09-670-314-652
6 US-09-739-449-204
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US-09-103-840A-1
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Sequence 2, Appli
Sequence 1, Appli
Sequence 5056, Ap
Sequence 7154, Ap
Sequence 5912, Ap
Sequence 216, Ap
Sequence 2218, Ap
Sequence 3188, Ap
Sequence 68250, Ap
Sequence 68250, Ap
Sequence 68250, A
Sequence 652, App
Sequence 204, Ap
Sequence 211, App
Sequence 211, App
Sequence 21385, Ap
Sequence 21385, Ap
Sequence 2563, Ap
Sequence 271, App
Sequence 277, App
Sequence 5769, Ap
Sequence 277, App
Sequence 377, Ap
Sequence 378, App
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ALIGNMENTS

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00 CURRENT APPLICATION NUMBER: US/19/103,840A CURRENT FILING DATE: 1998-06-24

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; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 198-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
Matches 241; Conserv
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                                          214742 agtgctgcaccgctgatgaccggctgatccccatcgagggcagccgtcgcctggtcga
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648 GGAGCTGGCCGTCGAGAACAAAACCCTGAGGGAGTTCGAGGGGGGCGTACCACGAGATATT
                                                                                         588 CCTTCTGATCGGCACTGGCGATGTAATAACCCCGCCTGAAGGCTCACGCAGACTCTTCGA 647
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    Mismatches

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Pred. No. 7.3e-06;
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 7154
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APPLICANT: Havukkala, Ilkka
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LENGTH: 309
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Best Local Similarity
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Best Local
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CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/171,432
PRIOR FILING DATE: 1999-12-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Polynucleotides, Material Incorporating TITLE OF INVENTION: Them, and Methods for Using Them FILE REFERENCE: 11000.1049BU
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SOFTWARE: FastSEQ for Windows Version
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ORGANISM: Eucalyptus grandis
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508 TCGGCCAAGCTGGGAAGGAGCATCTTCGTGAACATGGAGCTGGCCCACAGGGAGGCGGAC 567
                                                                                                    448 TCGAGGAACAGGGACGCCGTGAGGAGGTACGTTGAAGACCCACTCGRCCACGACAGGATT 507
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                                                           24 tggaaggtcctgtacattctttgcaaggacaaggacggcctacttcacaaagacacgatc 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 cgggccgtgtacgatgggagcttgttcgagcacatggagaaggagcacatggagaagggc
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nes 69; Conserv
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57.5%;
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                                                                                                                                                                  Score 39.6; DB Pred. No. 0.068;
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                                                                                                                                                Mismatches
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US-09-739-449-5912; Sequence 5912, Application US/09739449
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; LENGTH: 585
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-5912
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; ORGANISM: Eucalyptus
US-09-724-866A-18661
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US-09-724-866A-18661/c
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APPLICANT: Havukkala, Ilkka
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SEQ ID NO 18661
LENGTH: 518
                                                                                                                                                            Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                              Matches
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APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/514,000 PRIOR FILING DATE: 2000-02-23 NUMBER OF SEQ ID NOS: 13351
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CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/171,432
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 24913
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141 taatccgctgaaaagccgctccgaactggcgtctcttgaggaccgtatcgccgcctgtga 200
                                  411 AGTTGTTCTCCCAACGGCATAAAGCCGGAACTCCTCTCGAGGAACAGGGACGCCGTGAG 470
                                                                                                      351 CCCGGAAACGCCGGGCTTCATGGTGGCCCTCGCGAAGTTCCTTGGAAAGATCGCCCCGGG 410
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                                                                     cgccgaaatcgcgttgcgcagactgggcctcgaccagctctggtggatggtcacgccggg 140
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                                                                                                                                                         Score 36; DB 5
Pred. No. 0.75;
                                                                                                                                          Mismatches 145; Indels
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; LOCATION: (1)..(374732)
; OTHER INFORMATION: unsurus-
US-09-739-449-216
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SEQ ID NO 216
LENGTH: 374732
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mes 123; Conserv
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US-09-737-223-32498; Sequence 32498; Application US/09737223; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/737, 223
CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 09/332,782
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Pred. No. 2
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LENGTH: 452

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
RAME/KEY: misc_feature
LOCATION: (1)...(452)
OTHER INFORMATION: n = A,T,C or G
US-09-737-223-32498
                                                            밁
                                                                                                                                                                                                                                                                   ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(556)
; OTHER INFORMATION: n = A,T,C
US-09-737-223-29218
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Best Local S
Matches 70
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 29218
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Best Local Similarity
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CURRENT FILING DATE: 2000-12-13
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NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 38054
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/332,782
                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 556
 449
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                                                         tgatggggctggacctgctggtgttcgcccacgaccatgttggccacggacagagcgaag
                                                                                        TCAACTATGCCGGCTTTGGAGTTTACACCTTCGACTGGCCCGGCCACGGGAAGAGCCCCGG 166
                                                                                                                       tctttgtgtcccatggagccggagagcacagtggccgctatgaagagctggctcggatgc 388
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GGCTGGGTCGTTCATGGCCTCGGCGAGCACAGCGGAAGGTATGGAAGACTGATT 99

134;

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Gaps

0

Matches

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; LENGTH: 184668
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-207
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; LENGTH: 975
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-3188
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US-09-739-449-207
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GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TIFLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER: OF SEQ ID NOS: 13351
                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
                      Query Match
Best Local
                                                                                                                                                                              SEQ ID NO 207
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 207, Application US/09739449
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Best Local Similarity
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IITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C

CURRENT APPLICATION NUMBER: US/09/739,449

CURRENT FILING DATE: 2000-12-19
                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/514,000 PRIOR FILING DATE: 2000-02-23
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Local Similarity 46.4 es 116; Conservative
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                46.48;
Score 35.6; DB Pred. No. 2.8; 0; Mismatches
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Pred. No. 1.1;
0; Mismatches 134;
                                     DB 5;
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CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 68250
                                                                                                                                                                                                                                                                                           Sequence 652, Application US/09670314 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Swimmer et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
                                                   CURRENT APPLICATION NUMBER: US/09/670,314
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/060,756
PRIOR FILING DATE: 1998-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Synthetic -09-270-8498-68250
                                                                                                                                  TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA FILE REFERENCE: 3495-0169
                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                     APPLICANT: Cole, Stewart APPLICANT: Buchrieser-B
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCCTCTTCGGCCACAGCCTCGGTGGTCTAACTGTCATCAGGTACGCTGAGACGCGGCCCG 304
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                  PatentIn
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                                                                                                                                                                                                                                  Gordon, Stephen
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                  Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Best Local Similarity
Matches 133; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/08/276,163D CURRENT FILING DATE: 1994-07-15 NUMBER OF SEQ ID NOS: 15314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Human Genes, Sequences, FILE REFERENCE: PO14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Adams, et. al.
                                                                                                                                             NAME/KEY: misc feature
LOCATION: (279)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
LOCATION: (362)
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OTHER INFORMATION: n equals a,t,g, NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (143)
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NAME/KEY: unsure
LOCATION: (various)
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                                  NAME/KEY: misc feature LOCATION: (389)
                                                                   OTHER INFORMATION: n equals a,t,g,
                                                                                                                         OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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                                                                                         NAME/KEY: misc feature LOCATION: (363)
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NAME/KEY: misc feature LOCATION: (413) OTHER INFORMATION: n equals a,t,g, or

NAME/KEY: misc feature

OTHER INFORMATION: n equals a,t,g,

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PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 5042
LENGTH: 2922
TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
US-09-739-449-5042
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Best Local Similarity
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Best Local Similarity 48.6%;
Matches 87; Conservative
                                                                                                                                                                    Matches
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APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
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LOCATION: (488)
OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (457)
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (439)
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191 AGGAGGCGATGGAAATCATCGACTCGATAATCGAGGAGATCAGGGAGAAGCCCCTTCCTCT 250
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BE404062

BE604055

BE755050

BE755000

BE604369

BE793083

BE7416498

BE7581069

BE7416109

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9b est48:
9b est59:
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Description

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AN562949
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BE604369
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7 WHE0987-0
7 HVSMC98070005
2 WHE0403_E
2 WHE0403_E
3 WHE2160_D
3 WHE1405-0
3 WHE2160_D
3 WHE2160_D
4 WHE0403_A
0 HVSMEE0001
9 MUG011_D
9 MUG014_G
0 MUG004_G
0 MUG004_G
0 HVSMEE0001
2 HVSMEE0001
4 USMEE006.9
5 2a86f06.9

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RESULT
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                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence have been trimmed to remove vector quality sequence with phred score less than Seq primer: Stratagene SK primer.
                                                                                                                                                                    Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                            The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library Unpublished (2000)
                                                                                                                                                                                                                                       Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fe,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Seaton,C.L. and Tong,J.C.
                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
                                                                                                                                                                                                                                                                                                                                                                         BE500447 206 bp
WHE0987-0990_K09_K09ZS
                                                                                                                                                                                                                                                                                                              Triticum aestivum
                                                                                                                                          Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                  Triticum
                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum cDNA
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                                                                                                                                                    5105595818
                                                                                                                                                              5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0987-0990_K09_K09"
          /clone_lib="Wheat pre-anthesis spike cDNA library"
/tlssue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
  /note="Vector:
                                                                                /organism="Triticum aestivum"
                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            GI:9699064
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clone
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AW778156
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Lambda Uni-ZAP XR, excised phagemid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16891
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                                                                                                                     sequence and low 20
                                                                                                                                                                                                                                                              Fenton, R.D.,
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BE200927 fk83f09.y
AW281382 fj55c08.y
AW778156 fk45b02.y
AW376435 fj59d02.y
BE016848 fk69h03.y
AW778415 fk49b02.y
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AW595464 fk31b11.y
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AW281451 fj56d05.y
AW184547 fj15g04.y
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                                                                                                                                                                                        Service, Pacific
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fj59c02.y
fj21g06.y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 GCCTGCTGCACGACCTGCTCATCGAGCCCGAGAAGGAGGTGGTGCTCGGCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            689 GGGCGTACCACGAGATATTTGAAGACCCCGAGTGGGCCGAGGAGTTCCACGAAA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 55.7 nes 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTCACGCAGACTCTTCGAGGAGCTGGCCGTCGAGAACAAAACCCTGAGGGAGTTCGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 985)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,Y., Anderson,H., Dale,J., Henry,D., Kernoöle,S., Palmer,M., Ra, Y., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE454427 985 bp mRNA EST 26-JUL-2000
HVSMEh0094G18f Hordeum vulgare 5-45 DAP spike EST library
HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0094G18f,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clemson University Genomics Institute Clemson University
100 Jordan Hall, Clemson, SC 29634, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for barley genomics 
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Smagnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    barley.
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                                                                                                                /clone="HYSMEh0094G18f"
/clone_lib="Hordeum vulgare 5-45 DAP
HYCDNA0009 (5 to 45 DAP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Site_1: EcoRI; Site_2: XhoI; Plants were grown greenhouse. Whole spike with awns trimmed, where the state of 
                                        /tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                            /cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                        organism="Hordeum vulgare"
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55.7%;
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Pred. No. 0.0013;
lambdaZAP; Site_1:
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EcoR1; Site_2: Xho1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                               Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA
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660070B05.yl 660 - Mixed stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence
                                                                                                                                                                                                                                                                                                                                                   Email: walbot@stanford.edu
Plate: 660070 row: B colu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Walbot V
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Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae
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                                                                                                                        /note="organ: anthers; Vector: Lambda Zap; Site_1: EcoRI; Site_2: XhoI; Anther and pollen cDNA library.
Directionally sequenced with 5' end at the EcoRI site.
Created by Amile Franklin."
a 199 c 189 g 110 t
                                                                                                                                                                                                       /organism="Zea mays"
/cultivar="0hlo43"
/cultivar="htaxon:4577"
/db_xref="ftaxon:4577"
/clone_lib="660 - Mixed stages of anther and pollen"
/clsue_type="whole premieotic anthers to pollen shed"
/dev_stage="premieotic anthers to pollen shed"
/lab_host="xLOLR"
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0; Mismatches 81;
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Query Match Best Local Matches

Local Sin hes 111;

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Conservative

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Score 49.2; DB 166; Pred. No. 0.005; 0; Mismatches 103;

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WHE0403_E01_E01ZS Wheat etiolated seedling roc
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The structure and function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Virldiplantae; Embryophyta; Tracheophyta; (Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             800 Buchanan Street, Albany, CA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Olin Anderson
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                                                                                                                                              /lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized
germinated and grown aseptically in the dark at room
temperature on filter paper with water, nystatin and
cefotaxime in covered crystallization dishes. Roots were
harvested. The tissue, total RNA, and poly(A) RNA were
prepared, a cDNA library was made, and the cDNA clones
                    California, Riverside. Plasmid DNA preparations and DI sequencing were performed in the OD Anderson lab (all other authors)."

210 c 238 g 131 t
                                                                                    were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA
                                                                                                                                                                                                                                                                                                                                                                                                                     /cultivar="Chinese Spring"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                              /dev_stage="Five day old etiolated seedling"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                     'tissue_type="Root"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., H, P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
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                                                  /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized
, germinated and grown aseptically in the dark at room
temperature on filter paper with water, nystatin and
cefotaxime in covered crystallization dishes. Roots were
harvested. The tissue, total RNA, and poly(A) RNA were
prepared, a cDNA library was made, and the cDNA clones
were in vivo excised to give pBluescript phagemids in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oandersn@pw.usda.gov
                       other authors).
                                                                                                                                                                                                                                                                                                                                                          /dev_stage="Five day old etiolated seedling"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cultivar="Chinese Spring
/db_xref="taxon:4565"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Wheat etiolated seedling root cDNA library"
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Query Match

6.1%;

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GAAGAAGGTGACTGTCCCGTTTGTAGTCCTGCACGGCACGGCGGACCGGGTGACGGACCC
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98; Conservative
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,
Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M.,
Y., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hordeum vulgare
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Marmoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 864 656 7288 Fax: 864 656 4293
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/clone_lib="Hordeum vulgare seedling
HVcDNA0007 (etiolated and unstressed)
                                                                                                                                                                                                                                                                                                   /organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
                                                                                                                                                                            /note="Vector: lambdaZAP;
175 c 187 g 109
                                                                                                                                                                                                           /tissue_type="Seedling root"
/lab_host="TJC121"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: candersnew.usda.gov
Sequence have been trimmed to remove vector
quality sequence with phred score less than
Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.L., Tong, J.C. and Zhang, D.
The structure and function of the expressed portion of the wheat genomes - Drought stressed leaf cDNA library
Unpublished (2000)
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Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Han, P.S., Hsia, C.Kang, Y., Lazo, G.R., Miller, R., Nguyen H.T., Rausch, C.J., Seaton, C.L., Tong, J.C. and Zhang, D.
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                                                                                                                                                                                                                                                              /note-"Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were given a gradual stress down to 65% and 78% RWC at Texas Tech University (D. Zhang in HT Nguyen lab). Total RNA and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close), at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Triticum aestivum"
/cultivar="TAM W101"
/db_xref="taxon:4565"
/clone="WHE1405-1408_E04_E04"
/clone_lib="Wheat drought stressed leaf cDNA library"
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/dev_stage="Full tillering stage"
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Poaceae; Pooldeae; Triticeae;
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Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
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The structure and function of the expressed portion of the wheat genomes - Whole plant cDNA library from Triticum turgidum L. var
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                                                                                                      Simons). Tissues collected from seven-way controlled leaf, stem, root and seed; leaf from plant at fourth leaf stage; spike from pre-anthesis through 20 days after anthesis; flag leaf; leaf and stem tissue from tillers, and root. Total RNA and poly(A) RNA were prepared from each tissue and then pooled, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Akhunov. Chin, Panton, Kianian, Otto, Simons, Zhang) at the
University of California, Riverside. Plasmid preparations and DNA sequencing were performed Anderson lab (all other authors)."

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Triticum turgidum L. whole plant cDNA library"
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/dev_stage="Different growth stages"
/lab_host="E. coli SOLR"
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/clone="WHE2160_D03_G06"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
Sequences have deality 16. The threshold for highest quality sequences
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Plant Sciences Building, Rm. 2502,
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Department of Botany
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cordonnier-Pratt, M.-M., Gingle, A., Dean, R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE366333.1 GI:9307890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST database from Sorghum:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                706 542 1860
706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
two-week-old sorghum plants 48 hr after inoculation; vector: pBluescript II from Lambda Zap II; Site_1: XhOI; Site_2: EcoRI; Two-week-old sorghum plants (BTX 623 cultivar) were infected with pathogen (isolate FRM42I of Colletotrichum graminicola, which is a sorghum isolate). RNA was prepared from infected leaves harvested from 45 seedlings 48 hours after inoculation. Note: young seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they grow older (4 weeks or older), plants resume susceptiblity to anthracnose disease. The library, was made from poly-A
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                           /clone_lib="Pathogen induced 1 (PI1)"
/note="Organ: Anthracnose-infected leaves from
                                                                                                                                                                                                                                                                                     /organism="Sorghum bicolor"
/db_xref="taxon:4558"
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53.5%;
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Pathogen induced 1 (PI1) Sorghum bicolor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGACGGATTCTTGCACGACTTGCTCTTCGAGCCCGAGGCGCGACGAGGTCGGCGCCGAGAT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier, S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Hermann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.

International Trittceae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE416498 838 bp mRNA EST 24-JUL-2000 MUG011.D05R990330 ITEC MUG Wheat Spikelet Library Triticum aestivum CLONA Clone MUG011.D05, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                               Tel: 81 45 820 1903 Fax: 81 45 820 1901
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expressed Sequence Tags Unpublished (2000)
                                                                                                                                                                                                                                                                                            Email: ogihara@yokohama-cu.ac.jp
International Triticeae EST Cooperative (ITEC)
                                                                                                                                                                                                                                                                                                                                                                                         Kihara Institute for Biological Research, Yokohama City
Majoka-cho 641-12, Totsuka-ku, Yokohama 244-0813, JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Ogihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; I Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triticum aestivum
                                                                                                                                                                                                                                                                           http://wheat.pw.usda.gov/genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triticum
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/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; M13 Reverse sequencing primer used. 1.2 Kbp averainsort size."
                                                             /tissue_type="young spikelets"
/dev_stage="Feekes' scale 6-7"
                                                                                                           /clone_lib="ITEC MUG Wheat Spikelet Library"
                                                                                                                                    /db_xref="taxon:4565"
/clone="MUG011.D05"
                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                  /cultivar="Norin 26"
                                                                                                                                                                                                      /organism="Triticum aestivum"
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178 c 2
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; Poales; Poaceae; Pooideae; Triticeae;
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2-2H-ZO P
BE585068
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Qutob, D., Hraber, P.T., Sobral, B.W.S. and Gijzen, M.
Comparative analysis of expressed sequences in Phy
Plant Physiol. 123 (1), 243-254 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agriculture and Agri-Food Canada
1391 Sandford Street, London, On
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Phytophthora sojae"
/strain="race 2, strain P6497"
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RESULT 12
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yo, Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
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Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae;
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HVSMED0015A03f HOrdeum vulgare s
HVCDNA0002 (Dehydration stress)
HVSMED0015A03f, mRNA sequence.
                                                                                                 Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                 Clemson University
100 Jordan Hall, C
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High quality sequence start: 9
High quality sequence stop: 612
                                                Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                           Contact: Wing RA
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Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGAAGGTGACTGTCCCGTTTGTAGTCCTGCACGGCACGGCGGACCGGGTGACGGACCC 415
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                                                                                                                                                                                                                                                                                                                                     Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier, S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G. International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;86
                                                                                                                                                                                                                 Contact: Ogihara Y
Kihara Institute for Biological Research, Yokohama City
Maioka-cho 641-12, Totsuka-ku, Yokohama 244-0813, JAPAN
Tel: 81 45 820 1903
Fax: 81 45 820 1901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Triticum aestivum 
Eukaryota; Viridip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE416109 508 bp
MUG004.G04R990608 ITEC
CDNA Clone MUG004.G04,
                                                                                                                             http://wheat.pw.usda.gov/genome.
Location/Qualifiers
                                                                                                                                                                         Email: ogihara@yokohama-cu.ac.jp
International Triticeae EST Cooperative
                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bread wheat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cultivar="Morex"
/db_xref="taxon:4513"
/db_xref="taxon:4513"
/clone="HysMeb0015A03f"
/clone_lib="Hordeum vulgare seedling shoot EST library
/clone_lib="Hordeum vulgare seedling shoot EST library
HycDNA0002 (Dehydration stress)"
/tissue_type="Seedling shoot"
/tissue_type="Seedling shoot"
/tissue_type="Seedling shoot"
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/clone="MUG004.G04"
/clone_lib="ITEC MUG Wheat Spikelet Library"
                                                                    /organism="Triticum aestivum"
/cultivar="Norin 26"
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    215 c    238 g    164 t
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53.6%;
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Triticum aestivum
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                                                                                                                                                                                                                                                                                                                   Kihara Institute for Biological Research, Yokoham
Maioka-cho 641-12, Totsuka-ku, Yokohama 244-0813,
Tel: 81 45 820 1903
Fax: 81 45 820 1901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Clout, S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,J. Hotton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE416107 548 bp
MUG004.G02R990615 ITEC
CDNA Clone MUG004.G02,
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                                                                                                                                                                                                                                                                                                                                                                                                                           Expressed Sequence Tags Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Sorrells, M., Warburton, M. and Wenzel, G.
                                                                                                                                                                                                                                                                           Email: ogihara@yokohama-cu.ac.jp
International Triticeae EST Cooperative (ITEC)
                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Ogihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
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/dev_stage="Feekes' scale 6-7"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; M13 Reverse.sequencing primer used. 1.2 Kbp averaginsert size."
                XhoI; M13 Reverse sequencing primer used.
insert size."
                                                        /note="Vector: pBluescript SK(-); Site_1:
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/dev_stage="Feekes' scale 6-7"
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/clone_lib="ITEC MUG Wheat Spikelet Library"
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/db_xref="taxon:4565"
                                                                                                                                                                                                    /organism="Triticum aestivum"
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170
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                  Yokohama City
44-0813, JAPAN
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Triticum aestivum
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624 TGAAGGCTCACGCAGACTCTTCGAGGAGCTGGCCGTCGAGAACAAAACCCTGAGGGAGTT 683
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Local Similarity 54.8%;
                                   GAAGAAGGTGACTGTCCCGTTTGTAGTCCTGCACGGCACGGCGGACCGGGTGACGGACCC 413
                                                                      GGACAAGATAAAAGTCCCGATCCTCCTTCTGATCGGCACTGGCGATGTAATAACCCCGGC 623
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                                                                                                                l Similarity
96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hordeum vulgare
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 578.
High quality sequence stop: 578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 832)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF621752 832 bp mRNA EST 18-DEC-2000
HVSMEa0012F19f Hordeum vulgare seedling shoot EST library
HVcDNA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMEa0012F19f,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Development of a genetically and physically anchored EST resource for barley genomics Unpublished (2000)
Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
BF621752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF621752.1 GI:11885486
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                                                                                                                Conservative
                                                                                                                                                                                                                        /clone_llb="Hordeum vulgare seedling shoot EST library HVCDNA0001 (Cold stress)"
/tissue_type="Seedling shoot"
/lab_host="TJCl21"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1"
127 c 277 g 155 t
                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4513"
/clone="HVSMEa0012F19f"
                                                                                                                                                                                                                                                                                                                                                                                /cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                              5.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46; DB 100,
Pred. No. 0.036;
""matches 75;
                                                                                                              Score 43.8; DB 150;
Pred. No. 0.16;
0; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SC 29634, USA
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Search completed: June 2, 2001, 21:49:58 Job time: 28896 sec

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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                            'Cgn2_6/ptodata/2/pna/US08_COMB.seq:*
'Cgn2_6/ptodata/2/pna/US08_COMB.seq:*
'Cgn2_6/ptodata/2/pna/US09_COMB.seq:*
'Cgn2_6/ptodata/2/pna/US091_COMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US083_COMB.seq:*
/cgn2_6/ptodata/2/pna/US084_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Score

Match Length DB

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Description

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636 698 1155 380 851 248	44006000000	5522 562 562 568 486 491	412 412 412 453 757 757 759 548 548 570 548 474	4403765 4411529 415
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54078, 115000, 20, App 21707, 2618, A 2515, A	7728, 7728, 53190, 53190, 1903, 0290, 125, A 125, A 2167, 2121, 6922, 6922, 999, A	nce 144, nce 1298 nce 1222 nce 145, nce 145, nce 1402 nce 1402	nce 81660 nce 1902, nce 6072, nce 16234 nce 16234 nce 13158 nce 13158 nce 13168 nce 1431, nce 2521, nce 27014 nce 27014 nce 27014 nce 1731, nce 1731,	œ · · ·

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US-09-382-242-28
                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: GENOMIC DNA US-09-382-242-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 28, Applicat GENERAL INFORMATION:
                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 789 NUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INC
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                          LENGTH: 789 NUCLEOT
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLI
TOPOLOGY: LINEAR
 181
                                                          121
                             181
                                                                                       121
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                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
SOFTWARE: WORD PH
                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                          1 ATGGAGGTTTACAAGGCCAAATTCGGCGAAGCAAAGCTCGGCTGGGTCGTTCTGGTTCAT 60
                                                                                                                                                                                                                                                     Local Similarity
TTTGGAGTTTACACCTTCGACTGGCCCGGCCACGGGAAGAGCCCGGGCAAGAGAGGCCC 180
                                                          TTTGGAGTTTACACCTTCGACTGGCCCGGCCACGGGAAGAGCCCCGGGCAAGAGAGGGCCAC
                                                                                                                                 GGCCTCGGCGAGCACAGCGGAAGGTATGGAAGACTGATTAAGGAACTCAACTATGCCGGC 120
                                                                                                                                                                            ATGGAGGTTTACAAGGCCAAATTCGGCGAAGCAAAGCTCGGCTGGGTCGTTCTGGTTCAT 60
                                                                                                                  GGCCTCGGCGAGCACAGCGGAAGGTATGGAAGACTGATTAAGGAACTCAACTATGCCGGC 120
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WORD PERFECT 6.0
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VENTION: ESTERASES
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                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PS/2
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                                                                                                                                                                                                                                    99.9%; Score 788.6; DB 17; 100.0%; Pred. No. 1.7e-195; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                 Length 789;
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                                                         180
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231 CAGGGAGAAGCCCTTCCTCTTCGGCCACAGCCTCGGTGGTCTAACTGTCATCAGGTACGC 290

Query Match
Best Local Similarity
Matches 241; Conserv

Conservative

7.2%; 47.0%;

Score 56.6; DB 15; Pred. No. 0.0015; 1; Mismatches 265;

Indels Length

6; Gaps

2

4403765;

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Sequence 2, Application US/09103840A
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: VENTER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout ; OTHER INFORMATION: represent a, t, c or g US-09-103-840A-2
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                                                                                                                                SEQ ID NO 2
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                                                                                                                                                 SOFTWARE:
                                                                           ORGANISM: Mycobacterium tuberculosis
                                                                                                   TYPE: DNA
                                                                  FEATURE:
                                                                                                                LENGTH: 4403765
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Best Local Similarity 47.0%;
Matches 241; Conservative
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SOFTWARE: PatentIn Ve
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APPLICANT: VENTER, JOAN C.
TITLE OF INVENTION: DAN SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: U5/79/103,840A
CURRENT FILING DATE: 1998-06-24
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TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
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acaggacctggtgagcccggtagtggcggttgccgccaagcttctgggcgtcgtggtgcc 214561
                                           CCCGGAAACGCCGGGCTTCATGGTGGCCCTCGCGAAGTTCCTTGGAAAGATCGCCCCGGG
                                                                                     tgtcgaacgtccagacaactacgacctgatggtgctttcggcgccggcggtggc---ggc 214501
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Pred. No. 0.0015;
1; Mismatches 26
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NUMBER OF SEQ ID NOS: 152403

SEQ ID NO 43890

LENGTH: 415

TYPE: DNA
ORGANIEM: Zee mays
OTHER INFORMATION: Clone ID: uC-zmflb73274c04a1

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                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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CURRENT FILING DATE: 2000-05-30
NUMBER OF CPC
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                                 684 CGAGGGGGCGTACCACGAGATATTTGAAGACCCCGAGTGGGCCGAGGAGTTCCACGAAA 742
                                                                                            TGAAGGCTCACGCAGACTCTTCGAGGAGCTGGCCGTCGAGAAAACCCTGAGGGAGTT 683
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CGACGGGTTCCTGCACGACCTGCTTCGAGCCCGAGCGAGGGTCGGCGCGAGA 211
                                                                        GCTGGCGTCGCGCGAGCTCTACGGCGCGGCGGCGTCCGCGCACAAGGACCTGCGCCTGTA 270
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Lalgudi, Raghunath V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xu, Nanfei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sammons, R. Douglas
Shukla, Hridayabhiranjan
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                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                            6.98;
56.48;
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                                                                                                                                                                                                                      Score 54.2; DB 52;
Pred. No. 0.00094;
0; Mismatches 78;
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; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB148-048-Q1-E1-H7
US-09-394-745-1902
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NUMBER OF SEQ ID NOS: 295529
SEQ ID NO 81660
LENGTH: 412
TYPE: NOTE THE REPORT OF SEQ ID NO 81660
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US-09-304-517A-81660
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SEQ ID NO 1902
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Best Local Similarity 52.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lalgudi, Raghunath V.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PLANTS
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                           ENGTH:
589 CTTCTGATCGGCACTGGCGATGTAATAACCCCGCCTGAAGGCTCACGCAGACTCTTCGAG 648
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hes 112;
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                                                 79 gtgctgcacggcgccgacgacctggtgaccgaccccaggggctcgcggggcgctgtacgag 138
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52.3%;
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Pred. No. 0.0073;
                                                                                                                                                                                                                Score 50.8; DB 1
Pred. No. 0.0073;
                                                                                                                                                                                                Mismatches 102;
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                                                                                                                                                                                                Indels
                                                                                                                                                                                                                               Length 412;
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; LENGTH: 412
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB148-048-Q1-E1-H7
US-09-565-306-6072
                                                                                         ; TYPE: DNA ; ORGANISM: Arabidopsis thaliana columbia US-09-654-617-162340
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                                                                                                                             CURRENT APPLICATION NUMBER: US/09/54,617
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 463173
SEQ ID NO 162340
LENGTH: 453
TYPP: 707
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SEQ ID NO 6072
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     Matches
                                     Query Match
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Best Local
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APPLICANT:
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mes 112; Conserv
   Local Similarity es 92; Conserv
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     Conservative
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                                                                                                                                                                                                                                                                                  Kovalic, David K.
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                 6.48;
57.18;
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52.3%;
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                                                                                                                                                                                                                                                Annotated Plant Genes
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Score 50.6; DB 25;
Pred. No. 0.0084;
Prematches 69;
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     Indels
                                     Length
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564 GGACAAGATAAAAGTCCCGCGATCCTTCTGATCGGCACTGGCGATGTAATAACCCCGCC

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CURRENT APPLICATION NUMBER: US/09/654,617
CURRENT FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 463173
SEQ ID NO 131581
LENGTH: 757
TYPE: DNA
ORGANITY
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                                                                                                                                      ; ORGANISM: Arabidopsis thaliana
; OTHER INFORMATION: unsure at all n locations
US-09-654-617-131581
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PRIOR FILING DATE:
NUMBER OF SEQ ID NOS:
SEQ ID NO 162340
LENGTH: 453
                                                                                   Query Match
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Best Local Similarity
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38-21(15097)D

CURRENT APPLICATION NUMBER: US/09/684,016

CURRENT FILING DATE: 2000-10-10
                                                                                                                                                                                                                                                                                                                       APPLICANT: Liu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
564 GGACAAGATAAAAGTCCCGGATCCTCCTTCTGATCGGCACTGGCGATGTAATAACCCCGCC 623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 gaacaaagtgaaagttccctttcttgtgatgcacggtactgacgacacagttaccgatcc 208
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                                                                     Local Similarity
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                                                     Conservative
                                                                                                                                                                                                                                                                                                                       Jingdong
                                                                                                                                                                                                                                                                                                                                         Kovalic, David K.
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Pred. No. 0.0084;
                                                                   Score 50.6; DB 2
Pred. No. 0.0093;
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                                                  Mismatches
                                                                                   DB 25;
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                                                                                   Length 757;
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TYPE: DNA
ORGANISM: Pinus radiata
US-09-606-755-9659
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SEQ ID NO 131581
; LENGTH: 757
; TYPE: DNA
; ORGANISM: Arabidopsis t
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                                                                         FILE REFERENCE: 11000.1041U6
CURRENT APPLICATION NUMBER: US/09/606,755
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 17747
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9659
                                                                                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                        Sequence 9659, Application US/09606755
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Best Local Similarity
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                                                                                                                                                                                   APPLICANT: Shenk, Michael A.
TITLE OF INVENTION: Them, and Methods for Using Them
                                                                                                                                                                                                                                 APPLICANT: Havukkala, Ilkka APPLICANT: Shenk, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 200 PRIOR APPLICATION NUMBER: PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 38-21(15097)D
CURRENT APPLICATION NUMBER: US/09/684,016
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NAME/KEY: unsure
LOCATION: (1)..(757)
OTHER INFORMATION: unsure at all n locations
                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                            684 CGAGGGGGCGTACCACGAGATATTTGAAGACCCCGAGTGGG
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                                                           407
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57.1%;
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Pred. No. 0
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Sequence 5521, Application US/60171431

GENERAL INFORMATION:
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: them, and methods for using them.
FILE REFERENCE: 1049A
CURRENT APPLICATION NUMBER: US/60/171,431
CURRENT APPLICATION NUMBER: US/60/171,431
CURRENT FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 25199
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 5521
LENGTH: 589
TYPE: DNA
ORGANISM: Pinus radiata
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US-60-209-830-1431
; Sequence 1431, Application US/60209830
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US-60-209-830-1431
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                                                                     CURRENT APPLICATION NUMBER: US/60/209,830
CURRENT FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 62628
SEQ ID NO 1431
LENGTH: CALL
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Best Local S
                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                           APPLICANT:
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                             LENGTH: 600
TYPE: DNA
ORGANISM: Zea mays
              OTHER INFORMATION: Clone ID: LIB3591-004-P1-K6-E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 aggctgctcaactcacatggctttggagtttatgcaatggattggatcggtcatggtggg
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                                                                                                                                                                                                         La Rosa, Thomas J.
                                                                                                                                                                                                                                          Castiglioni, Paolo
Hardeman, Kristine J.
                                                                                                                                                                                                                             Kerk, Nancy M.
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                                                                                                                                                                        PLANTS
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63.1%;
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; NUMBER OF SEQ ID NOS:

; SEQ ID NO 284255

; LENGTH: 548

; TYPE: DNA

; ORGANISM: Zea mays

US-09-654-617-284255
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Best Local Similarity 55...
Conservative
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CURRENT APPLICATION NUMBER: US/09/654,617
CURRENT FILING DATE: 2000-09-05
NUMBER OF CON-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                    572 TAAAAGTCCCGATCCTTCTGATCGGCACTGGCGATGTAATAACCCCGCCTGAAGGCT
                              692 CGTACCACGAGATATTTGAAGACCCCGAGTGGGCCGAGGAGTTCCACGAAA 742
                                                                                                    632 CACGCAGACTCTTCGAGGAGCTGGCCGTCGAGAAACAAAACCCTGAGGGAGTTCGAGGGGG
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                                                                    CGCGCGAGCTCTACGGCGCGGCGCGTCCGCGCACAAGGACCTGCGCCTGTACGACGGGT
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TCCTGCACGACCTGCTCTTCGAGCCCGAGCGCGACGAGGTCGGCGCCGAGA 362
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Search completed: June 3, 2001, 01:28:37 Job time: 42015 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                             Query
Match
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Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/FCTUS_COMB.seq:*
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DВ
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US-08-471-033-30
US-08-471-043-30
US-08-463-483A-30
US-08-471-046A-30
US-08-471-046A-30
US-08-4838-219B-7
US-08-469-334-30
US-09-233-336A-7
US-09-233-752A-7
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US-08-232-463-14
US-07-640-476-6
US-09-060-756-652
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                                                                                                                               Sequence 82, Appl
Sequence 30, Appl
                                                                                                                                                                                                                                                                    Sequence 28, Appl
Sequence 14, Appl
Sequence 6, Appli
Sequence 652, App
Sequence 19, Appl
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BSULT 1 JS-08-602-359A-28 Sequence 28, Application US/08602359A Patent No. 5942430 GENERAL INFORMATION: APPLICANT: ROBERTSON, Daniel E. APPLICANT: MURHY, Dennis APPLICANT: MURHY, APPLICANT: MURHY APPLICANT: MURHY APPLICANT: MURHY APPLICANT: MAFTIA, Anthony	ALIGNMENTS	31.8 4.0 2370 2 US-08-838-219B-19	44 32 4.1 485 4 US-09-095-855-106 Sequence	2 4.1 485 3 US-08-873-970-106	32 4.1 485 3 US-08-873-970-41	32 4.1 485 2 US-08-997-362-106	32 4.1 485 2 US-08-997-362-41	32 4.1 485 2 US-08-997-080-106	32 4.1 485 2 US-08-997-080-41	32.6 4.1 49272 1 US-08-614-770A-1	32.6 4.1 2277 2 US-09-098-487-5	32.6 4.1 2277 1 US-08-676-974-5	32.6 4.1 2277 1 US-08-676-967-5	32 33 4.2 9723 3 US-08-532-384-21	33 4.2 9723 1 US-08-083-590A-21	30 33 4.2 4268 3 US-08-893-828-33	29 33 4.2 4268 3 US-08-532-384-12	28 33 4.2 4268	
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US-08-602-359A-28
               TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 28
SEQUENCE CHARACTERISTICS:
LENGTH: 789 NUCLEOTIDES
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: GENOMIC DNA
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOTTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/602,355
FILING DATE: February 16, 1996
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KOSMOTKA, Anna TITLE OF INVENTION: ESTERASES NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: LA JOLLA
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UZIP: 92037
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Best Local Similarity
Matches 789; Conserv
                                                                         sequence 14, Application US/08232463
Patent No. 5670367
                   GENERAL INFORMATION:
APPLICANT: CORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 CORRESPONDENCE
           NUMBER OF SEQUENCES:
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ADDRESS
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100.0%; Pred. No. 2.3e-222;
tive 0; Mismatches 0;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 harry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILIG DATE:
FILIG DATE:
APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1800 Diago
CITY: Alexandria
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                           510
                                                                                                                                                                                                                                                                                                                                                       450 GAGGAACAGGGACGCCGTGAGGAGGTACGTTGAAGACCCCACTCGRCCACGACAGGATTTC 509
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TOPOLOGY: li
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RRRRRRRRRRRRRRRATCGCAAGCTCC
                              TAAGTGGCTGGTTGAAAAATCGTACTCTTC 779
                                                                GGCCAAGCTGGGAAGGAGCATCTTCGTGAACATGGAGCTGGCCCACAGGGAGGCGGACAA 569
                                                                                              GGCGTACCACGAGATATTTGAAGACCCCCGAGTGGGCCGAGGAGTTCCACGAAACAATTGT
                                                                                                                                                            CTCACGCAGACTCTTCGAGGAGCTGGCCGTCGAGAACAAACCCTGAGGGAGTTCGAGGG
                                                                                                                                                                                                                         GATAAAAGTCCCGATCCTCCTTCTGATCGGCACTGGCGATGTAATAACCCCCGCCTGAAGG
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1800 Diagonal Road,
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                                                                                                                                                                                                                                                                                                                                                                                        Conservative 186; Mismatches 135;
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RESULT 3
US-07-640-476-6
; Sequence 6, Application
; Patent No. 5376536

GENERAL INFORMATION:

QUAX, WILHELMUS

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TELEX: 706141

INFORMATION FOR SEQ ID NO: 6

SEQUENCE CHARACTERISTICS:
LENGTH: 1164 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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ORGANISM: Streptomyces murinus
STRAIN: DSM 40091
                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION METHOD:
OTHER INFORMATION: /EC.
OTHER INFORMATION: /pro
OTHER INFORMATION: /ev.
OTHER INFORMATION: /st.
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NAME: Kate H. Murashige
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                  295
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                                                                                                                                                                                                              115 GCCGGCTTTGGAGTTTACACCTTCGACTGGCCCGGCCACGGGAAGAGCCCCGGGCAAGAGA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
SOFTWARE: Paten+T
                                                                                                                                                                                                                                        4.5%;
Local Similarity 44.0%;
les 150; Conserva+:...
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
ACGCGGCCCGATAAAATACGGGGATTAATAGCTTCCTCGCCTGCCCTCGCCAAGAGCCCG
                                                 GAGTACGTCACCGCCCAGGGCTACGACCTCCGCCTTCGCCATCGAGCCCCAAGCCCAACGAG
                                                                              GAGAAGCCCTTCCTCTTCGGCCACAGCCTCGGTGGTCTAACTGTCATCAGGTACGCTGAG
                                                                                                               GGCGCCAAGGACGTGCGCGACGCCCTCGACCGCATGAAGGAGGCGTTCGACCTCCTCGGC 498
                                                                                                                                                                                GCCGAACTGGGTGCCAAGACGTATGTCGCCTGGGGCCGGTGAGGGCGCCGAGTCCGGT 438
                                                                                                                                             GGGCACACGAGCGTCGAGGAGGCGATGGAAATCATCGACTCGATAATCGAGGAGATCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (415) 327-2951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible SYSTEM: PC-DOS/MS-DOS PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LUITEN, RUDOLF G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO
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FCC_number= 5.3.1.5

/FCC_number= 5.3.1.5

/product= "xylose isomerase (glucose isomerase)"

/evidence= EXPERIMENTAL

/standard_name= "D-xylose ketol isomerase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (various positions within the sequence) ; OTHER INFORMATION: applicants are uncertain of bases designated as US-09-060-756-652
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                                                                   US-08-387-942C-19
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CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 652
Sequence 19, Application US/08387942C Patent No. 5939289
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA FILE REFERENCE: 3495-0169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cole, Stewart APPLICANT: Buchrieser-Brosch, Roland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gordon, Stephen APPLICANT: Billault, Alain
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TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: unsure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 catctctcgcgaccctgaggtggtccaggcttacaacaccgacccactcgtgcaccacgg 170
                                                                                                                                                     351 ptatccccggctgtnccacnaggtgttcaacgaaccggancgcaaccaagtg
                                                                                                                                                                                                      681 GTTCGAGGGGGCGTACCACGAGATATTTGAAGACCCCGAGTGGGCCGAGGAG 732
                                                                                                                                                                                                                                                                                            621 GCCTGAAGGCTCACGCAGACTCTTCGAGGAGCTGGCCGTCGAGAACAAAACCCTGAGGGA 680
                                                                                                                                                                                                                                                                                                                                      231 ancaccggcattgaccgcgccgctgctagtgctgcacggcaccgatgaccggctgatccc
                                                                                                                                                                                                                                                                                                                                                                                   561 GGCGGACAAGATAAAAGTCCCGATCCTTCTGATCGGCACTGGCGATGTAATAACCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           501 CAGGATTTCGGCCAAGCTGGGAAGGAGCATCTTCGTGAACATGGAGCTGGCCCACAGGGA 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 GTTCTCCCAACGGCATAAAGCCGGAACTCCTCTCGAGGAA
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APPLICANT: APPLICANT: APPLICANT:

ERTESVAG, HELGA VALLA, SVEIN SKJAK-BRAEK, GUDMUND

CORRESPONDENCE ADDRESS:

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US-08-387-942C-1
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                                                                                                                                        Sequence 1, Application US/08387942C Patent No. 5939289
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Best Local Similarity
Matches 123; Conserv
                                                                                                       GENERAL INFORMATION: APPLICANT: ERTESV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPAX: 703-200 IN INC. 1
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
SEQUENCE I 1143 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Releacure APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: P.O.BOX 747
CITY: FALLS CHURCH
                                                     APPLICANT:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                   228 GATCAGGGAGAAGCCCTTCCTCTCCGCCACAGCCTCGGTGGTCTAACTGTCATCAGGTA 287
                                                                                                                                                                                                                                                 738 CGCCCTGGAAGGCGTGCTGTTCAAGATGACC 768
                                                                                                                                                                                                                                                                                  348 GAGCCCGGAAACGCCGGGCTTCATGGTGGCC 378
                                                                                                                                                                                                                                                                                                                                                      288 CGCTGAGACGCGGCCCGATAAAATACGGGGATTAATAGCTTCCTCGCCTGCCCTCGCCAA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                             558 CAACGTCGCCTACAACAACGACCGCCACGGCTTCAACATCGTCACCAGCACCTACGATTT 617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 CAACTATGCCGGCTTTGGAGTTTACACCTTCGACTGGCCCGGCCACGGGAAGAGCCCGGG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: SI
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ZIP: 22042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                  VALLA, SVEIN
SKJAK-BRAEK, GUDMUND
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                                                 LARSEN, BJORN
                                                                                                       ERTESVAG, HELGA
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                DNA COMPOUNDS COMPRISING SEQUENCES ENCODING MANNURONAN C-5-EPIMERASE
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Pred. No. 0.76;
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Best Local Similarity 45.4%;
Matches 123; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12588 base pai
5499 CGCCCTGGAAGGCGTGCTGTTCAAGATGACC 5529
                                                                                                                                                                                                                                                                      5259 CCACGACAACGGCCTCGACGGCTTCGTCGCCGACTACCTGGTCGACAGCGTGTTCGAGAA 5318
                                                                                                                                   5379 CGTCATGACCAACAACGTCGCCTACGGCAACGGCGGCGCCGGCCTGACGATCCAGCGGGG 5438
                                                                                                                                                                                                      5319 CAACGTCGCCTACAACAACGACCGCCACGGCTTCAACATCGTCACCAGCACCTACGATTT 5378
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ORIGINAL SOURCE:
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NAME: MURPHY JR, GERALD
REGISTRATION NUMBER: 28,
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SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                          108 CAACTATGCCGGCTTTGGAGTTTACACCTTCGACTGGCCCGGGCCACGGGAAGAGCCCGGG 167
                              348 GAGCCCGGAAACGCCGGGCTTCATGGTGGCC 378
                                                                                                 288 CGCTGAGACGCGGCCCGATAAAATACGGGGATTAATAGCTTCCTCGCCTGCCCTCGCCAA 347
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CITY: FALLS CHURCH
STATE: VA
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TYPE: nucleic acid
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                                                                 CTCGGAGGACCTGGCCCAGCCGATATCCTGATCGACGGCGCCCTACTACGACAA 5498
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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6702..9695
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2227..6438
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Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                         Mismatches 148;
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RESULT 8
US-07-989-847-7
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Best Local Similarity
Matches 131; Conserv
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SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/01
FILING DATE: 23-JAN-1995
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                         457
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                                                                                                                                                                                                                                                                898 GAGGGTGAGGTGGTGACGGCTGCAGAATTCCGCATCTACAAGGACTGTGTTATGGGGGAGT 957
                                                                                                                                                                                                                                                                                                                                         838 GAGTTCTCCCCTCGTCAGCGACACCACAAAGAGTTCAAGTTCAACTTATCCCAGATTCCT 897
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TYPE: n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Corstanje, Brahm J. REGISTRATION NUMBER: 34,804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                      AGGGACGCCGTGAGGAGGTACGTTGAAGACCCCACTCGRCCACGACAGGATTTCGGCCAAG 516
                                                                                                              GACTCTGACCTGTTTTTGTTGGACACCCCGTGTAGTATGGGCCTCAGAAGAAGGCT 1072
                                                                                                                                                 GTCCCGATCCTCCTTCTGATCGGCACTGGCGATGTAATAACCCCGCCTGAAGGCT 631
                                                                                                                                                                                       TTTAAAAACCAAACTTTTCTTATCAGCATTTATCAAGTCTTACAGGAGCATCAGCACAGA 1017
                                                                                                                                                                                                                            CTGGGAAGGAGCATCTTCGTGAACATGGAGCTGGCCCACAGGGAGGCGGACAAGATAAAA 576
                                                                                                                                                                                                                                                                                                                                                                              AAGATCGCCCCGGGAGTTGTTCTCCCAACGGCATAAAGCCCGGAACTCCTCTCGAGGAAC 456
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Pred. No. 1.5;
1; Mismatches 163;
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; LOCATION:
US-07-989-847-7
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Best Local Similarity 44.4%;
Matches 131; Conservative
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INFORMATION FOR SEQ ID NO:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/989,847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02140-2387
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
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POSITION IN GENOME:
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                   457
                                                                                                                                                       337 GCCCTCGCCAAGAGCCCGGAAACGCCGGGCTTCATGGTGGCCCTCGCGAAGTTCCTTGGA 396
                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: Stratagene catalog #936203 Human placenta LIBRARY: cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: HOTISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
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ZIP: 02140-2387
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                   AGGGACGCCGTGAGGAGGTACGTTGAAGACCCACTCGRCCACGACAGGATTTCGGCCAAG 516
                                                    GAGTTCTCCCCTCGTCAGCGACACCACAAAGAGTTCAAGTTCAACTTATCCCAGATTCCT 897
                                                                                    AAGATCGCCCCGGGAGTTGTTCTCTCCAACGGCATAAAGCCGGAACTCCTCTCGAGGAAC 456
                                                                                                                       GCCTTCCTCAACGACGCGGACATGGTCATGAGCTTTGTGAACCTGGTGGAGTACGACAAG 837
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BMP6C35
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87 CambridgePark Drive
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1282..1698
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                                                                                                                                                                                        Score 33.8; DB 2;
Pred. No. 1.5;
1; Mismatches 163;
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GAGGGTGAGGTGACGGCTGCAGAATTCCGCATCTACAAGGACTGTGTTATGGGGAGT 957
CTGGGAAAGGAGCATCTTCGTGAACATGGAGCTGGCCCCACAGGGAGGCGGACAAGATAAAA 576

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RESULT 9
US-08-469-411-7
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US-08-469-411-7
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/469,411
FILING DATE: 06-Jun-1995
CLASSIFICATION: <Unknown>
              NAME/KEY: mRNA
LOCATION: 1..2923
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: circular MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: GI-5192B-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-498-8622
TELEFAX: 617-876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
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TITLE OF INVENTION: Recombinant Bone Morphogenetic
Heterodimers, Compositions and
                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
TISSUE TYPE: Human placenta
IMMEDIATE SOURCE:
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MEDIUM TYPE: Tape
                                                                               FEATURE:
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                                                                                             NAME/KEY:
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LOCATION:
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STREET: 87 CambridgePark Drive
CITY: Cambridge
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TYPE: nucleic acid
STRANDEDNESS: double
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ZIP: 02140-2387
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1282..1698
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Methods of Use
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5187076-5
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                                                                                                                                                                            Matches
                                                                                                                                                                                              Query Match 4.3%;
Best Local Similarity 44.4%;
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Best Local Similarity
Matches 131; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 07-MAR-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                           397 AAGATCGCCCCGGGAGTTGTTCTCCCAACGGCATAAAGCCCGGAACTCCTCTCGAGGAAC 456
                                                                                                                                 337 GCCCTCGCCAAGAGCCCGGAAACGCCGGGCTTCATGGTGGCCCTCGCGAAGTTCCTTGGA 396
                                                                                    778 gccttcctcaacgacgcggacatggtcatgagctttgtgaacctggtggagtacgacaag 837
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APPLICATION NUMBER:
FILING DATE: 01-JUL
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 20-MAR-1987
APPLICATION NUMBER: 31,346
FILING DATE: 26-MAR-1987
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APPLICATION NUMBER: 347,559
FILING DATE: 04-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 329,610 FILING DATE: 28-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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gagttctcccctcgtcagcgacaccacaaagagttcaagttcaacttatcccagattcct 897
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                                                                                                                                                                            131;
                                                                                                                                                                            Conservative
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Pred. No. 1.5;
1; Mismatches 163;
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US-08-717-294-82
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                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SEED, BRIAN APPLICANT: HAAS, JURGEN
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF TITLE OF INVENTION: PROTEINS
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                              244 TTCCTCTTCGGCCAC 258
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                                                                                                                                                                                                                                                                             TYPE: n
                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Elbing, Karen L
REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/717,294 FILING DATE: 20-SEP-1996 CLASSIFICATION: 435
 27
                                                                87
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                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 617-428-02
TELEFAX: 617-428-7045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
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                                                            AGCGACCAGGAGGAGATCGACTACGACGACACCATCAGCGTGGAGATGAAGAAGGAGGAC 28
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nucleic acid
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                                                                                                                                          Score 33.4; DB Pred. No. 0.48;
                                                                                                                            Mismatches
                                                                                                                                                         DB 4;
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US-08-471-033-30
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                                                                     Matches
                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 09-SEF-19-1
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/218,018
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APPLICANT:
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ADDRESSEE: CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Estruch, Juan J TITLE OF INVENTION: No. 5770696el Pesticidal Proteins and NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8582
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APPLICATION NUMBER: US 08/314,594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                107 TCAACTATGCCGGCTTTGGAGTTTACACCTTCGACTGGCCCGGCCACGGGAAGAGCCCGG 166
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603 TGAAGAAGGACGGCAGCCCGGCCGACATCCTGGACGAGCTGACCGAGCTGACCGAGCTGG 662
                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 11..2389
OTHER INFORMATION: /no:
OTHER INFORMATION: sequ
                                                                                                                                                                                                                                                                               DESCRIPTION:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 0 FILING DATE: 25-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: P-40,403
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Koziel, Michael G
Mullins, Martha A
                                                                   Conservative
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                                                                                                                                                                                                                                                                           other nucleic acid
/desc = "Synthetic DNA"
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51.0%;
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sequence encoding VIP3A(a)"
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                                                                                   Score 33.4; D
Pred. No. 1.8;
                                                                   Mismatches
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                                                                                                    DB 1;
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                                                                                                                                                                                   TELEFAX: 919-541-8689
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 23-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0 FILING DATE: 09-SEP-1994 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANY: Estruch, Juan J
TITLE OF INVENTION: NO. 5840868el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                     MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 05-JUN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800 PRIOR APPLICATION DATA:
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NAME/KEY:
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CITY: Hawthorne
                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 40, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 25-MA
                                                                    DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/463,483 FILING DATE: 05-JUN-1995
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                                                                                                                                                      ENGTH:
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                                                                                                                                  nucleic acid
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Kostichka, N. Kristy
Duck, Nicholas B
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Koziel, Michael G
Mullins, Martha A
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misc_feature
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                                                                                 other nucleic acid
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; OTHER INFORMATION: ; OTHER INFORMATION: US-08-471-044-30
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                  TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPUTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                    REFERENCE/DOCKET NUMBER: CG
                                                                                                                        APPLICATION NUMBER: US 01
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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ADDRESSEE: CIBA-GEIGY Corporation
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: CIBA-GLICA CTREET: 7 Skyline Drive
                                                   TELEPHONE:
                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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10. 5849870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T: Estruch, Juan J
INVENTION: No. 5849870el Pesticidal Proteins and Strains
F SEQUENCES: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08463483A
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Koziel, Michael G
Mullins, Martha A
Nye, Gordon J
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Kostichka, N. Kristy
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                                                       919-541-8615
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sequence encoding VIP3A(a)"
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                                                                                                     32,943
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                                                                                      CGC 1695/CIP3
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Pred. No. 1.
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RESULT 15
US-08-471-046A-30
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                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDBER: US 08/463,483
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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DESCRIPTION: /desc = "Synthetic DNA"
                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30B CURRENT APPLICATION DATA: APPLICATION UNBER: US/08/471,046A FILING DATE: 06-JUN-1995
                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                       APPLICATION NUMBER: US 01 FILING DATE: 09-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: No. 5866326artis Corporation STREET: 3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 11..2389
OTHER INFORMATION: /note= "maize optimized DNA
OTHER INFORMATION: sequence encoding VIP3A(a)"
                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Research Triangle Park
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Local Similarity 51.0%;
les 79; Conservative
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STRANDEDNESS:
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Kostichka, N. Kristy
Duck, Nicholas B
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Koziel, Michael G
Mullins, Martha A
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23-MAR-1994
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                US 08/218,018
                                                                         US 08/314,594

 Mismatches

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Pred. No. 1.8;
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Search completed: June
Job time: 23128 sec
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Best Local
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                          107 TCAACTATGCCGGCTTTGGAGTTTACACCTTCGACTGGCCCGGCCACGGGAAGAGCCCGG 166
                                                                                                                                                                                   663 CCAAGAGCGTGACCAAGAACGACGTGGACGGCTTCGAGTTCTACCTGAACACCTTCCACG
                                                                                                                                                                                                                                                                    603 TGAAGAAGGACGGCAGCCCGGCCGACATCCTGGACGAGCTGACCGAGCTGACCGAGCTGG 662
                                                                                                                                                                                                                                                                                                                                          4.28;
Local Similarity 51.08;
nes 79; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 11.2389
OTHER INFORMATION: /note= "maize optimized DNA
OTHER INFORMATION: sequence encoding VIP3A(a)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
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                                                                                                    ACGTGATGGTGGGCAACAACCTGTTCGGCCGCAGC 757
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Pred. No. 1.8;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 20
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                      39.6
38.6
37.2
37.2
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43.2
43.2
42.8
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Match
                                                              N_Geneseq_0401:*
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SIDSZ/gcgdata/geneseq/geneseqn/Na1981.DAT:

SIDSZ/gcgdata/geneseq/geneseqn/Na1981.DAT:

SIDSZ/gcgdata/geneseq/geneseqn/Na1983.DAT:

SIDSZ/gcgdata/geneseq/geneseqn/Na1984.DAT:

SIDSZ/gcgdata/geneseq/geneseqn/Na1984.DAT:

SIDSZ/gcgdata/geneseq/geneseqn/Na1986.DAT:

SIDSZ/gcgdata/geneseq/geneseqn/Na1987.DAT:

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SIDSZ/gcgdata/geneseq/geneseqn/Na1998.DAT:
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Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGGAGGTTTACAAGGCCAA......CGTACTCTTCGGCTCAATAA 789
                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS2/gcgdata/geneseq/geneseqn/NA1999
/SIDS2/gcgdata/geneseq/geneseqn/NA2000
/SIDS2/gcgdata/geneseq/geneseqn/NA2001
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T79326
A49201
A49205
A64204
T85397
X25144
V32494
A38391
A38389
N90362
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            DNA encoding Therm Corn putative leci Corn putative leci cDNA sequence enco Pseudomonas fluore Pseudomonas fluore Wheat glutathione S. griseofuscus gl Pseudomonas sp. WF Pseudomonas sp. WF Pseudomonas sp. WF
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Piece 3 Piece 3 synBX08

ALIGNMENTS

RESULT T79326

T79326;

T79326 standard; DNA; 789 BP

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Callen W, Kosmotka A, Link S, Ma Reid J, Robertson DE, Swanson RV,
                                                      16-FEB-1996;
                                                                                                                                                        CDS
                                                                                                                                                                                                                                               DNA encoding Thermococcus esterase CL-2-30LC
                                                                                                                                                                                                                                                                 16-FEB-1998 (first entry)
                                                                           11-FEB-1997;
                                                                                              21-AUG-1997.
                                                                                                                                                                                    Thermococcus sp. strain CL-2.
                                                                                                                                                                                                       pulp; paper; lignin removal; su
disease resistance; feedstuff;
                                   (RECO-) RECOMBINANT BIOCATALYSIS INC.
                                                                                                                  WO9730160-A1.
                                                                                                                                                                                                                          Esterase; thermostable enzyme; ester; chiral compound; cheese;
                                                      96US-0602359
                                                                          97WO-US02039
                                                                                                                                                                 Location/Qualifiers
                                                                                                                                /transl_except= (pos: 493..495, aa:val)
                                                                                                                                              *tag=
                                                                                                                                                                                                                sugar; lignocellulose;
       Maffia AM, M
RV, Warren PV;
               Murphy D;
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Glucose isomerase

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This DNA sequence codes for thermostable esterase CL-2-30LC (W23073) CC of Thermococcus CL-2, a marine archaea isolated from a severed CC alvinellid worm, which grows optimally at 88 deg C. It can be CC amplified from a pBluescript vector by PCR (see T79310-11). Claimed, CC (W23069-77, W23088) were recovered from genomic gene libraries. CC (W23069-77, W23088) were recovered from genomic gene libraries. CC They can be used for recombinant production of the enzymes in host CC care stable at high temperature and in organic solvents, making them CC superior for use in production of pure chiral compounds used in CC method is claimed for transferring an amino group from an amino CC acid to an alpha-keto acid using a claimed esterase. The enzymes CC may also be useful as ripening starters in cheese making, in lignin CC synthesis, in fermentable sugar production from lignocellulosic composal in paper and pulp manufacture, in carbohydrate derivative synthesis, in fermentable sugar production from lignocellulosic composals, in the study of plant wall structure, plant resistance to CC disease and organic matter decomposition and to select plants bred CC for production of highly degradable animal feeds.
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Best Local
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ATGGAGCTGGCCCACAGGGAGGCGGACAAGATAAAAGTCCCGATCCTTCTTGATCGGC
                                                                  GAAGACCCACTCGRCCACGACAGGATTTCGGCCAAGCTGGGAAGGAGCATCTTCGTGAAC
                                                                                                  tocaacggcataaagccggaactcctctcgaggaacagggacgccgtgaggaggtacgtt
                                                                                                                                     TCCAACGGCATAAAGCCGGAACTCCTCTCGAGGAACAGGGACGCCGTGAGGAGGTACGTT
                                                                                                                                                                      ccgggcttcatggtggccctcgcgaagttccttggaaagatcgccccgggagttgttctc
                                                                                                                                                                                                                                        cccgataaaatacggggattaatagcttcctcgcctgccctcgccaagagcccggaaacg
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                                                acid encoding heat stable esterase from thermophilic
a - which is active in organic solvents, useful in cheese
anufacture, and to study plant resistance to disease
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                                                                                                    Polynucleotide encoding plant lecithin:cholesterol acyltransferase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expressitivaries -
                                                                                                                                                                                                                                                                                                                                                            Corn; lecithin:cholesterol
                                                                                                                                                                                                                                                                                                                                                                              Corn putative
                                                                                                                                                                                                                                                                                                                                                                                               12-DEC-2000
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                                                                                                                                              P-PSDB;
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phosphatidylcholine-sterol O-acyltransferase; heat shock
                                                                                  Claim 2;
                                                                                                                                                      WPI; 2000-412337/35
                                                                                                                                                                                      (DUPO ) DU PONT DE NEMOURS &
                                                                                                                                                                                                                                                                                                                                     Zea mays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RE,
                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                  Page 36-37;
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                             lecithin:cholesterol acyltransferase
                                                                                                                                                                                                        98US-0110782
                                                                                                                                                                                                                        99WO-US28586
                                                                                                                                                                                                                                                                        /product= "lecithin:cholesterol acyltransferase"
/partial
/EC_number= "2.3.1.43"
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                                                                                  49pp; English
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                                                                                                                                                                      JB,
                                                                                                           screening cDNA expression
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The present sequence is a putative coding sequence for a corn lecithin: Cholesterol acyltransferase (also known as phosphatidylcholine-sterol O-acyltransferase). This enzyme is found associated with high-density lipoproteins and Apolipoprotein-Al and The gene and protein can be used to produce transgenic plants which increased lipid metabolism and membrane fluidity, and therefore increased lipid metabolism and membrane fluidity, and therefore increasistance to heat and/or cold shock, to alter the content of phytos

lecithin

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identify potential

herbicides

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Sequence 921

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164 T; 1 other;

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Query Match
Best Local Similarity
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Best Local
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                                                                   The present sequence is a putative coding sequence for a corn lecithin:cholesterol acyltransferase (also known as phosphatidylcholine-sterol 0-acyltransferase). This enzyme is found associated with high-density lipoproteins and Apolipoprotein-Al and -D. The gene and protein can be used to produce transgenic plants which have increased lipid metabolism and membrane fluidity, and therefore increased resistance to heat and/or cold shock, to alter the content of phytosterol or lecithin in grains and to identify potential herbicides.
                                                                                                                                                                                                        Polynucleotide encoding plant lecithin:cholesterol acyltransferase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                            Claim
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                                                                                                                                                                                                                                                                                                                                              03-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corn putative lecithin: cholesterol acyltransferase gene
                                               Sequence 1660
                                                                                                                                                                                                     libraries
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                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1999;
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                                                                                                                                                                                                                                                                                                                      PONT DE NEMOURS & CO
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                                               B₽;
                                                                                                                                                                                                                                                                                                                                              98US-0110782
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/product= "lecithin:cholesterol acyltransferase"
/EC_number= "2.3.1.43"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 77..1396
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                                              361 A; 475 C; 499
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O-acyltransferase; heat shock; cold shock;
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Pred. No.
  Score 43.2; DB 21; Pred. No. 0.0086;
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            Length 1660;
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                                     The present sequence encodes a Zebrafish acidic ribosomal protein PO. The specification describes promoters from cytokeratin gene, the muscle creatine kinase gene, fast skeletal muscle isoform of the myosin light chain 2 gene, and an acidic ribosomal protein gene. The promoters of these genes are muscle- and skin-specific. They are capable of directing a structural gene to be predominantly expressed in skin epithelia when it is inserted in front of the structural gene and introduced into fish embryos. The promoters can be used in recombinant DNA molecules, or chimeric genes and the chimeric genes can be used to create transgenic fish or in a vector used to transform a cell. The transgenic fish can
                        be used in methods for detecting steroid hormones, or heavy metals such
                                                                                                                                                                                                                                                                                                                                                                (/XXDX)
(-ISXD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zebrafish; promoter; cytokeratin gene; muscle creatine kinase gene; fast skeletal muscle isoform; myosin light chain 2 gene; fish embryo; acidic ribosomal protein gene; structural gene; skin epithelia; chimeric gene; transgenic fish; steroid hormone; heavy metal;
                  as zinc,
                                                                                                                                                                                              Example
                                                                                                                                                                                                                       Zebrafish gene promoters, used to create transgenic zebrafish, for sensing steroid hormones and heavy metals in water samples
                                                                                                                                                                                                                                                                    P-PSDB;
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14-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A64204 standard;
                                                                                                                                                                                                                                                                                                                                      (YANT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                     (HEJJ/)
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                                                                                                                                                                                                                                                                  2000-558297/51.
DB; B08482.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66;
                                                                                                                                                                                                                                                                                                                                                   XU Y.
HE J.
                                                                                                                                                                                           1; Page 32-33; 72pp; English.
                                                                                                                                                                                                                                                                                                                                     YAN
                                                                                                                                                                                                                                                                                                                                                                                UNIV
                                                                                                                                                                                                                                                                                                           Lam TJ,
              copper,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                SINGAPORE NAT
 er, cadmium and monitoring and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             monitoring; ornamental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding a zebrafish acidic ribosomal protein PO.
                                                                                                                                                                                                                                                                                                                                                                                                          99SG-0000811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-SG00079.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "acidic ribosomal protein
1069..1074
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                                                                                                                                                                                                                                                                                                           ₩,
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mercury, in a water sample (i.e. for monitoring pollution). The t
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RESULT
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                                             Query Match
Best Local Similarity
                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                   The present sequence represents a DNA fragment which is involved in the present invention for isolating a lipase which is highly reactive with a highly unsaturated fatty acid ester. A host transformed by a vector containing the novel DNA can be used in the preparation of the protein having lipase activity. The transformant prepares the lipase efficiently in a large scale.
                                                                                               Sequence 1437
                                                                                                                                                                                                                        Lipase coding sequence - used to prepare a lipase reacting remarkably with a highly unsaturated fatty acid ester
                                                                                                                                                                                                                                                               WPI; 1997-484105/45
                                                                                                                                                                                                                                                                                                             26-FEB-1996;
                                                                                                                                                                                                                                                                                                                                 26-FEB-1996;
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132 CACCTTCGACTGGCCCGGCCACGGGAAGAGCCCCGGGCAAGAGAGGGCACACGAGCGTCGA 191
                                                                                                                                                                                                      Example 3;
                                                                                                                                                                                                                                                                                    (AMAN ) AMANO PHARM
                                                                                                                                                                                                                                                                                                                                                                                JP09224679-A
                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGACCCACTCGRCCACGACAGGATTTCGGCCAAGCTGGGAAGGAGCATCTTCGTGAACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gtgtttcatcgtgggcgcagacaatgtcggctccaagcagatgcagaccatccgtctgtc 211
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                                     155;
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                                                                                                                                                                                                   Page 9-10; 14pp; Japanese.
                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 fluorescens sequence
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48.7%;
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Pred. No. 0.0096;
1; Mismatches 11
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                                                Pred.
                                                          Score 41;
                                    Mismatches
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                                e 41; DB 18; Le
. No. 0.035;
lismatches 190;
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                                                                                            0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                            fatty acid ester;
                                                          Length 1437;
                                   Indels
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The present sequence represents a novel DNA fragment which encodes a protein having lipase activity. The lipase, which was isolated from Pseudomonas fluorescens, is highly reactive with a highly unsaturated fatty acid ester. A host transformed by a vector containing the novel DNA can be used in the preparation of the protein having lipase activity. The transformant prepares the lipase efficiently in a large

Sequence 3456 BP;

719

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1013 C;

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RESULT
T85397
ID TE
Claim 5; Page 6-7; 14pp; Japanese
                                                                                             P-PSDB;
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                                     Lipase coding sequence – used to prepare a lipase reacting remarkably with a highly unsaturated fatty acid ester
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                                                                                                                                               (AMAN ) AMANO PHARM
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                                                                                             W27247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fluorescens; lipase; unsaturated;
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Best Local :
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This cDNA sequence codes for a 25 kDa glutathione transferase (GST) subunit (see Y05537), which has been termed Triticum aestivum GST 1 (TaGST1). The cDNA was isolated from an expression library prepared from RNA extracted from 7-day wheat var. Hunter shoots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glutathione transferase; GST;
TaGSTl; herbicide resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Triticum aestivum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wheat glutathione transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1354
                                                                                                                                                                                                              New isolated glutathione transferase subunit polynucleotides
                                                                                                                                                                                                                                                                         WPI; 1999-244035/20.
P-PSDB; Y05537.
                                                                                                                                                                                                                                                                                                                                                                       Cole
                                                                                                                                                                                                                                                                                                                                                                                                                            (RHON ) RHONE-POULENC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09914337-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X25144 standard; cDNA; 1085 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 CACCTTCGACTGGCCCGGCCACGGGAAGAGCCCCGGGCAAGAGAGGGGCACACGAGCGTCGA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                    Ŋ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACGGGGATTAATAGCTTCCTCGCCTGCCCTCGCCAAGAGCCCCGGAAACGCCCGGGCTTCAT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGCCACAGCCTCGGTGGTCTAACTGTCATCAGGTACGCTGAGACGCGGCCCGATAAAAT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gaatttcaccggcgcctcgattggcgtgcacgacgcgccgaagga 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAGCCGGAACTCCTCTCGAGGAACAGGGACGCCGTGAGGAGGTA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gggcgggttcttcgccgactccaactacatcgcctatgcctcgccgacccagagcagcac 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        caatgacgtggtcgcctttgccaaggccaatggcctcagcggcaaggacgtgctggtcag 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGGCGATGGAAATCATCGACTCGATAATCGAGGAGATCAGGGAGAAGCCCCTTCCTCTT 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cgcgttcggccccaaggattacgccaagaactacgtcggcgaagcgttcggcaacctgct 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cgacaaagtgctcaacgtcggctacgagaacgacccggtgttccgcgccctcgacggttc 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTGGCCCTCGCGAAGTTCCTTGGAAAGATCGCCCCGGGAGTTGTTCTCTCCAACGGCAT 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cggccacagcctcggcgggctggcggtcaacagcatggcggatttgagcggcggcaagtg 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.2%;
Similarity 44.9%;
                                                                                                                                                     Page 76-77;
                                                                                                                                                                                                                                                                                                                                                                 Cummins I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97GB-0019727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-GB02802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
46..714
/*tag= a
                                                                                                                                                  101pp;
                                                                                                                                                                                                                                                                                                                                                                                                                            AGRIC LTD.
                                                                                                                                                                                                                                                                                                                                                                 Edwards R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 18
Pred. No. 0.049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glutathione peroxidase;
transgenic plant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subunit TaGST1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 190; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 18; Length 3456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          wheat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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RESULT
V32494
PT TAX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   broad-ranging activities toward xenobiotic substrates, including herbicides, and also have glutathione peroxidase. The invention provides cDNAs and genomic DNAs (see X25144-52) encoding wheat GST subunits (see Y05537-45) active in herbicide metabolism. This is fundamental to understanding the GST detoxification in wheat and in the development of transgenic herbicide resistant plants expressing wheat GSTs. The invention also provides methods of identifying compounds capable of metabolism by GST, or compounds that induce GST expression in graminaceous plants, and for determining the GST level in a sample of seed or flour.

Transgenic plants, host cells used for production of GST subunits
                                                                                                                                                                                                                                                                                                                                                                                                     ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           V32494;
          Improving heat resistance of glucose isomerase -
part of amino acid in specific position of amino
                                                                                                                                                12-SEP-1996;
                                                                                                                                                                             07-APR-1998
                                                                                                                                                                                                         JP10084956-A
                                                                                                                                                                                                                                                                                                                                Streptomyces
                                                                                                                                                                                                                                                                                                                                                                        Glucose isomerase;
                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V32494 standard; DNA; 1164 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1085 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             grown from seed treated with fenchlorazole-ethyl, a herbicide safener. TaGST1 homodimeric and heterodimeric isoenzymes have
                                                                                         (GODO ) GODO SHUSEI KK
                                                                                                                     12-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                            isomerised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 CTGGCCCGGCCACGGGAAGAGACCCCGGGCAAGAGAGAGGGCACACGAGCGTCGAGGAGGCGAT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 CCTCGG 266
                                                                                                                                                                                                                                                                                                                                                                                                    griseofuscus glucose isomerase encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GST dimeric proteins, and vectors are also provided
                                                  1998-264846/24
DB; W63617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAAATCATCGACTCGATAATCGAGGAGATCAGGGAGAAGCCCTTCCTCTTCGGCCACAG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gttcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggacatcctcaagaccctcgacggcgctcggggacaagcccttcttcggcggcgacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72;
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                                                                                                                                                                                                                                                                                                                                                            sugar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          506
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                                                                                                                                                                                                                                                                                                                                griseofuscus
                                                                                                                      96JP-0262370
                                                                                                                                                  96JP-0262370
                                                                                                                                                                                                                                 /transl_except= (pos:427..429, a:/transl_except= (pos:1138..1140, /product= "Glucose isomerase"
                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 A; 316 C;
                                                                                                                                                                                                                                                                                                                                                                        heat resistance; thermostable; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.0%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39.6; DB Pred. No. 0.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
          comprises replacing acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,:
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Best Local Similarity 44.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This DNA encodes a Streptomyces glucose isomerase. This glucose isomerase is used to create a mutant with improved heat resistance which comprises replacing an amino acid in a specific position of is sequence. The glucose isomerase is useful for the preparation of
                            Example 1; Page 17-18; 43pp;
                                                                                        New proteins useful for desulfurization of crude oil have ability control expression of benzothiophene oxidase group -
                                                                                                                                                                                                                WPI; 2000-378972/33
                                                                                                                                                                                                                                                                                                                                        28-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP2000093180-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                decontamination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Benzothiophene oxidase; bto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas sp. WF505 ORF6-3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A38391 standard; DNA; 1470 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1164 BP; 181 A; 443 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 3;
                                                                                                                                                                                                                                                                         (TOFU ) TONEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isomerised sugar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTCTCTCCAACGGCATAAAGCCCGGAACTCCTCTCGAGGAA 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ccccgcggcgacatcctcctgcccaccgtcggccacgccctggccttcatcgagcgcctg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gagtacgtcaccgcccagggctacgacctccgcttcgccatcgagcccaagcccaacgag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggcgccaaggacgtgcgcgacgcctcgaccgcatgaaggaggcgttcgacctcctcggc 495
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                                                                                                                                                                                                                                                                                                                                        98JP-0272744.
                                                                                                                                                                                                                                                                                                                                                                                                    98JP-0272744.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene cluster; desulphurisation; crude oil;
                               Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38.6; DB 19; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO:4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385 G; 155 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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A38389/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to proteins encoded by the benzothiophene oxidase (bto) gene cluster from Pseudomonas sp. WF505, specifically the protein which controls expression of the gene cluster (Y97827), the controls expression of the gene cluster (Y97827), the controls expression of the gene cluster (Y97827), the controls enzyme (Y97824), which controls benzothiophene activity via redox regulation. These enzymes are respectively encoded by the bto gene cluster open reading frames ORF2-16 (A38396), ORF4-9 (A38396) and ORF6-7 (A38395). The invention also encompasses genetic constructs and vectors comprising the genes encoding these proteins, hosts containing such constructs and the recombinant production of the enzymes. Pseudomonas sp. WF505 benzothiophene oxidase, benzothiophene oxidase co-enzyme and bto gene cluster regulator are useful in the desulfurisation of crude oil and containinated by organic sulphur compounds. Sequences A38390-A38400 crepresent genes of the Pseudomonas sp. WF505 benzothiophene oxidase gene cluster, while sequence A38399 is the entire gene cluster sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 123; Conserv
                                  WPI; 2000-378972/33
                                                                                                                                                                                    04-APR-2000
                                                                                                                                                                                                                                                         Pseudomonas sp.
                                                                                                                                                                                                                                                                                                 decontamination;
                                                                                                                                                                                                                                                                                                                 Benzothiophene oxidase; bto gene cluster; desulphurisation;
                                                                                                                                                                                                                                                                                                                                                   Pseudomonas sp. WF505 bto gene cluster, SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                A38389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A38389 standard; DNA; 11279 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1309 gccggcggcgttcgcgccagcatggg 1334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1470 BP; 273 A; 512 C; 489 G;
                                                                       (TOFU ) TONEN CORP.
                                                                                                           28-SEP-1998;
                                                                                                                                                28-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 ACGAGCGTCGAGGAGGCGATGGAAATCATCGACTCGATAATCGAGGAGATCAGGGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGGAGGTTTACAAGGCCAAATTCGGCGAAGCAAAGCTCGGCTGGGTCGTTCTGGTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCTTCCTCTTCGGCCACAGCCTCGG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCCTCGGCGAGCACAGCGGAAGGTATGGAAGACTGATTAAGGAACTCAACTATGCCGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gccgaccggtacttccaggaatcgaccaccggcaatcccaacaccgacaagctcgtgccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggccgcagctacaagagctaccgcggcatgggctccatcggcgcgatgcagcagggcagt 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gagggcatcgagggccgcgtgccctacaagggctcgatcgtctcgatcatctaccagatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.7%;
milarity 46.2%;
Conservative
                                                                                                           98JP-0272744
                                                                                                                                                98JP-0272744.
                                                                                                                                                                                                                                                             WF505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143;
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                                                                                                                                                                                                                                                                                                                   crude oil;
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New proteins useful for desulfurization of crude oil have ability to

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to proteins encoded by the benzothiophene oxidase (bto) gene cluster from Pseudomonas sp. WF505, specifically the protein which controls expression of the gene cluster (Y97827), the benzothiophene oxidase (bto) enzyme itself (Y97825) and a benzothiophene coxidase co-enzyme (Y97824), which controls benzothiophene activity via redox regulation. These enzymes are respectively encoded by the bto gene cluster open reading frames of office (A38398), orre-16 (A38395) and orf6-7 (C (A38395). The invention also encompasses genetic constructs and vectors (C comprising the genes encoding these proteins, hosts containing such comprising the genes encoding these proteins, hosts containing such (C constructs and the recombinant production of the enzymes. Pseudomonas sp. WF505 benzothiophene oxidase, benzothiophene oxidase co-enzyme and bto gene cluster regulator are useful in the desulfurisation of crude oil and containinated by organic sulphur compounds. Sequences A38390-A38400 crepresent genes of the Pseudomonas sp. WF505 benzothiophene oxidase gene cluster, while sequence A38399 is the entire gene cluster sequence.
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Best Local Similarity
Matches 123; Conserv
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                                                                                                 sig_peptide
                                                                                                                                        CDS
                                                                                                                                                                                                                                                       Glucose isomerase gene from Streptomyces
                                                                                                                                                                                                                                                                                                                          N90362;
                                                                                                                                                                                                                                                                                                                                                            N90362 standard; DNA; 2010 BP
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                                                                                                                                                                                       Streptomyces
                                                                                                                                                                                                                         Glucose
                                                                                                                                                                                                                                                                                          01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1266
                   24-MAY-1989
                                                     JP01137979-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGGAGGTTTACAAGGCCAAATTCGGCGAAGCAAAGCTCGGCTGGGTCGTTCTGGTTCAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCGGCGCGTTCGCGCCAGCATGGG 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCCTCGGCGAGCACAGCGGAAGGTATGGAAGACTGATTAAGGAACTCAACTATGCCGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCTTCCTCTCGGCCACAGCCTCGG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGGCATCGAGGGCCGCGTGCCCTACAAGGGCTCGATCGTCTCGATCATCTACCAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCGACCGGTACTTCCAGGAATCGACCACCGGCAATCCCCAACACCGACAAGCTCGTGCCC 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCCGCAGCTACAAGAGCTACCGCGCGCATGGGCTCCATCGGCGCGATGCAGCAGGGCAGT 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGATGGGCAGCATGTTCGCCGGCACCGAAGAGGCGCCCCGGCGAGATCGTGCTGTACCAG 1447
                                                                                                                                                                                                                     isomerase; Streptomyces; DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 11-15; 43pp; Japanese
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                                                                                                                                                                                                                                                                                         (first entry)
                                                                                   /*tag= a
666..675
/*tag= b
                                                                                                                                    Location/Qualifiers 666..1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.78;
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T85645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                                                   Catalysis; enzyme; methyl group;
catechol; pyrogarol; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T85645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T85645 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1341 aacttcccgcacggcatcgcgcaggccctgtgggcgggcaa
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21-DEC-1995;
                                                   21-DEC-1995;
                                                                                                         08-JUL-1997.
                                                                                                                                                               JP09173074-A.
                                                                                                                                                                                                               Pseudomonas paucimobilis SYK-6
                                                                                                                                                                                                                                                                                                                                                   DNA encoding enzyme for production of catechol or pyrogalol compounds
                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2010 BP; 292 A; 756 C; 674 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contained in recombinant etc
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P-PSDB; P90423.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NORQ ) NORINSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 GCCGGCTTTGGAGTTTACACCTTCGACTGGCCCGGCCACGGGAAGAGCCCCGGGCAAGAGA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccccgcggcgacatcctcctgcccaccgtcggccacgccctggccttcatcgagcgcctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGAAGCCCTTCCTCTTCGGCCACAGCCTCGGTGGTCTAACTGTCATCAGGTACGCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggcgccaaggacgtgcgcacgcctcgaccgcatgaaggaggcgttcgacctcctcggc 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGCACACGAGCGTCGAGGAGGCGATGGAAATCATCGACTCGATAATCGAGGAGATCAGG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTCTCCCAACGGCATAAAGCCGGAACTCCTCTCGAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gagtacgtcaccgcccagggctacgacctccgcttcgccatcgagcccaagcccaacgag
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                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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95JP-0349914.
                                                   95JP-0349914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
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Pred. No. 0.57;
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                                                                                                                                                                                                                                                                   vanillic acid; syringa; production;
paucimobilis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
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techniques, a
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RESULT 13
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This DNA encodes an enzyme which is capable of catalysing the reaction releasing a methyl group from vanillic acid or syringa acid. The DNA an transformed host cells can be used to produce a recombinant enzyme. This enzyme plays an important role in transforming natural components into those of catechol or pyrogarol structure.
                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                         19-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                    1132 gcgatcaaccagttcatcacggacaccgacgaggaaatggccatggt 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1072
           (PION-) PIONEER HI-BRED INT INC
                                   12-MAY-1998;
27-AUG-1997;
                                                                         24-AUG-1998;
                                                                                                  04-MAR-1999
                                                                                                                          WO9910498-A2
                                                                                                                                                                                                   Zea mays
                                                                                                                                                                                                                                        Maize;
                                                                                                                                                                                                                                                                Maize cinnamate-4-hydroxylase cDNA.
                                                                                                                                                                                                                                                                                                                 X25203;
                                                                                                                                                                                                                                                                                                                                         X25203 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1671 BP; 320 A; 560 C; 541 G; 250 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 9-10; 14pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pyrogarol containing molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene encoding enzyme which catalyses release of methyl group from vanillic or syringa acid - useful for production of catechol or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-397032/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MAZN ) COSMO OIL CO LTD.
(COSM-) COSMO SOGO KENKYUSHO KK
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                                                                                                                                                                                                                                                                                                                                                                                                                                AACATGGAGCTGGCCCACAGGGAGGGGGGACAAGATAAAAGTCCCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggcgtcaatctcgctcgccacatcgagaatgtccgccagttcggcgtgccggtggtggtc 113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     catggcggcgtcgacaaggccgatctcggcacggcgaacccggaggcggtccgcaagggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCTCCAACGCATAAAGCCCGGAACTCCTCTCGAGGAACAGGGACGCCGTGAGGAGGTAC 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anggcgggcctcangccctcggccgcagtgatcgtggcgacgatccgcgcgctcangatg 101:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTGAAGACCCACTCGRCCACGACAGGATTTCGGCCAAGCTGGGAAGGAGCATCTTCGTG 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                       cinnamate-4-hydroxylase; lignin;
                                                                                                                                                                                                                                                                                       (first entry)
                                   98US-0076851.
97US-0057082.
                                                                         98WO-US17519
                                                                                                                                                Location/Qualifiers
80..1597
/*tag= a
                                                                                                                                                                                                                                                                                                                                         CDNA; 1794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.68;
                                                                                                                                                                                                                                                                                                                                          ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36.2; D
Pred. No. 0.9;
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                                                                                                                                                                                                                                       transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1671;
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                                                                                                                                                                                                                                       plant;
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RESULT 14
A10594
ID A10594
XX A10594
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XX Cellul
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seeds. The claimed nucleic acids can be used to transform a plant to modulate lignin biosynthesis. A claimed method involves transforming a plant cell with a recombinant expression cassette comprising a lignin biosynthesis polynucleotide operably linked to a promoter, growing the plant cell under plant growing conditions, and inducing expression of the polynucleotide for a time sufficient to modulate (preferably increase) lignin biosynthesis in the plant. The plant lignins can be used as chemical feedstock. Plant material of increased lignin content can be used as a fuel source, and in the pulp and paper industry. Decreased lignin content improves the digestibility of fodder crops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acids (see x25196-216) that code for proteins (see Y05657-77) involved in lignin biosynthesis are claimed. A claimed are recombinant expression cassettes, host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This DNA sequence encodes a cinnamate-4-hydroxylase (see Y05664) of maize. A polynucleotide having this sequence can be amplified from a cDNA library prepared from immature ear of maize line AP9-using the primer pair given in X25231 and X25232. The invention
                                                                                                                                                     Vigna angularis
                                                                                                                                                                                                                                 Gene encoding a subunit of cellulose synthase.
                                                                                                                                                                                                                                                                     29-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                              A10594;
                                                                                                                                                                                                                                                                                                                                                  A10594 standard; DNA; 10732 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                               1403 gtcggccgcag 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1343 ytcgaggaggaggagcacgtcgaggccaacggcaacgacttcaggtacctgcccttcggc 1402
                                                                            29-FEB-2000
                                                                                                                JP2000060568-A.
                                                                                                                                                                                             Cellulose synthase; cellulose production; increase yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1794 BP; 376 A; 586 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 claimed are recombinant expression cassettes, host cells (especially maize or sorghum host cells), and transgenic plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             provides methods and compositions relating to altering lignin
biosynthesis and/or the lignin composition of plants. Isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 126-128; 166pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding plant lignin biosynthesis enzymes - transform plants to modulate lignin biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bowen BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 TTCGGCCACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGAGGCGATGGAAATCATCGACTCGATAATCGAGGAGATCAGGGAGAAGCCCCTTCCTC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tacctcgccaaccaccccgacagytggaggcggcccgaggagttccggcccgagcgattc 1342
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71; Conserv
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be amplified
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26-AUG-1998;

26-AUG-1998;

98JP-0239998 98JP-0239998.

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RESULT 15
Q03159
ID Q03159
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AC Q03159,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a gene encoding a subunit of the cellulose synthase complex of Vigna angularis. The invention relates to subunits cellulose synthetic equipment, that can be used to increase the amount cellulose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being
                                                    Q03159 standard; DNA; 1164
                                                                                                                                           8686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene encoding a cellulose synthetic equipment - for the amount of cellulose synthesised in a plant body
                                                                                                                                       cyssrassrsrvavaasnrsraagygasnaaassrysarggrsrgngassr
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                                                                                                                                                                      GTTCGAGGGGGCGTACCACGAGATATTTGAAGACCCCGAGTGGGCCGAGGA 731
                                                                                                                                                                                                        arghsvaasnashashassrsrarggysrvahsasthrgnasnrrgncyshscyssr
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                                                                                                                                                                                                                                                                                                                                                                                                                      raasrysaavathrgasnsrsrgthrgythrysgsrthrrgggyysgrvarashssrgnt
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTCTCGAGGAACAGGGACGCCGTGAGGAGGTACGTTGAAGACCCCACTCGRCCACGACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGTGGTCTAACTGTCATCAGGTACGCTGAGACGCGGCCCGATAAAATACGGGGATTAAT 323
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13.4%; Pred. No. 1.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mutant glucose isomerase enzymes -
obtd. by site-directed mutagensis of gene from Actinoplanes
missouriensis, used for prodn. of high fructose corn syrups
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                             GAAACGCCGGGCTTCATGGTGGCCCTCGCGAAGTTCCTTGGAAAGATCGCCCCGGGAGTT 414
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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- Web : www.genoscope.cns.fr)
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HSU67963
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LFL012710
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SC5F7
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HVU95374
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                                                                                                                                    sequence:
evolution
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                                                                                         e - Centre National de Sequencage
(E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                               BCT
segment 6/6.
                                                                                                                                          insights
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                                                                                                                                          into archaeal
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AF042732 Anopheles
Z11165 R.capsulatu
AL096872 Streptomy
AP002998 Mesorhizo
AL137242 Streptomy
A98031 Sequence 1
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AF176640 Pseudomon
AP003010 Mesorhizo
AF202538 Pseudomon
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AL353870 Streptomy
E13698 DNA encodin
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AB025596 Pseudomon
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AC012975 Drosophil
AC007821 Drosophil
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Complement (5633. .6655)
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transl_table=11
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                                                                              CGGAGACGTTATAACCCCCACCTGAAGGTGCCAAGAGATTTTACGAGAGGCTGAAAGTTGA
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KIDVGHLDKLMNLVGELVITKGRLEQIGERLEGRELFALSTLSRLLTELQDEIMEMR
LTPIAEVFNKFPRMVRDLARKHGKEVETVEVMEGADIEVDRTILEKLGDALVHLLRANVD
HGIEPPEERVKLGKPRVGRUELLAKREKNHVVIIVRDDGRGIDPEKVKKKAIERGLIT
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GAACAAAACCCTGAGGGAGTTCGAGGGGGGCGTACCACGAGATATTTGAAGACCCCCGAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGACCCACTCGRCCACGACAGGATTTCGGCCAAGCTGGGAAGGAGCATCTTCGTGAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGAAAAGAATTTGAGGAAACGATAATCAAGTGGCTAGTTGA 54853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 39
99287316
2 (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haft,D.H., Hickey,E.K., Peterson,J.D., Nelson,W.C., Ketchum,K.A., McDonald,L., Utterback,T.R., Malek,J.A., Linher,K.D., Garrett,M.M. Stewart,A.M., Cotton,M.D., Pratt,M.S., Phillips,C.A., Richardson,D., Heidelberg,J., Sutton,G.G., Fleischmann,R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evidence for lateral gene transfer from genome sequence of Thermotoga Nature 399 (6734), 323-329 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nelson,K.E., Clayton,R.A., Gill,S.R., Gwinn,M.L., Dodson,R.J., Haft,D.H., Hickey,E.K., Peterson,J.D., Nelson,W.C., Ketchum,K.A., McDonald,L., Utterback,T.R., Malek,J.A., Linher,K.D., Garrett,M.M. Stewart,A.M., Cotton,M.D., Pratt,M.S., Phillips,C.A., Stewart,A.M., Cotton,M.D., Pratt,M.S., Phillips,C.A., Richardson,D., Heidelberg,J., Sutton,G.G., Fleischmann,R.D., Ferson, M. B., M. Stewart, A.M., Cotton, M.D., Pratt,M.S., Phillips,C.A., Stewart, A.M., Cotton, M.D., Pratt,M.S., Phillips,C.A., Stewart, A.M., Cotton, M.D., Pratt,M.S., Phillips,C.A., Elson, M.D., Heidelberg,J., Sutton,G.G., Fleischmann,R.D., France, M.D., M.D., Pratt,M.S., Phillips, C.A., Phillips, Phillips
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Thermotogales; Thermotoga.
1 (bases 1 to 13280)
Nelson, K.E., Clayton, R.A., Gill, S.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermotoga maritima
AE001789 AE000512
AE001789.1 GI:49819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (01-JUN-1999) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 13280)
Nelson, K.E., Clayton, R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White, O., Salzberg, S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eisen, J.A., Fraser, C.M. et, al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermotoga maritima.
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                                                                                                                                                                                                                                                                                              /gene="TM1345"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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section
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                                                                                                                                                                                                       PID:1184680
70.04; ident
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gill, S.R., Gwinn, M.L., Dodson, R.J.,
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                                       phosphorylase
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maritima
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                                                                                                                                                                                                            by sequence
                                                                                                                                                                                                                                                       GB:AL009126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUN-1999
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gene

SdC

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KPLRGPSRREIGHGHLÆFRALKNMLPPEEFFYTIRVSEILESUGSSSMATVCSGSL
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                                                                                                                                                                                                                                                                                                                                                                                                                          sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSADRYGQEGENKFVPEGIEGMVPYKGTVKDVVHQLVGGLRSGMGYIGARTIKELQEK
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GGIRYSGDIVKALAAGAESVMVGSIFAGTEEAPGETILYQGRKYKAYRGMGSLGAMRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISLEKAKEILHQHRIEKLPLYSKDNKLYGLITIKDIMSYIEHPNAARDEKGRLLYGA
AVGTSPETMERVEKLYKAGYDVIVIDTAHGHSRRVIETLEMIKADYPDLPYVAGNVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVFGIGPESGKIIEKHEMIV"
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YLGKLDMVTDNPAGMMSFVIDDLSNDSLETIEERVERIKNVSKEDYRRAYERFIAGNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKISSEDLREYHRKNYNLPDTKIILAGKVNDDYLSLLEKELSELERNKPGDPLPPPPS
FEHTEPRYIVRNDLEQVHIAMARPICGRISEDIYPLYALNTALGSGMSSILFHEIREK
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/db_xref="GI:4981908"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(4861. .5919)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(4861. .5919)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mKEALTFDDVLLVPQYSEVLPKDVKIDTRLTRQIRINIPLVSAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="inosine-5′-monophosphate dehydrogenase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to GB:AE000657 percent identity: 85.71;
identified by sequence similarity; putative"
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identified by sequence similarity; putative"
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/gene="TM1346"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILSEFNVEKIPVVEPTPPEGLVEAFKDLLNKEELERRILVKVKKEREVALKEYEEQLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="TM1348"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="TM1348"
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                                        .6932)
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                                                             complement(9808. .10119)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="GI:4981911"
/tabs1stion="MURVFR-PSPTGFLHVGGARTALENFLEARKEKGKFILRIEDTD
/trabs1stion="MURVFR-PSPTGFLHVGGARTALENFLEARKEKGKFILRIEDTD
LERSSREYEEKLMESLERHGLILMDEGPDVGGDHGPYRQSERVEIYREHAERLVKEGKA
YYVYAYPELIEEMREKLLSEGKAPHYSOEMFEKFDTPERREYEEKGLRPAVFFKMPR
KDYULMDVVKGEVVFKTGA1GOFVIMSNGLFTYNFACVVDDMLMEITHVIRGDDHLS
NTLRQLALYEAFEKAPPVFAHVSTILGPDGKLSKRHGATSVEAFRDMGYYLRNMPIEKLA
LALGWSHPEGKELLTULEELISSFSLDRLSPNFAIFDDQKLKWNNGYYLRNMPIEKLA
ELAKPFFEKAGIKIIDEEYFKKVLEITKERVEVLSEFPEESRFFFEDPAPVEIPEEMK
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                                                                                                                                                                                                                            VPAFLKMKKLVVPGIEIQTVEDVHVLGFFSDIESALKVTKIVYEHLPSVKHDHEKMGY
QLFVDEKGNYTGYEDVPLGFPSDLTLSQAVELIRSFGGIPVYAHVEKRFGVLYQLGFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVFSQLKEELQNVRWTMEEITPVFKKVLKQHGVKPKEFYMTLRRVLTGREEGPELVNI
IPLLGKEIFLRRIERSLGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(7710. .9119)
/gene="TM1351"
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GYTVFYIREIASFFVLIYPKSVRAEAREFFRDVYASMGRYIRVIFINAVIIGLSYWIV
FEAFNLKYSAIISLWAFVTNFIPIVGVVLEYIPVLLFSLTLGVKGVLLIALFAILIHA
                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein"
/protein_id="AAD36423.1"
/db_xref="GI:4981912"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(9113. .9811)
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/protein_id="AAD36420.1"
/protein_id="AAD36420.1"
/db_xref="G1:4981909"
/translation="MKEFRKILEDKAFFFTTLYILISFLVFKIFPDVFAVIVLMVFFT
LLLDPVIRFLEKLKFGKYFSRVAALLLFFFVMVYSLYMIIPPVFNEFGSFIEFMTKVF
                                                                                                                                                               ILNSEYTLGGVLNW"
                                                                                                                                                                                                 PDLEIPVAEVVSREGKENAQKKNLRVIVTSDAHFPSDIGRRYIDISGAPNSPEEVLKK
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/protein_id="AAD36421.1"
/db_xref="GI:4981910"
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identified by sequence similarity; putative"
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/protein_id="AAD36422.1"
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identified by sequence similarity;
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      note="similar
                                                                                                                                                                                                                                                                                                translation="MKADLHVHTCLSPCADLLMIPPVVERASGDVQILGIVDHNSAKN/
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dentified by sequence similarity; putative"
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.y; putative"
percent identity: 0.00; identified
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                                                                                                                                GAGCACCAGAAAGAGTTTTTCAAAACGATAGTCGAGTGGAGTCTCGAAAAA
                                                                                                                                                                  GAGTGGGCCGAGGAGTTCCACGAAACAATTGTTAAGTGGCTGGTTGAAAAA 768
                                                                                                                                                                                                                                                                                                      GGCACTGGCGATGTAATAACCCCGCCTGAAGGCTCACGCAGACTCTTCGAGGAGCTGGCC
                                                                                                                                                                                                                                                                                                                                                         CATATGAAAAAGGTTCTCAAAGACGCTGAAAGGATAAAGGTTCCTGTTCTCATTTTTCAC
                                                                                                                                                                                                                                                                                                                                                                             AACATGGAGCTGGCCCACAGGGAGGCGGACAAGATAAAAGTCCCGGATCCTCTTCTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATAAGAGATCCCCTCGTTCACGACAGGATCTCTTTCAAGCTCGCTTCAGATATGCTCTCC 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATTCTCCGGTCCTTGAATTCATGGTGAGGTTTCTGTCCTTTTTTGTTCCATTCCTCACG 729:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCCTCGGCGAGCACAGCGGAAGGTATGGAAGACTGATTAAGGAACTCAACTATGCCGGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGGAGGTTTACAAGGCCAAATTCGGCGAAGCAAAGCTCGGCTGGGTCGTTCTGGTTCAT 60
                                                                                                                                                                                                         ACAGAGAAAAAA----CTGGTGAGCTTTCCTGGAGGATACCATGAACTTTTTGAAGATCCA
                                                                                                                                                                                                                                            GTCGAGAACAAAACCCTGAGGGAGTTCGAGGGGGGGGGTACCACGAGATATTTGAAGACCCC
                                                                                                                                                                                                                                                                                 GGAACTGATGACAGGGTGTGTCTTTTGAGGGAAGCAAGAAGTTTTTTCGAAGCACTGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGCCGGGCTTCATGGTGGCCCTCGCGAAGTTCCTTGGAAAGATCGCCCCGGGAGTTGTT
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AE000982 13099 bp
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/protein_id-"AAD36424.1"
/db_xref-"GI:4981913"
/translation-"MEKLGLEHVCGDLNTEVEHGFTCDLLSEVLGKAQDSTLWITVQS
/translation-"MEKLGLEHVCGDLNTEVEHGFTCDLLSEVLGKAQDSTLWITVQS
HVNIIAVATVVGIKGIVLCDGHEYEKDTVKKAEENGVVLLKSQENSFIVSGKVYELGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(10100. .11065)
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Pred. No. 4.7e-25;
Pred. No. 351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (15-DEC-1997) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
In order to show the genes in ascending order on the genome, the origin of this version has been moved by TIGR to position 2093570 of the original version and the opposite strand is shown from the
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Klenk, H.P., Clayton, R.A.,
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607. .1143
                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAB89505.1"
/db_xref="GI:2648806"
/taanslation="MLDILKTIWLLLPCYTDNNFAVLVGGGTPIDFGKTFVDGKRIL
/translation="MLDILKTIWLLLECYTDNNFAVLVGGGTPIDFGKTFVDGKRIL
GDGKTWRGFVGGVAGGVLTANLQYAIEKLSGLAIYSSLPFNEFFTLTFLLAFGAMFGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to 39.53; identified
                                                                                                                                                                                       /note="similar to
48.99; identified
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/protein_id="AAB89505.1"
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                                                       /product="orotate phosphoribosyl
/protein_id="AAB89504.1"
                                                                                        /product="orotate
                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                     /gene="AF1741"
                                                                                                                                                                                                                                                                                                                                                                                                         LCGSF1KRRFGYERGSRFL1VDQLMFLLVALL1ASLYPPFWKLFTAEI1ALAV11TPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Archaeoglobus fulgidus"
translation="MVMLADALVKRMIEVGALKFGDFVLSSGKRSRVYVDVKLASTFP"
                                                                                                                         transl_table≔11/
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                                                                                                                                                                                GB:L77117 PID:1592320 percent identity:
by sequence similarity; putative"
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/gene="AF1746"
3990. .5396
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KVSGKSYRVWILAKYSEEPLSGVVRVGILIAKSEYPRVMRASKKLMAHIRVYDSSIEITK
DLVYGFIDIAASPFITQAVFGILMKNITIVRKVALNGGGLVFSGISSDYWGCSEFSTM
ERNLRKYLELKGLKGSIRYFROPESMIKSLGELRAIAIWEPYFTMLEGKKEAFNBHIG
DYLCCTLAVNNNFSECNSDLLEEFIREFDRAKVGKKDGKVLAELIGFPTEVVVRSFES
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DRIGEVKEGEKVVVVEDVITTGSSALSAARRVEESGASVAAIIAVVDREESGRNFMSL
LKLSDLIEAHDSIQPTES"
                                                                                                                                                                                                                                                                                                             /note="hypothetical protein; identified by GeneMark; putative"
                                                                                                                                                                                                                                                                                                                                                               complement(3340. .3867)
/gene="AF1745"
                                                                                                                                                                                                                                                                                                                                                                                                           complement(3340.
/gene="AF1745"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MALRLSKLGVKPNHLTLAGLVFALISSYLIIEGRILHASIFVLL
SSLCDLLDGALARKAELTTKFGGYLDSVTDRYVDVILFISLGIYGVDWVAIAMAMSGA
LLVSYTRARAETIIEKCDVGIAERSERLLILLLGMLTGYIYEAVLIIAVLSHITALHR
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/product="CDP-diacylglycerol--glycerol-3-phosphate
/probsphatidyltransferase (pgsA-2)"
/protein_id="AAB89506.1"
/db_xref="GI:2648809"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to GB:L42023 SP:P44528 PID:1003150 PID:1222037 PID:1204382 percent identity: 26.71; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="AF1744"
2825. .3343
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GDESCTNCNYMKIDLCLGCPVTGHYKGTLWK"
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VLFIYVKNLGHFRTPLSLSPSTYKKLAECPAPYLNNLSKHLNSCRNQALKILRITLNT
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/gene="AF1742"
                                                                                             CEIREDLMKLRITKA'
                                                                                                                         {	t AEEFSGKDLEYVLRRLEACNFFRLQVKKNEFVLLLNHEKTKKFVKMLMEVLLEKMGFE}
                                                                                                                                            /translation="mrnpvrvTiALDDESvKIFEELKKELGLSQSEIIrrvIKFYrDY
KFLEKFDREKVSTYIEMLGEGEHVVLDIDHWISLLEFIESHPSGEDFWKLHREIAKAH
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/transi_table=11
/product="A. fulgidus predicted coding
/protein_id="Ana89511.1"
/db_xref="GI:2648812"
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2203. .2778
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identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                              167
                                                                                                                                                                                                                                                                                       107
  281
                                                                                                                                                                                                                                                                                                                                                                                     47
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gene CDS gene

gene

CDS

gene

CDS

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Local Sin
hes 280;
TCAGGTACGCTGAGACGCGGCCCGATAAAATACGGGGGATTAATAGCTTCCTCGCCTGCCC 340
                                                           GTTTGGATTACGACTGCCCGAAGATACTCTACGGCCACAGCATGGGCGGGAATCTCGCTC 1126
                                                                                                                                                                                                                                         GCAAGAGAGGGCACACGAGCGTCGAGGAGGCGATGGAAATCATCGACTCGATAATCGA--
                                                                                                                                                                                                                                                                                                                                                                                                                          TCTGTCTTGTTCATGGTCTGGGGGGAGCACTCTGGAAGATACGAGCACGTTGCAAGGTTTT 11444
                                                                                                                                                                                 GGAAGAGGGGGCATGCTGAATATCAGCAGTTAATGGATGACATCACCCTTTTCCTCCAAA 11324
                                                                                                                                                                                                                                                                                                    TCAACTATGCCGGCTTTGGAGTTTACACCTTCGACTGGCCCGGCCACGGGAAGAGCCCGG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGTTCTGGTTCATGGCCTCGGCGAGCACAGCGGAAGGTATGGAAGACTGATTAAGGAAC 106
                                                                                                                      ----GGAGATCAGGGAGAAGCCCTTCCTCTTCGGCCACAGCCTCGGTGGTCTAACTGTCA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="AF1747"
5393. 5777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGFLVMFMQAGFAMLEAGFSRAKNVANVMKNLMDFAVGSLAFFAVGFALMMGADWQG
LAGTTGWFLAGESYDVSTIELWFFMLVFAATAATIVSGSIAERFKFVSVLVYSAVVSA
VIYPIYGHMLMGGGMLSSEEPWKLGGGYAALAFATLYSGSIAERFKFVSVLVYSAVVSA
VIXPIYGHMLMGGGMLSSEEPWKLGGGYAALDFAGSGVVHALGGYIALAAVMLLER
LGKXDSDGNPRAIFGHNLAFAVIGTFILWFGWFGFNAGSTLSAHELRVSIIASNTNLA
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WGFFIYQLISAIVNFAMAFGTGFALFWILKKVIGIRVSPEEEMLGLDIAEHAAVAYPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="AF1749"
6544. .7710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="AF17.5738. .6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identity:
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MKKIEAIVRAEKFPEVKAALEERGFYGMTVTDVKGRGQQGGMQI
QFRGRTMEVTLLPKVKLEIVVKDDAVEEVIGLIVNSAFTGSPGDGKIFIIPVEDVVRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to PID:1001734 SP:P54147 PID:1208463
percent identity: 49.04; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTFPDAEY IAKMLGLTEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mimyrrihnniyqikpgrlsshcylitaelnalidsgtardfpk
LERELGEIGLNAKDIDIVINTHEHfDHIGGNLFLQKNSIIMAHRHAAVKIIYGDDEVM
MCRTHGQREVGYRVHYWLNNIDAVDLGGVFLRVMHTPGHTSGCICLYDPRNRILFSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="nitrogen re
/protein_id="AAB89507
/db_xref="GI:2648808"
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/db_xref="G1:3648804"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLFANGTLSSIYNSGSLGEYFNSLRKIKTMKIDLLLPGHGRISGNVEVDIERTLENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTGERGDDSL'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FVCTETELPLAMKQGGGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to GP:1]
identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="AF1748"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="similar to GB:L77117
dentity: 58.04; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="AF1747"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF1748"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 87.6; DB 1;
Pred. No. 3.3e-09;
0; Mismatches 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GP:1787158 percent identity:
uence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulatory protein P-II (glnB-2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SP:Q60381 PID:1592259 percent
by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 13099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                               224
                                                                                                                                                                                                                                                                                                    11384
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gene CDS	Q 0	SOURCE DO ORGANISM DO REFERENCE 1 1 AUTHORS WILL WILL WILL WILL WILL WILL WILL WIL	963 97/c 110N N	Oy 401 TCGC Db 11143 TTGC Oy 461 ACGC Oy 161 ACGC Oy 521 GAAC Oy 581 CGAX OY 581 CGAX	11263 341 11203
/organism= Delinococus radioquirans /otrain="R1" /otrain="R1" /otrain="R1" /otrain="R1" /otrain="M1530" /gene="DR1530" /gene="DR1530" /gene="DR1530" /note="identified by Glimmer2; putative" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="AAFI1102.1" /db_xref="GI:6459300" /translation="MTLALDINILSAIFRAEETAEAVLGVLEAQPPGTLVVSGAAFSE	Heidelberg, J., Gwinn, M.L., Jiang, L., Pam P., McDonald, d.L., Daly, M. Chum, K.A., Ne C. and Fraser 9) The Instit ckyille, MD 2 lifters	Deinococcus radiodurans Deinococcus radiodurans Deinococcus radiodurans Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus. 1 (bases 1 to 10603) White,O., Eisen,J.A., Heidelberg,J.F., Hickey,E.K., Peterson,J.D., Dodson,R.J., Haft,D.H., Gwinn,M.L., Nelson,W.C., Richardson,D.L., Moffat,K.S., Oin,H., Jiang,L., Pamphile,W., Crosby,M., Shen,M., Vamathevan,J.J., Lam,P., McDonald,L., Utterback,T., Zalewski,C., Makarova,K.S., Aravind,L., Daly,M.J., Fraser,C.M. et,al. Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1 Science 286 (5444), 1571-1577 (1999) 20036896	ACA 10 10 000 GI	ACGCAT ATGGCAT ACCCACT ACCCCT ACCCCT ACCCCT ACCCCT	
gene CDS	CDS			gene .	gene CDS

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QEAAQPAQSPFRRYVGIAPPLEGGSVEYHRQQLGYEE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(4319. .5218)
/gene="DR1533"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to GB:D26185 SP:P37474 PID:467444 GB:AL009126 percent identity: 61.27; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(882. .4046)
/gene="DR1532"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(882. .4046)
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/transl_table=11
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                                                                                   putative"
                                                                                                                                                              complement(5246. .5794)
                                                                                                                                                                                                                                                                                                                                                      /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(4319. .5218)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIDKRGIKPDEYARMLIEVLGYFG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNARLTPEYFVDADGQPNEGERIATYGRLSDARTLQAISRVERDLRKKYGPPTPEVQN
FIDLAKLRLTALAKRVLSIGETMTQLQITFAYKALDYDAPGLKKFPHKTEVVTFPPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(502. .747)
/gene="DR1531"
                                                                                                                                                                                                       complement(5246. .5794)
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identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(502. .747)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLASPNIAEASAFAFLRDTGVRADWQMDEDLWLCAARAFRGYSVRRRQSGGGQPRRIL
ADFMIGAHALLRADALVTLDPQHYRLNFPELRVINPAEG"
                                                                                                    note="similar to identity: 49.42; i
                                                                                                                                                 /gene="DR1534"
                                                                                                                                                                                        /gene="DR1534"
                                                                                                                                                                                                                                                                                                                                                                                                                  transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="DR1533"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                              codon_start-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="identified by Glimmer2; putative"
                                                                                                        SP:P05332 identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ai protein"
3.1"
                                                                                                    GB:X07542 PID:39573 by sequence similari
                       putative"
                                                                                                        similarity;
                                                                                                                          percent
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gene

CDS

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/gene="DR1538"
9996. 1051
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TPAAPQTAT PVVDDQYA PLQWAF PLMGYGAVWRDMDAGGYTREVTVAVADSGYWRDH
PDLAGQLWTPQEGALDVLSGTUNGDGDGPDRDTDESFAGRKTESHGTHVTGII VARW
GONAP SCAGC SPTGVVGASYKAP I KVLP I RVLDTQGNTDLADV I NAVRYAAGLPVKLG
EQVYTNPH PAQVLNLSLGGEGGISTAEAQPMCDAVAQARERGTLIFAAAQNSGTGQPYF
PAACRPAVAVGSVTLTA KAGTFYHATYSNHYAQVQLSAPGGSSVLAPTYYAGGTFGGEYF
PAGCPAVAVGSVTLTA KAGTFYHATYSNHYAQVQLSAPGGSSVLAPTYYAGGTFGGEYF
PDDDIVSTGWDYQKDEPNYVAMAGTSQATPQVAAVAALLLSKGVTQGPDDTLARLTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="serine protease, subtilase family"
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TGDIALTVTAHRRPNAFPAADOPQLRGVIEVSSTRPDGTVQSTARWTVTADQYRLSGR
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/note="similar to SP:P23929 GB:X57433 PID:42181
PID:1742412 percent identity: 63.04; identified
sequence similarity; putative"
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LPVYTFGHSLGGLITÄASAARDPRGLSGVILSSPALLIGEGQPQLTKALAPLLARVAP
RLPVSELGTDALSRRSDEVRAYQDDENIYHGKVTAQTAWTMLRLSGELWPDYVRWQLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                putative"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MPILYIHGIAVREEGEHGWSAVRPFVQRVAWSDVEAKLREYVAPVLRPEREDVLLEQVVWGDLCWQPVPPDEGWAPPADADLDDALAERLEGQVRREIPVVLRPEREDBOAMPADADLDDALAERLEGQVRREIPVQAWFELIEAVWAATAHODLTRAHWEIEDEGWAPADADLDDALAERLEGGVRREIPVLAWFULGOOFFROIFRSDLMHRVTELRSPLEGFLPYFMGDLLRVLAGRGTPEQPGPIPQRVLAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to 57.89; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(9171. .1:0019)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(9171.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="conserved h
/protein_id="AAF11098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(5791. .6894)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(5791. .6894)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mttspvfpiltprlklrlyesrdldallgyyrQpavtrylleep
wtradaeeqgqkreqrrgldtpagalalvwdyggrvigdaalwlsdetrqvaeigwvm
dpayagqglateavaplltlafdsyglhrvtaqmdarnvasarlcerlglrqeahlrq
                                                                                                                                                                                                                                                          AAHTAG"
                                                                                                                                                                                                                                                                                       TLVVHGDQDQLADVKGSQRF1ET1PAADKTLRVFEGGYHELLNDEPSDEVRQ11LDWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="lipase, putative"
/protein_id="AAF11100.1"
/db_xref="GI:6459298"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identity: 51.46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGEGDYRVLAGRDLDANGLFGEAHEPRSQAAQATLSPAQPQVELGELTVKP*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STDLGAPGRDDFYGFGMVNAAAALGAPAVSNTLGVLLSDGQGHTYRPALNALGHFTAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to PID:1890101 percent identity: identified by sequence similarity; putative"
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                                                                                                            /gene="DR1538"
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identity: 51.46; identified by sequence similarity;
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Deinococcus radiodurans
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Bacterla; Thermus/Deinococcus group; Deinococcales; Dei
Chases 1 to 10129)
White,O., Eisen,J.A., Heidelberg,J.F., Hickey,E.K., Pet
Dodson,R.J., Haft,D.H., Gwinn,M.L., Welson,W.C., Richar
Moffat,K.S., Qin,H., Jiang,L., Pamphile,W., Crosby,M.,
Vamathevan,J.J., Lam,P., McDonald,L., Utterback,T., Zal
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GNGTITTESGVLSQAQYSFKTRFENGKGTNPEELLASAHAGCFTMQLSALLAEHGHEI
KALDTDATCEMVKDGPGFKINHMHLRVRAQLTGSDQADFEAHVKDAAEKCPLSRIMQG
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/protein_id="AAF11101.1"
/db_xref="G1:6459299"
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    Shen, M.,
    Zalewski, C.,

                                                         Peterson, J.D.,
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//occe legitited by Gilmmet 2; putative //codon_start=1 //codon_start=1 //codon_start=1 //codon_start=1 //product="hypothetical protein" //product="hypothetical protein" //protein id="AAR12062.1" //protein id="AAR12062.1" //protein id="AAR12062.1" //db_xref="GI:6460344" //translation="MALQGROHRCQPTPGRAATARRLRRPGRAPGRAPGRAAGF //translation="MALQGROHRCQPTPGLARQDLESLDDSPTDRLAYQARAAGF //translation=1 //daggroundeductor=1 //daggro	338" 338" 338" 338" 338" 338" 338" 338"	/transl_table=11 /transl_table=11 /transl_table=11 /product="hypothetical protein" /product="lapvothetical protein" /product="lapvothetical protein" /protein_id="AAFI2061.1" /db_xref="01:6460343" /db_xref="01:6460343" /translation="MSPTWNNRPHTLGSRAALACLRLSGWTPLLAPVPGPRLVAPAAP /translation="MSPTWNNRPHTLGSRAALACLRLSGWTPLAPAPGPRLVAPAAP /translation="MSPTWNNRPHTLGSRAALACLRLSGWTPLAPAPAPGPRAPAVGGIPIDRRRRGGNFVDA VVEIIREREEIVLLVAPEGTRAGGDYWKTGFYYMALEAGWYANALDWGRKQVGIVG YVTPTGDIDADFAEIRRLLEGVRGKHPRFETPAFPRADPA" complement(8201971) /gene="DR2515" /complement(8201971) /gene="DR2515" /foote="similar to Sp:P55680 PID:2182691 percent identity: 46.60; identified by sequence similarity; putative" /codon_start=1 /transl_table=11		aly,M.J., Fi resistant ba 7 (1999) 7 (1999) 7 (1999) 8 berg,J.F., Fin,M.L., Nelson,M.L., Wally,M.J., Walson,Fraser,C.M.
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/ Ldibscable=1. /product="hypothetical protein" /protein_id="AAF12064.1" /db_xref="G1:6460346" /translation="MSTWAWSALPLGLEGLLNIFLAFVAPTQAWGTTGASAVFMAAAL /translation="MSTWAWSALPLGLEGVAPVWMGVL" complement(73778951) /gene="DR2521" complement(73778951) /gene="DR2521" complement(73778951) /gene="BR2521" /note="similar to PID:1652359 percent identity: 57.45; identified by sequence similarity; putative" /codon_start=1 /transl_table=11 /product="conserved hypothetical protein"	/product="transcriptional regulator, MerR family" /protein_id="AAF12058.1" /protein_id="AAF12058.1" /db_xref="G1:6460340" /translation="MAPLPSISIREVAERSGCPASALRYYEDAGLIAALPRLETAARC /translation="MAPLPSISIREVAERSGCPASALRYYEDAGLIAALPRLETAARC YDPRVLDTLSVITALRGVGFGIREIRALLDIRQPGDPAPLRLKKAEQALDRLTEVLAE RRRTLEEAEKLLRRWEAEVAEAQOS" complement(71127339) /gene="DR2520" /gene="DR2520" /note="dentified by Glimmer2; putative" /codon_start=1 /franslation="1"	PLEDAPOPLARE INTO V PY DIDUGUE PLANK FF F THE LUTGER I TRUG PLEDAPOPLARE ITAAAER SKALHHYDS V PY DIDUGUE PLANK FF F THE LUTGER I TRUG LSEQTRILITRSCYTLGTPAYMAEBQAKGGVDARSDLY ALGAVLY RVAGGSPEYGDS DQSVLYQHYYEPVPDPDLNPAVPDAVBAVLLKULLAKRADRRPQSGAALAHLWALARR DLWTTHARGQY KGGRARTGEHPDOPARVSDWQELLWSVALDGEVYMPPAAVVGEGDLYAY GTRGGQLVLITHTGGRPRATYAARDEVTAPATLIGGHVLYGAWDGTLRRVELQSGSEVW RHQARAEFTGAPTVWGGRLLAPSRDGHLHALSLRTGELAMAYRAGGSLAASPLVWAGA ALQCDETGWLHALDARSGTPLWKYEVGTWHATPALLDGPPGTATLVIATWRGEVHAIG GWGKVRGLRLADGEDLWERTLDGRVTASPALTALDGPPGTARLVIATWRGEVHAIG LEVQNGRAALAGEDA IRTTYDVEDEVWASPALTALDGPPGTARLTYDASAGREVHVVA GWGKVRGLRLADGEDLWERTLDGRVTASPVISAGLVFLATEGGELLALDVRNGEVRW TCRESGYQATPLAASGTLYVAFWDGTLKAYRNAHPEWRSEQEG" complement (6664 . 7047) /gene="DR2519" . /gene="DR2519" . /gene="DR2519" . /dentified by sequence similarity; putative" /codon_start=1	46.36631 /gene="DR2518" 46.56631 /gene="IR2518" /gene="IR2518" /gene="similar to PID:2344821 percent identity: 56.09; /note="similar to PID:2344821 percent identity: 56.09; /dentified by sequence similarity; putative" /codon_start=1 /codon_start=1 /product="serine/threonine protein kinase, putative" /protein_id="AAF12057.1" /db_xref="GI:6460339" /translation="MPLIPGTLLAGRYELLALLGEGGSAQVYRAQDGLLGREVALKYM /protein_serine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threonine-threoni	REAN BRACE TO DE 1

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/translation="MTQPNSWTIPHLPVAGYAWEVADPAGAVLLTHALAEYAQRYQDR
/transachinaegysvrsydlreheperswydaefyqyddhlaeraelaereceplpl
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IVPINKAGLSKLPEEYAAYQADERIYGGQVTLLTASTWAQLSQQLWPTYSNWALPTLV
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/gene="DR2522"
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/protein_id="AAF12060.1"
/db_xref="GI:6460342"
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identity: 50.80; identified by sequence similarity;
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/db_xref="GI:6460341"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGTAATAACCCCGCCTGAAGGCTCACGCAGACTCTTCGAGGAGCTGGCCGTCGAGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colè, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E., Tekaia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A., Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Squares, S., Squares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
                                                                           implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                           been renumbered from the original cosmid submissions but the ogene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes
                                                                                                                                                                                                                                                                                                                                                                     available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk On Jun 26, 1998 this sequence version replaced gi:2213497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA Unite de Genetique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete genome sequence
Nature 393 (6685), 537-544 (1998)
98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis. Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis H37Rv complete z97050 AL123456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkhill, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Erratum:[[published erratum appears
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barrell,B.G.
Deciphering the biology of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTCI28
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Details of M.
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                                                      initiation codon.
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                     Location/Qualifiers
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.36300
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/product="adhE"
/product="adhE"
/product="adhE"
/protein_id="cab09757.1"
/protein_id="cab09757.1"
/db_xref="GI:2213499"
/db_xref="GI:2213499"
/db_xref="SPTREMBI:007407"
/db_xref="SPTREMBI:00740
/note-"Rv0163, (MTCI28.03), len: 151. Unknown, but similarto AFAGBD 4 Alcaligenes eutrophus/sp[044017] 4-HTDROXYBUTYRATE DEHYDROGENASE (GBD) (145 aa); opt: 155 z-score:214.4 E(): 0.0002; 26.6% identity in 139 aa overlap. Also similar to other dehydrogenases. eg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dehydrogenase alpha chain (374 aa), opt: 619 z-score: 741.5 E(): 0, 34.7% identity in 363 as overlapContains PS00059 Zinc-containing alcohol dehydrogenases signature. Also similar to other tuberculosis alcohol dehydrogenases eg. MTCY369.06c (34.0% identity in 365 as overlap), MTCY322_9, (35.0% identity in 371 as overlap),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATHVVVNRASVVPVPHEVPPTVAALLGCAVLTGGGAVLNVGDPQPGQSVAVVGLGGVG
MAAVLTALTYTDVRVVAVDQLPEKLSAAKALGAHEIYTPQQATAGGVKAAVVVEAVGH
PAALHTAIGLTAPGGRTITVGLPPPDVRISLSPLDFVTEGRSLIGSYLGSAVPSHDIP
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/gene="adhE"
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AEEVARVLRVCRDAGAXVTVQGGRT5LVAGTVPEHDDVLLSTERLCVVSDVDFVERRI
EIGAGVTLAAVQHAASTAGLVEGVDLSARDTATVGGMASTVAGGLRTVRYGNMGEDVV
GLDVALPDGTVLRRHSRVRRDNTGYDLPALFVGAEGTLGVITALDLRLHPTPSHRVTA
VCGFAELAALVDAGRMFRDVEGIAALELIDGRAAALTREHLGVRPPVEADMLLLVELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Rv0161, (MTCI28.01-MTV032.04), len 449; possible oxidoreductase, similar to AIP2_YEAST P46681 actin interacting protein 2 (530 aa), fasta score; opt: 356 z-score: 775.7E(): 0, 33.3% identity in 357 aa overlap at to DLD1_YEASTP32891 d-lactate dehydrogenase (cytochrome) (587 aa), fastascores opt: 311 z-score: 490.9 E():
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REVSLWQSGRLPVESLVTSTIRLDDINEAMDHLADGIAVRQLISFTGDL'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dehydrogenase,
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/gene="adhE"
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PLSAISGFARDAVALVHRHVPDSPEALPLLFGHIGEGNLHLNVLRCPPDREPALYAKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    physical
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dehydrogenase, similar to eg.ADH_MACMU P28469 alcohol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:1773"
/clone="128"
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/protein_id="CAB09760.1"
/db_xref="GI:3256009"
                                                                                                                                                                                                                                                                                                2615. .3070
/gene="Rv0163"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="PS00059 Zinc-containing alcohol dehydrogenases"
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                                                                                                                                                                                                                                                                                                                                                                                                               'gene="Rv0163"
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                                                                                                                                                                                                                                                                         /note="Rv0166, (MTCI28.06), fadD5, probable fatty-acid CoAligase len: 554; similar to several eg. LCFA_ECOLI P29212 long-chain-fatty-acid-coa ligase (561 aa), fasta scores; opt: 612 z-score: 764.6 E(): 0, 29.4% identity in 534 aa overlap. Contains PS00455 Putative AMP-binding domain signature. Also similar to many other M. tuberculosis CoA ligases eg. MTCY07A7.11c (35.3% identity in 487 aa overlap), MTV013_10, MTY25D10_30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Rv0165c, (MTCI28.05c), possible transcriptional regulator, len: 264 aa; some similarity to several eg. NTRA_CHELE P54988 nta operon transcriptional regulator (231 aa), fasta scores; opt: 154 z-score: 197.2 E(): 0.00058, 32.0% identity in 125 aa overlap. Also simila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNTR_BACLI GLUCONATE OPERON TRANSCRIPT, GNTR_BACSU GLUCONATE OPERON etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..... RVUL64, (MTCI28.04), to gp|Z95398|MLCL622_27 Myco (156 aa) opt: 7-7
VFGYEDLLNEAGDVHEPVDIPNDSPALIMYTSGTTGRPKGAVLTHANLTGQAMTALYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4491. .6155
/gene="fadD5"
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COMplement(4444. .4446)
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LDRINNALAGAIGSGDAKTIASIEFAFHRVFNKASRRIKLAWFLLNAARYMGAGVRGR
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PLSAKPRSQLPLRRAQLSDEVAGHLRAAIMSGALRSGTFIRLDETAAELGVSVTPVRE
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/protein_id="CAB09759.1"
/db_xref="GI:2213502"
/db_xref="SPTREMBL:007410"
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TAINAWINTSTGVDPLAMPVLGIVAESGCRYESELREPESLMVGLAVTRLGRSSVTYR
LGVEKEPDDAGVITALGHWYHYYDRTSRRPVPIPEAIRSLLSTACVSG"
                       LRFVGNTMTWADLRRRVAALAGALSGRGVGFGDRVMILMLNRTEFVESVLAANMIGAI
AVPLNFRLTPTEIAVLVEDCVAHVMLTEAALAPVAIGVRNIQPLLSVIVVAGGSSQDS
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/protein_id="CAB09758.1"
/db_xref="GI:2213500"
                                                                               'db_xref="SPTREMBL:007411"
'translation="MTAQLASHLTRALTLAQQQPYLARRQNWVNQLERHAMMQPDAPA
                                                                                                                                       /protein_id="CAB09749.1"
/db_xref="GI:2213503"
                                                                                                                                                                                            /product="fadD5"
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/transl_table=11
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Query Match
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         Submitted (08-NOV-2000) The Institute for Medical Center Dr. Rockville, MD 20850,
                                                                               Submitted (03-NOV-2000) The In Medical Center Dr. Rockville, 4 (bases 1 to 90459)
Town,C.D. and Kaul,S.
                                                                                                                                                                                                 Medical Center Dr, Rockville, 3 (bases 1 to 90459)
Town, C.D. and Kaul, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                Submitted (27-OCT-1999) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org
                                                                                                                                                                                                                                                                                                  Lin, X. and Kaul, S. Direct Submission
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            cdtown@tigr.org
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                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RN/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tb/tgi.shtml). Annotated genes are named indicate the level of evidence for their annotation. Genes with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes were identified אין מיניייייייין (Chris Burge, prediction programs including Genescan+ (Chris Burge, prediction programs including Genescan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GenemarkHMM (Mark Borodovsky, http://CCR-081.mit.edu/GeneMark/), GlimmerA (a variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Nov 8, 2000 this sequence version replaced gi:11079536 Address all correspondence to:at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GeneSplicer (Mihaela Pertea and Steven Salzberg, contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of GlimmerM, see Mihaela Pertea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genes were identified by a combination of several methods: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The orientation
                                                                                                                                                                                                                                                                                                                                          /gene="T9L24.28"
2516. .2854
                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein, 3' partial"
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/protein_id="AAG30966.1"
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GAYESSDFDEFGESEPKSEEELDPGSWRRIFETNESTVHASASPQYYSCLHKILSAAS
EQNTTLMEEAVSEIDSSASSGDPHAQSVMGFVYGIGMMRETSRSKSILHHHFAAAGGN
MQSKMALAFRYLRQNMYDKAVELYAELAETAVNSFTLISKDSPMAEPVRLHIGTEENKD
ALRKSRGEEDEDFQILEVQAEKGNSVAMHKIGLFYYFGLERCHRADHAKALYWFSKAEF
NGLGYLYVKGYGVGVKRNYTKAREYFEMAANNEDPSGHYNLGVLYLKGTGVKKDVRHAT
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HSLNPPPPPPSCCGPMKEIVEKDAPCLCIAFNNPEVLKALNLTKENALLLPKACGVNPD
                                                                                                                                                                                                                                                                       /note="contains
GI:2627141 from
                                                         VSLCSKIASE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1. .1980)
/gene="T9L24.27"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(<1. .73,432. .647,958. .1023,1079. .1375,
comprement(3212. .3233)
/rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                              <2516. .>2854
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                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                          /gene="T9L24.28"
                                                                                                                                                                                                                                                     2516. .2854
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/gene="T9L24.28"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Arabidopsis thaliana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="T9L24.27"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="T9L24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis
/cultivar="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /chromosome="I"
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the sequence is from SP6
                                                                                                                                                                                                                                                                         similarity to lipid (Picea abies)"
                                                                                                                                                     al protein<sup>†</sup>
}.1<sup>*</sup>
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complement(5484. .515)
/rpt_family="(G)n"
complement(11574. .1160.
/rpt_family="ar_rich"
l2616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="contains similarity to lipid transfer protein GI:2627141 from (Picea ables)" join(4436. 4769,4878. 4948) /gene="T9L24.29"
                                                                                           /translation="MAIEKQEINESSIGFNLISEKRRHNKTHDDKPYLVDSLTLNSWASQPSTDEIIIIDDEEKEVTLEPKRKKPRLGSWWDNVEAVDELCCVVKGSPPKAKEDN GVASKADSYFSSTDLLETMENKKINEDKRSLPEKDKDESTVGESNTKNKGMNT"
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9854. .10321
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LIHMMVMDXVANRPXGFAFLRYETEEEAMKAIQGMHGKFLDGRVIFVEEAKTRSDMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to RNA binding glycine rich protein (RGP la) GI:436789 from (Nicotiana sylvestrie)"
join(7586. 7832, 8692. .8760, 8845. .8951, 9049. .9171)
/genc="T9L24.48"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTABS 1 at 10n="MNMNIPSKKIVPVPTPSEKVVSLVSRTGRDLQRYNTAGYRQVVGCVPYXYKKHGGGEIEVLLISAQKKGKOMLLPKGGWEIDESIEEAALTRETIEEAGVTGQLESSLGKWQYKSKHTIMIHDGHMFPLLVSQQFEIWPESEFRQRKWVSLSEAIELCQNSWMREALEAFINRKGQTQ"
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/rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                        RAKPRRDFPKPQSKPRTFRTW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="RNA-binding glycine-rich protein, putative"
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/db_xref="GI:11120799"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7586. .9171
/gene="T9L24.48"
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/gene="T9L24.48"
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/protein_id="AAG30977.1"
/db_xref="GI:11120797"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(6464.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mnITRILGVVTTVVILYSVQVTAQFFGDVQQAMRCVAKLMPCQP
YIHLSIPPPPLCCNPMKQIAEKDVSCLCTAFKHPDLLRFLALTKENAIKILDSCGINH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="AT_rich"
join(<4436. .4769,4878.
/gene="T9L24.29"
                                                                                                                                                                                                                                                                                              note-"predicted by
                                                                                                                                                                                                                                                                                                                       /gene="T9L24.31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(6464. .6594,6690. .7092)
/gene="T9L24.30"
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/gene="T9L24.30"
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/gene="T9L24.30"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAGCGCCTCAAAGAAGCTCTACGAGGAAGCTGCCTCGTCAGACAAATCACTCAAGCTCTA 20574
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                                                                                                                               Seeger, K.J.
Unpublished
3 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Streptomyces.
Direct Submission
Submitted (08-MAR-1999) Streptomyces coelicolor sequencing project,
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
                                                                                                                                                                                                                                               Kinashi,H. and Hopwood,D.A.
A set of ordered cosmids and a detailed genetic and physical map
for the 8 mb Streptomyces coelicolor A3(2) chromosome
mol. microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acetyl-coenzyme A synthetase; acsA; anti-sigma factor; ATP-binding protein; bldG, anti-sigma factor antagonist; DNA polymerase; DNA topolsomerase I; helicase; hydrolase; integral membrane protein; lipoprotein; oxidoreductase; proteinase; pyrophosphate synthase; secretory protein; septum site determining protein; serine protease; slpD; sodlum/proton antiporter; transferase; transposase;
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                                                                                                Bentley, S.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 40544)
Redenbach, M., Kieser, H.M., Denapaite, D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(13997...14021)
/rpt_family="AT_rich"
complement(14718...14753)
/rpt_family="(TAAA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="MAP kinase, putative"
/protein_id="AAG30984 1"
/db_xref="GI:11120804"
/ta_nslation="MALVRERROLNLRLPLPPISDRRFSTSSSSATTTTVAGCNGISA
/CLAUSIALION="MALVRERROLNLRLPLPPISDRRFSTSSSSATTTTVAGCNGISA
CDLEKLNVLGCGNGGIVYKVRHKTTSEIYALKTVNGDMDPIFTRQLMREMEILRRTDS
PYVVKCHGIFEKPVVCEVSILMEYMDGGTLESLRGGVTEOKLAGFAKOLLKGLSYLHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(14983. .15005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEFRSFVECCLRKDSSKRWTAPQLLAHPFLREDL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGGSSDIYAGDIWSFGLMMLELLVGHFPLLPPGQRPDWATLMCAVCFGEPPRAPEGCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"similar to MAP kinase kinase 5 GI:3219273 from
(Arabidopsis thaliana)"
                                                                                                                          1 to 40544)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKIVHRDIKPANLLLNSKNEVKIADFGVSKILVRSLDSCNSYVGTCAYMSPERFDSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="T9L24.32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="T9L24.32"
12616. .13881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="T9L24.32"
                                                                                                                                                                          and Harris, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40544 bp
coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50.6; DB 12; Pred. No. 0.21; ); Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cosmid H5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BCT
                                                                                                                                                                                                                                                                                                                                                  Eichner, A., Cullum, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 90459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            °.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transposase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20634
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FEATURES
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                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                    trna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid H5 lies between E2 and H17 on the Asel-H genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 available on the World Wide Web.
(URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Notes:
Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Details of S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by the BBSRC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT: This sequence MAY NOT be the entire insert of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="SCH5.01, partial CDS, possible transposase, >228aa; similar to many eg. TR:O54404 (EMBL:Z11519) probable transposase from Tn4811 of Streptomyces li 66 (320 aa) fasta scores; opt: 535, z-score: 648.0, 8.7e-29, (41.0% identity in 227 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="IlylnrTGIPWKYLPHDFPGHGTVYFYYAAWRDEGIFTQLNYDL
TALARVKEGRKPEPTASVIDTQSVKTSTNVPLTSQGTDAAKKIVGRKRGILTDTIGLI
LAVTVTGAGLSENAVGIRLLDQAKRTYPTIVKSWVDTGFKNAVIEHGATLGIDVEVVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SCH5.01"
<1..691
                                                                                                                                                                           complement(1103.
/gene="SCH5.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DETTPTWRGTY"
/gene="SCH5.02c"
/note="SCH5.02c, slpD, proteinase, len: 539aa; identical
to the previously sequenced TR:Q54398 (EMBL:L42758) slpD,
                                                                                                        complement(1103. .2722)
                                                                                                                                                                                                                                                                                complement(918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNPEKRGFHVVKRRWVVERSIGWIMMHRRLARDYETLTTSSEAMIHIASIDNLAKRIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative transposase"
/protein_id="CAB38475.1"
/db_xref="GI:4539556"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
/db_xref="taxon:100226"
                                                                                                                                                                                                                                             /note="tRNA Thr anticodon CGT,
                                                                                                                                                                                                                                                                                                                                                                                  /gene="SCH5.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=2
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SCH5.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="cosmid H5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                           /note="slpD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=SCH5.01
                                                                                                                                                                                                                                                                                                                                               'note="Nominal overlap with Streptomyces coelicolor cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coelicolor sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                    . 994)
                                                                                                                                                                                                              .2722)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         648.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lividans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
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complement(4193. .7462)

'db_xref="GI:4539559"

translation="MSVPPRTMEGAPRISAAARCHGSVSRLGVTALCEGSV"/

/product="small hypothetical protein" /protein_id="CAB38478.1"

complement(4193.

.7462)

complement(4060.

.4173)

/codon_start=1 /transl_table=11 /gene="SCH5.04c"

note="SCH5.04c, unknown,

len: 37aa"

'label=SCH5.04c

```
fasta scores; opt: 661, z-score: 598.9, E(): 1.7e-28, (32.6% identity in 562 aa overlap). Contains probable N-terminal signal sequence. Also contains Pfam match to entry PF00561 abhydrolase, alpha/beta hydrolase fold, score 56.80, E-value 4.7e-13."
                                                                                                                                                        /product="putative DNA polymerase"
/protein_id="CAB38477.1"
/protein_id="CAB38477.1"
/db_xref="GI:4539558"
/db_xref="GI:4539558"
/translation="MTWDDLVGQEKVCEPLAAAARDADAFVTAAATAGPLPQSTSMTHAWLETGPPGSGVARTARAFAAALQCVSPDRALGGVPGCGFCDGCHTALVGTHADVSTVAMGAEIRAQDMRDTYWRKSFTSPANGRWQIILVEEAERLNERGSANAVLKAVEEPAAPAFVAMALCAPSTEDVLPTIRSGCRHLNLRTPSVEAVADMLVREGIEPDVAAAARAFATQGHIDRAARDARATQGHIDRAARDARATQGHIDRAARDARATQGHIDRAARDARATGGHIDRAARDARATGGHIDRAARDARATGGHIDRAARDARATGGHIDRAARDARAAVLKIPLEVEDVGGALRAAQGLVDAAAEDAKQLAEEMDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          limited region of similarity to many DNA polymerase III subunits eg. SW:DP3X_SALTY DNA polymerase III subunits gamma and tau from Salmonella typhimurium (642 aa) fasta scores; opt: 327, z-score: 338.5, E(): 1.5e-11, (32.1% identity in 246 aa overlap). Contains probable coiled-coil from 245 to 285 (41 residues), max score: 1.601, (probability 0.99)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hydrolase fold, score 5 complement(2835. .4040)/gene="SCH5.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="proteinase"
/protein_id="CAB38476.1"
/protein_id="CAB38476.1"
/db_xref="GI:4539557"
/tabslation="MDTERTHRETETGGTREFRATILITAALLATACSAGGASTSAGSPA
AKAAGATEAATATLTPLPKATPAELSPYYEQKLGWRDCGVPGFQCATMKAPLDYAKPA
BGDVELAVARKKATGPGKRLGSILVNPGGPGGSAIGYLQQYAGIGYPAKVRAQYDMVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mycelium-associated (lipoprotein) proteinase from Streptomyces lividans 66 (539 aa) fasta scores; opt: 3608, z-score: 3750.3, E(): 0, (100.0% identity in 539 aa overlap). Also similar to two other peptidases from Streptomyces coelicolor SC9C7.15c (EMBL:AL035161) fasta scores; opt: 666, z-score: 603.6, E(): 9.4e-29, (35.7% identity in 502 aa overlap) and SC185.03c (EMBL:AL03517)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(2835. .4040)
/gene="SCH5.03c"
/note="SCH5.03c, possib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(1145. .2257)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLPAGDADGRKLTESLATTGVIAAMYDEGAWQQLRESLTSAIKEKDGAGLLILSDSYY
EREADGGYSNLMFANAAVNCLDLPAAFSSPDEVRDALPDFEKASPVFGEGLAWSSLNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDPRGVARSEPVECLDGREMDAYTRTDVTPDDAGETDELVDAYKEFAEGCGADAPKLL
RHVSTVEAARDMDVLRAVLGDEKLTYVGASYGTFLGATYAGLFPDRTGRLVLDGAMDP
SLPARRLNLEQTEGFETAFQSFAKDCVKQPDCPLGDKDTTPDQVGKNLKSFFDDLDAK
                                                  complement(4060.
                                                                                                                      VLALQLGSRVATANADAEDALERLARGSTPESTLRRIEAVAACGEALDRNVPPLLAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAYGRGSSCIDSAINTYLLTGTAPEDGKRCS*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AYWPVKPTGEPHRIEAAGATPIVVVGTTRDPATPYRWAEALSDQLTSGHLLTYEGDGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
/label=SCH5.03c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Pfam match to entry PF00561 abhydrolase, alpha/beta
nydrolase fold, score 56.80, E-value 4.7e-13."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SCH5.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label=slpD
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gene="SCH5.04c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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                                          .4173)
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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
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                        JOURNAL
MEDLINE
                                                                                                                                                                                                                                                             ORGANISM
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Best Local
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTCAACTATGCCGGCTTTGGAGTTTACACCTTCGACTGGCCCGGCCACGGGAAGAGCCC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCCAGGCGCTCGGCCCATGCTCGGGGACGTCCGCCAGA 38524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCCAAGAGCCCGGAAACGCCGGGCTTCATGGTGGCCCTCGCGA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACGGCCGCCGATGCGGCCCAAGCTCGTACGACGGCTCGCGGTGTCCTCGATGCCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCCCTCGGCGAGCCGGGCGCGCGCTGGTCACGACCTCGGCGGCTACCTGGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGCACCCCGCGCGTTACGACCCCGCGGGCCTCGCCCTCGACATCACCGGCGTGATCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGCA---AGAGAGGGCACCACGAGCGTCGAGGGAGGCGATGGAAATCATCGACTCGATAAT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTCGCCGACGCCGGTTTCCGCGCGGTCGCCATGGACCTGCGCGGCGTCGGCGGCAGCGA 38300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTGCTGCTGCACGGCTTCCCGCAGTTCTGGTGGACCTGGCGGCACCAGCTGGTGGC 38240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTCGTTCTGGTTCATGGCCTCGGCGAGCACAGCGGAAGGTATGGAAGACTGATTAAGGA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGTACGCTGAGACGCGGCCCGATAAAATACGGGGGATTAATAGCTTCCTCGCCTGCCCT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAGGAGATCAGGGAGAAGCCCTTCCTCCTCCGCCACAGCCTCGGTGGTCTAACTGTCAT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166;
                                                                                                                                                                                                                                                                                                                                                                                  AF128272 2689 bp DNA BCT 14-MAR Streptomyces spectabilis TDP-glucose synthase (spcD) and TDP-glucose-4,6-dehydratase (spcE) genes, complete cds.
                                                                                                                                                                                                                               Streptomyces spectabilis.
Streptomyces spectabilis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                   FEMS
                                                                                    1 (bases 1 to 2689)
Hyun,C., Kim,S.S., Sohng,J.K., Hahn,J., Kim,J. and Suh,J.
Hyun,Cl., Kim,S.S., Sohng,J.K., Hahn,J., Kim,J. and Suh,J.
An efficient approach for cloning the dNDP-glucose synthase gene
An actinomycetes and its application in Streptomyces spectabili
                                                                                                                                                                                                                                                                                                                                            AF128272.1
10650224
                                                                                                                                                                                                    Actinomycetales; Streptomycineae; Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                 spectinomycin producer
MS Microbiol. Lett. 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to several thymidylate kinases eg. SW:KTHY_ECOLI thymidylate kinase, tmk, from Escherichia coli (213 aa) fasta scores; opt: 423, z-score: 339.7, E(): 1.3e-11, (38.4% identity in 198 aa overlap). 710-800aa (approx.) glutamic acid-rich region which may form a hinge structure. 800-1089aa has no distinguishing features or significant database similarities. Further clues to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         function may be indicated by the presence of matches to PS00217 Sugar transport proteins signature 2 and PS00017 ATP/GTP-binding site motif A (P-loop). Contains Probable coiled-coil from 711 to 875 (165 residues), max score: 2.135, (probability 1.00).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /notee SCH5.05c, probable integral membrane protein with kinase activity, len: 1089aa; a multidomain protein. The N-terminal 480aa (approx.) contains several probable membrane spanning hydrophobic regions, 510-710aa similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="integral membrane
/protein_id="CAB38479.1"
/db_xref="GI:4539560"
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Pred. No. 0.87;
0; Mismatches 17
                                              183 (1),
                                                 183-189 (2000)
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KEYWORDS SOURCE

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                       CGGCATAAAGCCGGAACTCCTCTCGAGGAACAGGGACGCCGTGAGGAGGTACGTTGAAGA 485
                                                                                                                                                                                                                                                                                                                                                                           TAAAATACGGGGATTAATAGCTTCCTCGCCTGCCCTCGCCAAGAGCCCCGGAAACGCCGGG
GCAGGCCTCGGAGTACGTGCGCGTCATCGAGGAGCGCCAGGGCCTGAAGATCGGCTGTGT
                                      GCTGGCCCACAGGGAGGCGGACAAGATAAAAGTCCCGATCCTCCTTCTGATCGGCACTGG
                                                                                                                                                                  GCGCGGCGAGCTGGAGATCACCGGGGTCAACGAGGAGTACCTGCGGCGCGGCGCCTGTC
                                                                                                                                                                                                                                                GGGTCTGTACTTCTACGACGAGCACGTCGTCGACATCGCCGGGGGCTCCGCCCGAGCGA
                                                                                                                                                                                                                                                                                         CTTCATGGTGGCCCTCGCGAAGTTCCTTGGAAAGATCGCCCCGGGAGTTGTTCTCTCCAA
                                                                                                                                                                                                                                                                                                                                    CGGCACGGCCCTGTCCATCGAGGAGAAGCCCCAAGCCCCAAGTCCCCGGTACGCCGCCGT
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                                                                                CGTGACGGTGCTCGACCGGGGCACCGCCTGGCTCGACACCGGCACGTTCACGGCGATGGT
                                                                                                                         CCCACTCGRCCACGACAGGATTTCGGCCAAGCTGGGAAGGAGCATCTTCGTGAACATGGA
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Hyun, C.G. and Suh, J.W.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (13-FEB-1999) Biological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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VSDHCRGVELALRHGRAGEVYHIGGGTELTNEQLTGHLLAATGRGWEQVERVPDRKGH
DARYSLDCTKAATELGYAPLVGFERGLADTVAWYAGNRSWWEPLQRRAALRASA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="TDP-glucose-4,6-dehydratase"
/protein_id="AAD31797.1"
/db_xref="G1:4884769"
/tanslation="MRITUTGGAGFIGSEFVRSMLLAPGAANDIRITVLDKLTYAGVR
ENLDPVAGHPRHAFVHGDICDGDFLDQVVPGHDAVVHFAAETHVDRSITGSAPFVTTN
VLGTQLLLDAARRHGYGRFLHYSTDEYYGSIFYGSWSBESPLAPNSPYAATKAGSELL
VLGTQLLLDAARRHGYGRFLHYSTDEYYGSIFYGSWSBESPLAPNSPYAATKAGSELL
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1350. .
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ALILGDNIFHGRSFGVHVREHTAÞDGGRIFAYPVADPTAYGVVEIGEDGTALSIEEKÞ
AKÞKSRYAAVGLYFYDEHVVDIAAGLRÞSERGELEITGVNEEYLRRGALSVTVLDRGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="TDP-glucose synthase"
/protein_id="AAD31796.1"
/db_xref="GI:4884768"
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/db_xref="ATCC:27741"
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/strain="ATCC27741"
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (16-MAY-2000) Department of Medicine and Genetics,
Submitted (16-MAY-2000) Department of Medicine and Genetics,
Submitted (16-MAY-2000) Department of Medicine and Genetics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 12131)
Stover.C.K., Pham,X.-Q.T., Erwin,A.L., Mizoguchi,S.D., Warrener,P.,
Hickey,M.J., Brinkman,F.S.L., Hufnagle,W.O., Kowalik,D.J.,
Lagrou,M., Garber,R.L., Goltry,L., Tolentino,E.,
Westbrook-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N.,
Folger,K.R., Kas,A., Larbig,K., Lim,R.M., Smith,K.A., Spencer,D.H.,
Wong,G.K.-S., Wu,Z., Paulsen,I.T., Reizer,J., Saier,M.H.,
Hancock,R.E.W., Lory,S. and Olson,M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stover,C.K., Pham,X.Q., Erwin,A.L., Mizoguchi,S.D., Warrener,P.,
Hickey,M.J., Brinkman,F.S., Hufnagle,W.O., Kowalik,D.J., Lagrou,M.,
Garber,R.L., Goltry,L., Tolentino,E., Westbrock-Wadman,S., Yuan,Y.,
Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lim,R.,
Smith,K., Spencer,D., Wong,G.K., Wu,Z. and Paulsen,I.T.
Complete genome sequence of Pseudomonas aeruginosa PA01, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Washington Genome Cer
Box 352145, Seattle, WA 98195, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa.
Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        opportunistic pathogen
Nature 406 (6799), 959-964 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20437337
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                                                 EAVSQASANQRKGRCGRVEPGICVRLYSEEDFNARPAFTDPEILRTNLAAVILAMLH
RIGDIBAFPFIEPPDGKAIKOGFTLLGELSAVWREGOLFPLGRCHARLPIDPRLGRML
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                                                                                                                                                                                                                                                                                                                                                                                        QGILAALDEIAAHEREVGKRPGDVLVFLPGEREIRDAAEMLRKANLRHTEVLPLYARL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="PAO1"
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9359. .9829
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PLGKSALIDELSFGSENKAFKENRTAFDWLSRDPQEVDRYVADPLCGFRCSNQLWVDL
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VNTNPLYTARELEHQPNDSGAKAVVCLANMAHLVEGVLPKTGVKQVIYTEVGDILPPL
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IVDRKKDMILVSGENVYPNELEDVLATLPGVLQCAAIGIPDEKSGESIKVFVVVKPGA
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TGVAKGAMLTHRNLVANMLQCKALMGANLNEGCEILIAPLPLYIIYAFTFHCMAMMLT
GUNAILLITNPRDLPSMLKDLGQWKFTGFVGLMTLFVALCUNGTFRKLDPSALKLTLSG
GMALQLATAERWKEVTGCAICEGYGMTETAPVVSVNPFQNIQVGTIGIPVPSTLCKVI
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RLPISRRLELTQALLHRAGPEVKRQWPPVAEDRLADCRAGTADALPLAEMLKRLGR"
complement(4554. .6242)
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                              PEARHELFNESNRDAVTQDLIDWLEQALRHRRDHSTKERT"
                                                                       LGGLADITPPTHLRQIDADLPLLIIGGERDPVSQGKRLGDLADALRGAGLRQVTLKTY
                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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                                                                                                                                   Haloferax volcanii ORF1,
AJ238878
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                                                         ABC-transporter; permease Haloferax volcanii. Haloferax volcanii
                                       Archaea; Euryarchaeota;
                                                                                                                   AJ238878.1 GI:4775468
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VVAPDVSGwVTDLEVKDNQVVKVGDVLmRIDQERYQANLEQARAVAETRHQQYLLRQN
EAARRSRLGIGAISAEDKENAQINAAIARSEYQEALAQVKIAELNLKRSELRAARNGQ
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/gene="PA3304"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="conserved hypothetical protein"
/protein_id="AAG06692.1"
/db_xref="GI:9949432"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGVGLGAALGGLVVAALGVAATPWVGLALVLAALACALGASTLDGATQALPFSPPAR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="probable MFS transporter"
/protein_id="AAG06691.1"
/db_xref="GI:9949431"
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/codon_start=1
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DAAVAATTQEKERIAHGMLSGALISAAIATVLPGPGTIYLGQTLRFTRPVKLGDDLKV
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/protein_id="AAG06690.1"
/db_xref="GI:9949430"
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              Haloferax volcanii.
Haloferax volcanii
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Haloferax volcanii plasmid
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Archaea; Euryarchaeota;
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Johann Wolfgang Goethe-Universitaet,
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                                                                                                      mid pHV3 putative sulfate/thiosulfate partial cds, and aldehyde dehydrogenase
Halobacteriales; Halobacteriaceae;
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                                                                                                             942
   Conservative
                                                                                                                                                                                               /translation="mttledidldfvpfgQTgLQTseLQFgTwrfgKeTgQGnveIde
ERAHELLDAYEAAGGRFIDTADIYGGGASERWIGDWLEDRDRERFTIASKIYWQIRDG
DPNSRGTNRKNVRHRIDALLDRLDTDYVDVLYIHRWDDETPTREMMKTLNGLVEDGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="aldehyde dehydrogenase"
/protein_id="AAB71806.1"
/protein_id="AAB71806.1"
/db_xref="GI:2459733"
/t-ans1ation="MYDDIATDADWNALYIDGEWTESESGESIAVEDPSTRETVAHVP
/t-ans1ation="MYDDIATDADWNALYIDGEWTESESGESIAVEDPSTRETVAHVP
RGTEADVDAAYEAAEAQESWAEAPPARRQEVVEQFLQALNEYEDEIIDLLAHEVGGS
RIMGETSIQIASDHASEAATLPRRNRGEHVASNIPGKENIVQKNPKGVVTVISPWNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="expressed during exponential growth; similar to sulfate/thiosulfate transport protein encoded by GenBan Accession Number U67576"
                                                                                                                                                               HYLGASTLRPNAWKVARANEIARAEGWEPFTVAQPRYNLVDREIEGDYLEMTRSYGIA
VCPWSPLGQGFLTGKYTREDGLTGESRAAESSRFEESYLTEENFDVHDELDAVAGEVD
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HFGPIAPVIPFSDVDEAVELANATEYGLSGSVHAGDLATGKEIALRMETGNVHVNDQP
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/translation="VTAKTAFDGVDRQLEAAARSLGEDRVGSVRRVTLPLAKQGILAG
VTLTFARAIGEFGATLMLAYYPRTLPVQIWVSYLSTGLDAAFPVALVLVGIAVGAILL
                                                                                                                                            ATPAQTALAWLMHRDGVTAPIVGARTVEQLTENLEAATIDLTDEQVDRLTGAKPDPYV
                                                                                                                                                                                                                                                    /product="oxidoreductase"
/protein_id="AAB71807.1"
/db_xref="GI:2459734"
                                                                                                                                                                                                                                                                                                                                                                                   alcohol dehydrogenase
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/protein_id="AAB71805.1"
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/strain="DS2"
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                  5.5%;
45.0%;
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1 (bases 1 to 1104)

Ju, B., Xu, Y., He, J., Liao, J., Yan, T., Hew, C.L., Lam, T.J. and
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Singapore 119260, Singap
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               /product="acidic ribosomal phophoprotein PO"
/protein_id="AAD54776.1"
/protein_id="AAD54776.1"
/db_xref="GI:5880681"
/translation="MPREDRATWKSNYFLKIIQLLDDFPKCFIVGADNVGSKQMQTIR
LSLRGKAVVLMGKNTMMRKAIRGHLENNPALERLLPHIRGNVGFVFTKEDLITEVRDLL
LANKVPAAARAGALAPCCTVVPAQANTGLGPKTSFPQALGITKISRGTIEILSDVQL
IANKVPAAARAGALAPCTVVPAQANTGLGPKTSFPQALGITKISRGTIEILSDVQL
IKPGDKYGASEATLLNMLMISPESYGLIQVYDNGSVYSPEVLDITEDALHKRE
LKGVRNIASVCLQIGYPTLASIPHTIINGYKRVLAVTVETDYTFPLAEKVKAYLADPT
AFAVAAPVAAATEQKSAAPAAKEEAPKEDSEESDEDMGFGLFD"
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/db_xref="taxon:7955"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      onstein, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 189370)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Paces, J.
                                                                                                                                                                    complement(453. .2471)
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/db_xref="GI:3128258"
                                                                                                                                                                                                                                                                                                                                                 complement(<1. .456)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paces, V., Maltsev, N., Paces, J., Haselkorn, R. and
                                                                                                                                                                                                                                                            /product="CobD protein"
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                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                   /chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                        /strain="SB1003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 to 189370)
                                                                                                                                                       codon_start=
                                                                                                                                                                                                                                                                                                                                                                                    'db_xref="taxon:1061"
                                                                                                                                                                                                                                                                                                                 transl_table=11
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Pred. No. 22;
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LLDRTDPARGLAQAHLRA I KARAAAETA FDAANAAMDT I TTGAAAAAETVLGR I DGTS
GAVHDRTSGA I GTLLALAGLSA I FGLLA PLLAWLG I VRPLQRVTQA TARLAAGDTGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLDVAGQATVRDSVAAGESRMQDKTVATEPTGPLAPLRADLARLAGLARDLARPGSRD
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TALLGLRRAGVEAVVLVGAYKPVAEFARVAHRIGYRPEMVNISFVGTDALLAELGAEG
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                                                                                                                                                               9544. .10413
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LSSLMGVPTVYVMTHDSIGLGEDGPTHQPVEHLAICRATPNTWTFRPADVIETAEAWE
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                                                                                                                                                                                       TGRIRPSFAQDYQDLALVRREGGHS"
                                                                                                                                                                                                                                   EITAAVNQLDQVTQHNAAMFEENAAATQALLGEAQTCGSVRGLRMQGATGAAVAAGRI
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aı protein"
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DVFPPALAHVALGHLERPQSJLDGGRVBYSGAPFPLSASEIGYDHGVTLLDLAGGAAPR
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complement(12010...12912)
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18245. .21130
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                                                                                                                                                                                                                HIPLPRPVPMLRLPAQGTAPLPEILAALDRLALPDRPRAEGPFLYLALRADRPVTEIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="exonuclease SbcD homolog"
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/protein_id="AAC16116.1"
/db_xref="GI:3128264"
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146016 GGTCATCCGCTCCGCTTCGGACGCCCGGGGCGCTTTACGGCTCGGTCACGCCCCGCGACG 146074
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                                                                                                                                                                                 145896 CGCCAACGACGCCAACATCAAGAGCTTCGAAGCCCGCAAGGCGCAGCTGGAAGCCCGCAA 145955
                                                                                                                                                                                                                                                                        145836 GGTGAAAGTGCGCGGACGGCTACGCCCGCAACTTCCTTGCCGCAAGGCAAGGCGCTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                          351 CCCGGAAACGCCGGGCTTCATGGTGGCCCTCGCGAAGTTCCTTGGAAAGATCGCCCCGGG 410
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                                          TCTGATCGGCACTGGCGATGTAATAACCCCGCCTGAAGGCTCACGCAGACTCTTCGAGG 649
                                                                                         CCTCGAGACCAAGAAGAAGCCGAGGCGGCCGCCGCCAAGCTTGAAGGTCAGAAGTTCGT 146015
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/protein_id="AAC16120.1"
/db_xref="GI:3128268"
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Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 189370;
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Search completed: June 2, 2001, 20:50:58 Job time: 25356 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2000 Compugen Ltd.
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1308.428 Million cell updates/sec
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Result
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AZ207320 SP_0134_A
AL069494 Drosophil
AL109856 Drosophil
AL108856 Drosophil
AL108877 Drosophil
AL10877673 Drosophil
AL098379 Drosophil
AL098379 Drosophil
AL068607 Drosophil
AZ648867 DROSOPhil
AZ648867 MO518D20
BF109918 7171905: X
AL065906 Drosophil
AV559504
AL1098595 Drosophil
AL525973 AL525973
B91654 CIT-HSP-216
BE130527 L48-72173
AL067738 Drosophil
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RESULT
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                                                                                                                                                                                                                                                                                                                                                           AZ207320 655 bp DNA GSS 31-AUG-2000 SP_0134_A1_C01_SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratugenomic clone Plate=134 Col-1 Row-E, DNA sequence.
                                                                                Seq primer: SP6
Class: BAC ends
                                                                                                   Email: acameron@caltech.edu
Plate: 134 row: E column:
                                                                                                                                         Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
                                                                                                                                                                                                                                            Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Swartzell, S., Wallace, J.C., Poustka, A.J., Livingst
                                                                                                                                                                                                                                                                 Strongylocentrotidae; Strongylocentrotus.
1 (bases 1 to 655)
                                                                                                                                                                                                                                                                                            Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
                                                                                                                        Tel: (626) 395-8421 Fax: (626) 793-3047
                                                                                                                                                                         Contact: Cameron, RA, Davidson, EH,
                                                                                                                                                                                    20402566
                                                                                                                                                                                                    additional resources
                                                                                                                                                                                                                                                                                      Echinoidea; Euechinoidea; Echinacea; Echinoida;
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                                                            quality sequence stop: 655.
Location/Qualifiers
                                                                                                                                                                                             Natl. Acad.
                                                                                                                                                                                                               urchin genome project: Sequence scan, virtual map, and
                                                                                                                                                                                                                                    Ettensohn, C.A., Lehrach, H., Britten, R.J,
/clone="Plate=134 Col=1 Row=E"
/clone_lib="Strongylocentrotus purpuratus,
urchin, sperm genomic BAC library"
                               /organism="Strongylocentrotus purpuratus"
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                                                                                                                                                                                                                                    Davidson, E.H. and
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AQ802401 HS_3111_A
AW154885 EST290177
BF258253 HVSWE£001
A2550251 ENTEO39TR
AL067863 Drosophil
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AZ263165 RPCI-23-1
AL206096 Tetraodon
BF363913 QVO-NN102
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AI399010 NCSC5B2
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AZ278955 RPCI-23-1
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

[ bases 1 to 1080)
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DH10B"
                                                           /organism="Drosophila
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR29N07"
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                             /note="end :
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                    2 TGTTTAATATCAATGTCTTTGTTAATATATCTTGGCTGTATTTTCAGGGATAGTTATGA 61
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACRZ6H16 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fly), genomic survey sequence. AL059400
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                                                                                                                                                                                                                    /note-"end
                                                                                                                                                                                                                                         /clone_lib="RPCI-98"
/clone="BACR26H16"
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/db_xref="taxon:7227"
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                                                                                          TGCACGATCAAAGGGGACATGGGGAGAACGGCAAGCGATAGAGAAAGAGGGGTATGTGGAGG
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                                                                                                                                  AKARTTTKAKTKTKATTKAKAKGTATKAATKTKATGKAGGKKKTGKKKKKKGAKGKKAKT
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                                                                                                                                                                                                             , 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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/clone="BACN37F08"
/note="end : SP6"
a 25 c 90 g
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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TTGCTAGGCACGGATTTGGATTCTGCATGCACGATCAAAGGGGACATGGGAGAACGGCAA 268
                                                          WDKWDTKWKDDRWTKRWATRGDGRAGRAKRRDDRRGDRGRRRRRTRKWRWWRRAAWWT
                                                                                                                                     TKRDWRGAATRRARWATAATTATADDTWKRTTGTKTRTWKWKWWARRAAKWRDWWRDTDW
                                                                                                                                                                       AAACAGGCGTAAGAGTGTTTTATCGGTGTGTAATCCCGGAGAAAGCTTTTAACACTTTGA 148
                                                                                                                                                                                                                                                    TATCTTGGCTGTATTTTCAGGGATAGTTATGAAGACTGTGGAAGAGTATGCGCTACTTG 88
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                                                                                             TAATAGGTTCACACGGATTGGGGGCGCACAGTGGAATCTACATTAGTGTTGCTGAAGAAT 208
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP)-

http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37F10 of DrosBAC library from Drosophila melanogaster (fruit
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genos
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Similarity 17.2%;
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/clone="BACN37F10"
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a 84 c 159 g
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/plasmid="pBeloBAC11"
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RARRARRAGAGAARRRRGRRGRGAGARRRGRGRGRRRGAGARRRRGRRMRTRRAR
                                         TGCATGCACGATCAAAAGGGGACATGGGAGAACGGCAAGCGATAGAGAAAAGAGGGTATGTG
                                                                                                                      GCGCACAGTGGAATCTACATTAGTGTTGCTGAAGAATTTGCTAGGCACGGATTTGGATTC
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                                                                                  Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDCP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDCP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/clone="BACR12K22"
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/db_xref="taxon:7227"
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survey sequence TET3 end of BAC #
rom Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ct
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AAADATAAATAAKATAWATKTTTKKTTTTTTTKTTTTTTTKKTTTARKADRDDDDK
                                 TDKTKTGTDTKWGWKDKWTDKKRDGKRGDGDRKDKGTGGDGDSKAKGDRAWAWRAKATRA
                                                                                                         AACACTTTGATAATAGGTTCACACGGATTGGGGGCGCACAGTGGAATCTACATTAGTGTT 198
                                                                                                                                                 KTDGWGTTTKADTTDDTDADWWDWKDWDWKDADTKAGRKRGWGKKGGWKKTTKTKKKK
                                                                                                                                                                                    GCGCTACTTGAAACAGGCGTAAGAGTGTTTTATCGGTGTGTAATCCCGGAGAAAGCTTTT 138
                                                                                                                                                                                                                       DTKKTKTRTGTKKKTDRGMRKTDTWGWGDWRADRTDGARADRAANAKDKDADGKADTDAT 593
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Wheb: www.genoscope.cns.fr)

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Cenevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

[ bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster genome survey sequence SP6 end of BAC BACN03G04 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL098379
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70; Conservative
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/clone="BACN03G04"
/note="end : SP6"
a 108 c 131 g
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98. and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library or filters for hybridization from the BACPAC Resource Center can be found at http://hacpac.med.buffalo.edu/drosophila bac.htm.
                     AGTTATCGCGCTAGCCCCGGCCCTCCAAATCCCCTTAACCCCGGCTAGAAGACTTGTTCT
                                                                                                           CAGTATGGGCGGGCTGATAGCGCTCGGAACAGTTGCAACTTATAAAGAAATCGCCAAGGG
                                                                                                                                                                                                  GGCCTTCTCCGATTATGCCAAGTGGCGCGCGTGGGAGGTGACGAAATAATATTGCTAGGACA 383
                                                                 NMNKNKKMAGNMAMAKAKAGMMAMMAAMAMAMAKBDMAKAMMMMMMGMMMMMVKMGMMGG
                                                                                                                                                        GNNMNNNKNKNNNGNKNNNNNMMNNKNNGKNNTNNTKNNCNNTNNNMNKNKMNNNMMM
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1 (bases 1 to 1101)
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BACR17F22 of RPCI-98 library from Drosophila melanogaster (fruit
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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TTRTTTTTTTKTKKKKKKKKKTKGTTKTDDKNAKVDAAKARTDDKKTKAKTGWRGKKKKTTT 1040
                                          TTGTTAATATATCTTGGCTGTATTTTTCAGGGATAGTTATGAAGACTGTGGAAGAGTATG 79
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                                                                                               th 4.3%; Similarity 17.5%; 60; Conservative 13
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BACR32D23 of RPCI-98 library from Drosophila melanogaster (frui
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0518 row: D column: 20
Seq primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Utah
University of Utah
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42Tv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the DAkson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                              /sex="Male"
                                                                                                                                                                                                                                                                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC1M0518D20"
                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 TGTTTAAAATTTCTGTGTAAGCTCAGAAACACAAACTTTGTTATGCAAGGTTTGTTATGC 432
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7171g05.x
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75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 555)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 476.
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Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NDHSF pool 1: 309384-310319, 323208-325895 Soares NDHSF pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NDHFB-9W pool 1:
                                                                                                                                                                                                                        /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro.
                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE: 3526857"
                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 GATTAACAGCTCATTGGTCTTTTGTTAAGTGAGGGAGAGAGGGAGTCGGCCTGTGCTAGT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          642 GATTAAAGCATCATCTATGTCTTGGACCATAGCAGGGGAAATTAATACTCCCGTCCTGCT 701
                                                                                                                                                                                                                        Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGF is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gooegawa and haron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library. Or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insectä;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 938)
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AL065906
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
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                                             /organism="Drosophila m
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14J11"
/note="end : T7"
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                           681 AATTAATACTCCCGTCCTGCTTATTCATGGGGAAAAACAGAATGTCATACCTCCGGAGGC 740
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 AATCAAGGTTCCGTTTCTTGTGATGCACGGCACAGCTGATACAGTTACTGATCCTAAAGG 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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                                                          94;
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                                                                                                                                                                                                                                                                                                                               Yana
                                                                                                                                                                                                                                                                                                                                           The First Laboratory for Plant
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                          Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                 Email:
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                                                          Conservative
                                                                                                                                                                                                                                                                                                               asamizu@kazusa.or.jp,
                                                                                                                                                                                      /clone="5Q118f05F"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
/strain="Columbia"
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 KDDKKDAKADKKKWKKDRAKDKAKKDDDKKDKAKDKDKDKKDADAKAWAKAKADADAKAK 988
                                                                                                                                                   KKKRAKDRKKKKKKDKAWGDKKKAKKDKAAAKAKADAAGDAKAKRRRAGDKDKAKADAKA 868
                                                                                                                                                                                                                                                                 ATATCAATGTCTTTGTTAATATATCTTGGCTGTATTTTTCAGGGATAGTTATGAAGACTG 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the European Drosophila Genome Project (EDC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster genome
BACN03K20 of DrosBAC library fr
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/clone="BACN03K20"
/note="end : T7"
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/plasmid="pBeloBAC11"
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AL525973 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC015XJ02 5
prime, mRNA sequence.
AL525973
AL525973 GI:12789466
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BP 191 91006 EVRY cedex - France
Email: segref@enoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 784)
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                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Freng Lilang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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Search completed: June 2, 2001, 21:49:52 Job time: 28890 sec

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Result
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US-09-270-849B-3883 US-08-956-171C-37 US-08-956-171C-102 US-08-956-171C-102 US-60-248-505-210 US-09-270-849B-2073 US-09-270-849B-1399 US-09-737-223-32806 US-09-737-223-13292 PCT-US01-01392-7528 PCT-US01-01392-7528 PCT-US01-01392-2386 US-09-270-849B-13030 US-09-270-849B-33030 US-09-270-849B-33030 US-09-270-849B-33030 US-09-270-849B-108901

ALIGNMENTS

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TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 2041-756
CURRENT APPLICATION NUMBER: US/09/737,223
CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 09/332,782
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 28329
LENGTH: 469
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; GENERAL INFORMATION:
; APPLICANT: Hyseq, In
US-09-737-223-15344/c ; Sequence 15344, Application US/09737223 ; GENERAL INFORMATION:
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ORGANISM: HOMO sapiens
FEATURE:
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Local Similarity '48.78;
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; ORGANISM: Saccharomyces cerevisiae
US-09-335-032-12216
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US-09-335-032-12216/c
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US-09-737-223-15344
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SEQ ID NO 12216
LENCTH: 924430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12216, Application US/09335032 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 09/012,031 PRIOR FILING DATE: 1998-01-22 NUMBER OF SEQ ID NOS: 12219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: Characterization of the
TITLE OF INVENTION: Transcriptome
FILE REFERENCE: 01107.78572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/035,917 PRIOR FILING DATE: 1997-01-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Velculescu, Victor APPLICANT: Vogelstein, Bert APPLICANT: Kinzler, Kenneth
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                                                                                                                                                                                     517 AGGCTTGCCCCGCATTCTAAGATCACCTTACAAAGGAGATTGCCGCAGAAACCAGAGGGT 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TGGAGTTTATAATATAAATTAGATCATCCTAGCATACACTTCGGCAATTTGTTTTTATTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TTTTATTTCTATTTAAATGTACACATATATAGTATTTATAATAATAATAATAATTTAGATT 122
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GAAATGATTAAAG 649
                                                              TTGCTGAGAGTCAAGTTCCCCGATAGAAGCCATATTCAAATAGCATTCAAACCCAATGAA 404679
                                                                                                   TTTCAAAGAGCAAAAGATATAGAATACAGTCTGAGTGAAATATCAGTCAAGCTCGTGGAC 636
                                                                                                                                              AGACTTAGAGAGCAATCAGCCAACAACTTGCCAAAGAAAAATAAGGCTATATCTGAGTGT 404739
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50.0%;
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Pred. No. 20;
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Pred. No. 0.42;
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US-09-270-849B-13957; Sequence 13957, Appl; GENERAL INFORMATION:
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-849B-1276
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US-09-270-849B-1276
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APPLICANT: Swimmer et al.
TITLE OF INVENTION: Insect genome survey devices
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/270,849B
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13957
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CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
SOFTWARE: PatentIn Ver: 2.0
SEQ ID NO 1276
LENGTH: 789
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Best Local 9
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Best Local :
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TITLE OF INVENTION: Insect genome survey devices
FILE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                           531 TTCTAAGATCACCTTACAAAGGAGATTGCCGCAGAAACCAGAGGGTTTTCAAAGAGCAAA 590
651 ATCATCTATGTCTTGGACCATAGCAGGGGAAATTAATAC 689
                                                                            591 AGATATAGAATACAGTCTGAGTGAAATATCAGTCAAGCTCGTGGACGAAATGATTAAAGC
                                                                                                                  654 tacgaagcttagctatgtattggtacttccctctaaacaagcgtgtatataaatatcctt 713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551 taatttaatttaagtataaggaagtgtgttttttgtctttttaaccatttgaaaattatt 610
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                                     agaattaaagtccaatgtcaatgtagtgcaaaacatacacgagaaggatattcaacaggc
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Pred. No. 5;
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Pred. No. 5
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RESULT 8
US-09-270-849B-97733
; Sequence 97733, Application US/09270849B
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PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 207
LENGTH: 184668
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CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 3188
LENGTH: 975
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
ETLE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
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APPLICANT: Slater, Steven C.

TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                         146 TGATAATAGGTTCACACGGATTGGGGGCGCGCACAGTGGAATCTACATTAGTGTTGCTGAAG 205
                                                                                                                          206 AATTTGCTAGGCACGGATTTGGATTCTGCATGCACGATCAAAGGGGACATGGGAGAAC 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 tcatggcgaaacagggtttcgaggtctatgcccatgatcatcgcggccacggccgcac 233
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                                                                                                     tcatggcgaaacagggtttcgaggtctatgcccatgatcatcgcggccacggccgcac 154449
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54.2%;
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54.2%;
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Pred. No. 54;

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Pred. No. 11;
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; SEQ ID NO 4615
; LENGTH: 330
; TYPE: DNA
; ORGANISM: Eucalyptus g
US-09-724-866A-4615
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 195450
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 97733
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Polynucleotides, Material Incorporating TITLE OF INVENTION: Them, and Methods for Using Them FILE REFERENCE: 11000.1049BU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: CURRENT APPLICATION NUMBER: US/09/270,849B
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ORGANISM: Artificial Sequence
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125 ggtttgctgtatggagaaacaccagagaatgccgaaatcgtctt 168
                                   811 AACTTGTTTTTGAACCAGGCGCGGTGAAAATCGTCACAGACAT 854
                                                                                                                                                                                         691 CCCGTCCTGCTTATTCATGGGGAAAAACAGAATGTCATACCTCCGGAGGCGAGCAAAAAA 750
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                                                                                                                751. GCCTACCAATTAATACCTTCATTCCCTAAAGAGTTGAAAAAATACCCCGGATCTTGGACAC 810
                                                                         65 ctctacgactctgctttgagttcggacaagacattcaaattgtatccaggcatgtggcac 124
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Pred. No. 9.9;
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US-09-724-866A-2131 ; Sequence 2131, Application US/09724866A

GENERAL INFORMATION:
APPLICANT: Havukkala, Ilkka

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; SEQ ID NO 4971
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Eucalyptus 9
US-09-724-866A-4971
US-08-276-163D-11300/c
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                  RESULT
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Best Local Similarity
Matches 81; Conser
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SEQ ID NO 2131
LENGTH: 336
TYPE: DNA
ORGANISM: Eucalyptus grandis
5-09-724-866A-2131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4971, Application US/09724866A GENERAL INFORMATION:
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Best Local Similarity
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PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 24913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/724,866A CURRENT FILING DATE: 2000-11-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/171,432
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                                                                                                                                                                   751 GCCTACCAATTAATACCTTCATTCCCTAAAGAGTTGAAAAAATACCCCGGATCTTGGACAC 810
                                                                 125 ggtttgctgtatggagaaacaccagagaatgccgaaatcgtctt 168
                                                                                                    811 AACTTGTTTTTTGAACCAGGCGCGGTGAAAATCGTCACAGACAT 854
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CURRENT APPLICATION NUMBER: US/08/276,163D
CURRENT FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 15314
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11300
LENGTH: 455
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GENERAL INFORMATION
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                                             NAME/KEY: misc feature
LOCATION: (363)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
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LOCATION: (275)
OTHER INFORMATION: n equals a,t,g,
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            OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
 NAME/KEY: misc
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LOCATION: (308)
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LOCATION: (368)
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NAME/KEY: misc feature
LOCATION: (366)
OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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                NAME/KEY: misc feature LOCATION: (449)
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; TYPE: DNA
; ORGANISM: human
US-60-248-505-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 48
                                                                                                                                                       Sequence 9, Application US/60248505
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN
TITLE OF INVENTION: RECEPTORS, NUC
TITLE OF INVENTION: PROTEINS, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/270,849B
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8139
LENGTH: 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8139, Application US/09270849B GENERAL INFORMATION:
APPLICANT: Swimmer et al.
                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                          FILE REFERENCE: c1000918
CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Insect genome survey devices
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                   297 GNCCTTNAANAAAACCCCTATCNCNAAAACCCAGAGGCTTACAAAGTGGATTGTGTACAC
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                                                                                                                                                                                                                                                                                                                     gaatacttccataatg
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                                                                              FastSEQ for Windows Version 4.0
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                                                                                                                                                       ISOLATED HUMAN G-PROTEIN COUPLED RECEPTORS, NUCLEIC ACID MOLECULES PROTEINS, AND USES THEREOF
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Pred. No. 11;
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US-60-248-505-308

US-60-248-505-308

Sequence 308, Application US/60248505

GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
ITITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
ITITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
ITITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: C100918
CURRENT FILLING DATE: 2000-11-15
CURRENT FILLING DATE: 2000-11-15
SEQ ID NO 308
SEQ ID NO 308
LENGTH: 203032
TYPE: DNA
ORGANISM: human
FEATURE:
NAMEJKEY: misc_feature
NAMEJKEY: misc_feature
OTHER INFORMATION: n = A,T,C or G
US-60-248-505-308
Search completed: June 3, 2001, 02:00:32 Job time: 20651 sec
                                                                                                                        Db 172100 aggtgaatcaatcttacactgttacgtcatctttacagacccatctat 172147
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                                                                                                                                                                                                                        Db 172040 gagggtcctgctaaaacaggctggctacaccagaggaaaaggtaaagccttctacctttg 172099
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Best Local Similarity 52.3%;
Matches 69; Conservative
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                                                                                                                                                                                                                                                         552 GAGATTGCCGCAGAAACCACAGGGTTTTCAAAGAGCAAAAGATATAGAATACAGTCTGAG 611
                                                                                                                                                                              612 TGAAATATCAGTCAAGCTCGTGGACGAAATGATTAAAGCATCATCTAT 659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  606 TCTGAGTGAAATATCAGTCAAGCTCGTGGACGAAATGATTAAAGCATCATCTATGTCTTG 665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31.2; DB 6; Length 27807; Pred. No. 40; 0; Mismatches 63; Indels 0;
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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:*
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Gapop 10.0 , Gapext 1.0
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894
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44: /cgn2_6/ptodata/2/pna/US6012_COMB.seq:*
45: /cgn2_6/ptodata/2/pna/US6013_COMB.seq:*
46: /cgn2_6/ptodata/2/pna/US6014_COMB.seq:*
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50: /cgn2_6/ptodata/2/pna/US6019_COMB.seq:*
51: /cgn2_6/ptodata/2/pna/US6019_COMB.seq:*
53: /cgn2_6/ptodata/2/pna/US6019_COMB.seq:*
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56: /cgn2_6/ptodata/2/pna/US6025_COMB.seq:*
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59: /cgn2_6/ptodata/2/pna/US6025_COMB.seq:*
59: /cgn2_6/ptodata/2/pna/US6027_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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36 35 3.9 453 25 US-09-654-C17-162340 Sequence 16234 37 35 3.9 453 27 US-09-664-C17-162340 Sequence 16224 38 35 3.9 488 16 US-09-205-070-14049 Sequence 14049 39 35 3.9 488 17 US-09-340-623-14049 Sequence 14049 40 35 3.9 505 46 US-60-147-499-15639 Sequence 15639 41 35 3.9 505 46 US-60-147-499-15639 Sequence 15339 41 35 3.9 536 23 US-09-657-700-6810 Sequence 13158 42 35 3.9 757 25 US-09-654-017-131581 Sequence 13158 43 35 3.9 1737 27 US-09-684-016-131581 Sequence 13158 44 35 3.9 1137 19 US-06-234-6809-11233 Sequence 11233	35			9	21	-09-540-764-349	e 34982
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43 35 3.9 757 27 US-09-684-016-131581 Sequence 13158 44 35 3.9 1103 55 US-60-234-690-11233 Sequence 11233 45 35 3.9 1103 15 US-60-234-690-11233 Sequence 11233				u) n	-09-605-700-	equence 131581
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; Sequence 27, Applicat
; GENERAL INFORMATION:
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TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 NUCLEOTIDES
                                                                                                                                                                                              Query Match 100.0%; Score 894; DB 17; Best Local Similarity 100.0%; Pred. No. 3.6e-267; Matches 894; Conservative 0; Mismatches 0;
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APPLICANT:
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NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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CITY: LA JOLLA
STATE: CALIFORN
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OPERATING SYSTEM:
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TOPOLOGY: LIP
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KOSMOTKA, Anna
ESTERASES
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TTD, John
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                                                 GAGTTGAAAAAATACCCCGATCTTGGACACAACTTGTTTTTTGAACCAGGCGCGGTGAAA
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US-08-466-194-14/c Sequence 14, Application US/08466194
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08 FILING DATE: 06-JUN-1995 PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08 CORRESPONDENCE ADDRESS: PRIOR APPLICATION DATA: NUMBER OF SEQUENCES: COUNTRY: ADDRESSEE: Foley & Larc STREET: 3000 K Street, FILING DATE: STATE: CITY: Washington 20007 엉 USA Foley & Lardner 22-APR-1994 52 US 08/232,463 US/08/466,194 Suite 500 Version

07/935,313

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US-09-565-309A-12262
, Sequence 12262, Application US/09565309A
; GENERAL INFORMATION:
APPLICANT: ALEXANDROV, NICKOLAI
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-0853P
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US-08-466-194-14
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
CURRENT APPLICATION NUMBER: US/09/565,309A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 68449
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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 CTTTTAACACTTTGATAATAGGTTCACACGGATTGGGGGCGCACAGTGGAATCTACATTA 193
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                                                                                                                                                                                                                                                                                                                                                                                                                    374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 26-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                 TGCTAGGACACAGTATGGGCGGGCTGATAGCGCTCGGAACAGTTGCAACTTATAAAGAAA 433
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                                                                                   DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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; NAME/KEY: misc_feature : LOCATION: (1)..(568) : LOCATION: (1)..(568) : OTHER INFORMATION: any n = a, g, c, t, unknown, or other : NAME/KEY: misc_feature : LOCATION: (1)..(568) : OTHER INFORMATION: 15284:105521 (Clone Number:Unique Sequence Identifier) US-09-565-309A-12262
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/565,309A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 68449
SEQ ID NO 47131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 47131, Application US/09565309A GENERAL INFORMATION:
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LENGTH: 568
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Best Local
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Best Local
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-0853P
                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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ORGANISM: Arabidopsis thaliana
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1098 ttgtataatcaggcaccatcagttttcaaagacatcaaactctatgacggtttcttacac 1157
                                                                                          691 CCCGTCCTGCTTATTCATGGGGAAAAAACAGAATGTCATACCTCCGGGAGGCGAGCAAAAAA 750
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mes 98; Conserv
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Pred. No. 0.0033
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Pred. No. 0.0051;
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RESULT 5
US-09-565-309A-55932
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; GENERAL INFORMATION:
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                                              NUMBER OF SEQ ID NOS: 9796
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1429
                                                                                                                                                                                                                                                           Sequence 1429, Application US/09652123
GENERAL INFORMATION:
APPLICANT: Holtman, Douglas A.
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CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 68449
SEQ ID NO 55932
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Best Local Similarity
Matches 98; Conserv
                                                                                                                        TITLE OF INVENTION.

FILE REFERENCE: 1600.1186-001

CURRENT APPLICATION NUMBER: US/09/652,123

CURRENT FILING DATE: 2000-08-30

CURRENT FILING DATE: 60/151,135
                                                                                                                                                                                               TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES TITLE OF INVENTION: THEREFOR FILE REFERENCE: 1600.1186-001
                                                                                                             PRIOR APPLICATION NUMBER: 60/:
PRIOR FILING DATE: 1999-08-30
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LOCATION: (1)..(1406)
OTHER INFORMATION: any n = a, g, c, t, unknown, or other
NAME/KEY: misc_feature
LOCATION: (1)..(1406)
OTHER INFORMATION: 15284 : OVERLAP (Clone Number : OVERLAP)
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ORGANISM: Arabidopsis thaliana
FEATURE:
        TYPE: DNA
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Pred. No. 0.0051;
0; Mismatches 86;
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; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-07938-5
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; LOCATION: (1)...(769)
; OTHER INFORMATION: n = A,T,C
US-09-652-123-1429
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; Sequence 5, Application PC/TUS0007938
; GENERAL INFORMATION:
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Sequence 5, Application US/09534061
GENERAL INFORMATION:
APPLICANT: Ling, Vincent
APPLICANT: Wu, Paul
APPLICANT: Gray, Gary
TITLE OF INVENTION: MICROSATELLITE REPEATS IN THE COSTIMULATORY RECEPTOR
TITLE OF INVENTION: LOCUS AND USES THEREOF
FILE REFERENCE: GNN-5343CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity 52.5%;
Matches 83; Conservative
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CURRENT FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/126,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                         43997 aaatcctaccaagtcatattttaagtccagaaaagaaattttaaaccaactggatcttctg 44056
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                                                                                                                                                                                                                                                                                                     808 CACAACTTGTTTTTT 822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.5%;
Local Similarity 56.3%;
les 76; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics Institute, Inc
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 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40.6; DB 1;
Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
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Gaps

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US-09-521-640-150845/c ; Sequence 150845, Application US/09521640 ; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-534-061-5
                   US-09-565-240-49927, Application US/09565240; Sequence 49927, Application US/09565240; GENERAL INFORMATION:
Abad, Mark S.
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                                                                                                                                                                                                                                                                                                                              ΔÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Glycine max
US-09-521-640-150845
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                                                                                              RESULT
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SEQ ID NO 5
LENGTH: 50000
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Best Local Similarity 56.3%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.3%;
Best Local Similarity 56.2%;
Matches 72; Conservative
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SEQ ID NO 150845
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CURRENT FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/126,215
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Halling, Conrad H.

APPLICANT: Kovalic, David K.

TITLE OF INVENTION: Nucleic Acid Mo:
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15750)D
CURRENT APPLICATION NUMBER: US/09/521,640
CURRENT FILING DATE: 2000-03-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           688 ACTCCCGTCCTGCTTATTCATGGGGAAAAACAGAATGTCATACCTCCGGAGGCGAGCAAA 747
                                                                                                                                                                                                                                                                                                                       679 GAAATTAATACTCCCGTCCTGCTTATTCATGGGGAAAAACAGAAATGTCATACCTCCGGAG 738
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                                                                                                                                                                                                                                                                                              191 GAAATTAAGTGTCTCGATCAGCTTTCGCATCATCATGAGCAGTAGGTCCTAGAACCGATC 132
                                                                                                                                                   71
                                                                                                                                                 CATTIGGG
                                                                                                                                                                                                                         GCGATCAGCAAACCCGAACAAAAACTAGATGAAATTGATAATGGCATTAGACAATTCAAC 72
                                                                                                                                                                                                                                                           GCGAGCAAAAAAGCCTACCAATTAATACCTTCATTCCCTAAAGAGTTGAAAAAATACCCC 798
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Abad, Mark S.
La Rosa, Thomas J.
                                                                                                                                                 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acid Molecules and Other Molecules Associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304701
                                                                                                                                                                                                                                                                                                                                                                     Score 38.4; DB 19;
Pred. No. 0.85;
0; Mismatches 56;
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Pred. No. 1.7;
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CURRENT APPLICATION NUMBER: US/09/565,240
CURRENT FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 54005
SEQ ID NO 49927
LENGTH: 413
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3167-019-p1-K1-B8
US-09-565-240-49927
                                                                                                                                                                                                                                                                                            ; FEATURE:

NAME/KEY: misc_feature

: LOCATION: (1)...(176787)

: OTHER INFORMATION: n = A

US-60-212-664-184
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Best Local Similarity
Thes 77; Conserve
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                                                     Db 144893 attgcattccgggtctgatgacccgcacggttttccccagatatgagaaactcatagatgc 144952
                                                                                                                           Db 144833 tcacctggcagaggagatgccatgatcacaaaggtggttttctccagggtgagacttatgg 144892
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US-60-212-664-184
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: F
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/60/212,664
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TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: UCLEIC ACID MOLECULES ENCODING &
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000687
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TITLE OF INVENTION:
FILE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 176787
                                                                                                                                                               539 TCACCTTACAAAGGAGATTGCCGCAGAAACCAGAGGGTTTTCAAAGAGCAAAAGATATAG 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 CTTTGATAATAGGTTCACACGGATTGGGGGCGCACAGTGGAATCTACATTAGTGTTGCTG
                     659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 AAGAATTTGCTAGGCACGGATTTGGATTCTGCATGCACGATCAAAGGGGACATGGGAGAA 262
                                                                                          599 AATACAGTCTGAGTGAAATATCAGTCAAGCTCGTGGACGAAATGATTAAAGCATCATCTA 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 CGGCAAGCGATAGAGAAAGAGGG 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 ctaagaaaaaggaacacaaggagttattgagatntgaaaatcctaacttggtaaagcca 78
TGTCTTGGACCATAGCAGGGGAAAATTAATACTCCCCGTCCTGCTTATTCATGGGGAAAAAAC 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aagagcttgaaagctagagatgttgatgttggaaaaaaccaacagaactttcaaggcgtgaa 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Greenberg, Simon
Rabkin, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ladunga, Steve
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53.8%;
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                                                                                                                                                                                                  ; Score 37.8; DI
; Pred. No. 23;
0; Mismatches
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Pred. No. 1.2;
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NAME/KEY: misc_feature

: LOCATION: (1)...(469)

: OTHER INFORMATION: n = A,T,C

US-09-235-076-28329
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; LENGTH: 67878
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-534-859-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-534-859-27
   Matches
                  Best Local
                               Query Match
                                                                                                                                                                                                SOFTWARE: Fas
                                                                                                                                                                                                                                                                                                                                       Sequence 28329, Application US/09235076 GENERAL INFORMATION:
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Best Local Similarity 53.48;
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CURRENT APPLICATION NUMBER: US/09/235,076
CURRENT FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                         APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCE:
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/534,859
CURRENT EILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 1127
EQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                   LENGTH: 469
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36259 atgagtaatatatatatatgtatatatacctcggctggatatttctggaatatgggcg 36318
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                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ATCCCGGAGAAAGCTTTTAACACTTTGA 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AAGACTGTGGAAGAGTATGCGCTACTTGAAACAGGCGTAAGAGTGTTTTATCGGTGTGTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGTITAATATCAATGTCTTTGTTAATATATCTTGGCTGTATTTTTCAGGGATAGTTATG 60
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   93;
              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parnell, Laurence D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09534859
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   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s, Susan R
                                                                                                                                                                                                                                                                                                          NOVEL NUCLEIC ACID SEQUENCES OBTAINED
              4.2%;
48.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLANT POLYMORPHIC MARKERS AND USES THEREOF
Score 37.2; D
Pred. No. 2.2;
0; Mismatches
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F
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Pred. No. 17;
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                              DB 16;
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NUMBER OF
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US-09-332-782-28329
; Sequence 28329, Application US/09332782A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-289-768-30823
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Best Local Similarity 48.7
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30823
LENGTH: 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: Hyseq, Inc
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CURRENT APPLICATION NUMBER: US/09/289,768
CURRENT FILING DATE: 1999-04-08
CURRENT APPLICATION NUMBER: US/09/332,782A CURRENT FILING DATE: 1999-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)...(469)
OTHER INFORMATION: n = A,T,C or
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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 28329
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(469)
; OTHER INFORMATION: n = A,T,C or G
US-09-332-782-28329
Search completed: June 3, 2001, 00:45:43 Job time: 39441 sec
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                                                                                                                                        138 aagatccaagataaggaaggcatccctcctgatcagcagaggttgatactttgctgggaa 197
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DB seq length: 2000000000
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    of hits satisfying chosen parameters:
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
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/cgn2_f/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/FCTUS_COMB.seq:*
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US-08-727-034-5
US-08-727-034-5
US-08-781-891-79
US-08-862-765-1
US-08-945-296-3
US-09-405-112-3
US-09-602-359A-28
US-08-960-780-18
US-08-201-118-8
US-08-238-821B-8
PCT-US95-05744-8
US-08-874-186-42
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US-09-265-315-18
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US-08-602-359A-24
US-08-687-080-68
US-08-987-980-68
US-08-448-170-7
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               US-08-233-609-2
US-08-444-083-2
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US-08-232-463-14
US-09-040-984-13
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8-727-034-5
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RESULT 1 US-08-602-359A-27 Sequence 27, Appric Application US/08602359A ROBERTSON, Daniel E.

ALIGNMENTS

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,359A
FILING DATE: February 16, 1996 GENERAL INFORMATION: APPLICANT:
APPLICANT:
APPLICANT: APPLICANT:
APPLICANT: CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: TITLE OF INVENTION: APPLICANT: MAFFIA, Anthony ADDRESSEE: FISH & F STREET: 4225 EXECUT CITY: LA JOLLA STATE: CALIFORNIA APPLICANT: COUNTRY: U ZIP: 92037 E: FISH & RICHARDSON P.C.
4225 EXECUTIVE SQUARE, STE 1400 USA MURPHY, L. John KOSMOTKA, Anna KOSMOTKA, Anna KOSMOTKA, Anna KOSMOTKA, Anna LINK, SWANSON, Ronald V. WARREN, Patrick V. Steven Dennis

TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 894 NUCLEOTIDES FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070 TOPOLOGY: LI MOLECULE TYPE: CLASSIFICATION: 435 PRIOR APPLICATION DATA: TYPE: NUCLEIC STRANDEDNESS: APPLICATION NUMBER: NUCLEIC ACID LINEAR GENOMIC DNA SINGLE 27: 09010/010001

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RESULT 2
US-08-232-463-14/c
; Sequence 14, Applicatic
; Sequence 1570367
; Patent No. 5670367
; GENERAL INFORMATION:
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Best Local Sim
Matches 894;
APPLICANT:
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                                                                                                                                          ATCGTCACAGACATTGTAGAGTGGGTTAAGAATCTACCCAGGGAAAATCCTTAA 894
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                                                                                                                                                                                                   Similarity
                                                        Application
DORNER, F. SCHEIFLINGER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 894; DB 2; llarity 100.0%; Pred. No. 1.3e-298; Conservative 0; Mismatches 0;
                                                        US/08232463
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; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14
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Best Local S
Matches 29
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FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/ACENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)683-4109
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FALKNER, TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                           194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 6.1%; Score 54.8; DB 1; Local Similarity 6.8%; Pred. No. 2.2e-08; hes 29; Conservative 219; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
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CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/232,463
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ZIP: 22313-0299
TCGCCAAAGGGAGTTATCGCGCTAGCCCCGGCCCTCCAAATCCCCCTTAACCCCCGGCTAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                               AGTATGCGCTACTTGAAACAGGCGTAAGAGTGTTTTATCGGTGTGTAATCCCGGAGAAAAG 133
                                                                                                                                                                                                  AGGATATGAAGGCCTTCTCCGATTATGCCAAGTGGCGCGTGGGAGGTGACGAAATAATAT
                                                                                                                                                                                                                                                                      CTTTTAACACTTTGATAATAGGTTCACACGGATTGGGGGGCGCACAGTGGAATCTACATTA 193
                                                                                                                                                                                                                                                                                                                                                                                                                  TGCTAGGACACAGTATGGGCGGGCTGATAGCGCTCGGAACAGTTGCAACTTATAAAGAAA 433
                                                                                                                           ATGGGAGAACGGCAAGCGATAGAGAAAGAGGGTATGTGGAGGGCTTTCACAACTTCATAG
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RECOMBINANT
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Patent No. 6210883
                                                                                                       Sequence 18, Application US/08714918 Patent No. 6037123
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                      Patent No.
                                                                                        GENERAL INFORMATION:
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                   APPLICANT:
APPLICANT:
APPLICANT:
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NAME: Maki, David J.
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS TITLE OF INVENTION: OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Reed, Steven G. APPLICANT: Wang, TongTong
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OPERATING SYSTEM:
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/U-
FILING DATE: 18-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
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                                                                                                                                                                                                                                        CCGCAGAAACCAGAGGGTTTTCAAAGAGCAAAAGATATAGAATACAG 605
                                                                                                                                                                                                                                                                    GTTCTTTCCATCTGTTAAAGTAGTACACTCCAAAGGGAAATGACCAGTAAAAAATGATCC 420
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Lee, Ving
Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
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                                                                    Benton, Bret
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Pred. No. 0.43;
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; Sequence 18, Application US/09265315

; Patent No. 6187541
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                    GENERAL INFORMATION:
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APPLICATION NUMBER: 60/003
APPLICATION SEPTEMBER: 15,
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: September CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                                   APPLICANT:
                                                    APPLICANT:
                                                                    APPLICANT:
                                                                                  APPLICANT:
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TITLE OF INVENTION:
   TITLE OF INVENTION:
                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                      154 GGTAGAGATTGCTAAGCGTAACGCTGAAGAAGTTGGGTTGTCTGATATTATTAAATTTAG
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les 86; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (213)
TELEX: 67-3510
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STREET: Suite 4700
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                                                                                                                                                                                                                                                                                                                                                                                                     6 TAATATCAATGTCTTTGTTAATATATCTTGGCTGTATTTTTCAGGGATAGTTATGAAGAC 65
                                                                                                                                                                                                                                    TGTAAAAGATGTCAATACATTAACAATTGATACAGAAGAACCGGTGGCGTTAATTGGAA 36
                                                                                                                                                                                                                                                                  GGAGAAAGCTTTTAACACTTTGATAATAGGTTCACACGGATTGGGGGCGCGCACAGTGGAA 184
                                                                                                                                                                                                                                                                                                                                     TGTGGAAGAGTATGCGCTACTTGAAACAGGCGTAAGAGTGTTTTATCGGTGTGAATCCC 125
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                             Benton, Bret
Lee, Ving J.
Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
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633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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 METHODS OF SCREENING FOR COMPOUNDS
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ber 22, 1995
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Pred. No. 2.9;
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93;

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Gaps

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95

Length 1962; Indels

NUMBER OF SEQUENCES: TITLE OF INVENTION:

ADDRESS

ACTIVE ON STAPHYLOCOCCUS AUREUS TARGET GENES

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Patent No. 610,...
Patent No. 610,...
Patent No. 610,...
Panton
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Best Local Similarity 48.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (213) 955-044
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                      APPLICANT:
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LENGTH: 1962 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: September 15, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/:
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                               126 GGAGAAAGCTTTTAACACTTTGATAATAGGTTCACACGGATTGGGGGGCGCACAGTGGAA 184
                                                                                                                                                                                                                                                                                                                      154
                                                                                                                                                                                                                                                                                                                                                                                            214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 195
APPLICATION NUMBER: 60/003,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                           6 TAATATCAATGTCTTTGTTAATATCTTGGCTGTATTTTTCAGGGATAGTTATGAAGAC 65
                                                                                                                                                                                                                                             TGTAAAAGATGTCAATACATTAACAATTGATACAGAAGAACCGGTGGCGTTAATTGGAA 36
                                                                                                                                                                                                                                                                                                                  GGTAGAGATTGCTAAGCGTAACGCTGAAGAAGTTGGGTTGTCTGATATTAATTTAAATTTAG 95
                                                                                                                                                                                                                                                                                                                                                                                          TAAGATGGCTGATTATGATAAAGAAATCGAAGTATATGCTTCTGATATCGATCCAGAAAT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86; Conservative
                                                                                                                                  18, Application US/09265315
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633 West Fifth Street
Suite 4700
                     Lee, Ving J.
Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
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   Sun,
                                                                                             Benton, Bret
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Pred. No. 2.9;
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Sequence 24, Application US/08602359A Patent No. 5942430 GENERAL INFORMATION:

APPLICANT:

ROBERTSON, Daniel E.

APPLICANT: APPLICANT:

MURPHY, Dennis REID, John MAFFIA, Anthony

APPLICANT:

LINK, Steven

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US-08-602-359A-24
                RESULT
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APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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                                                                                                     126 GGAGAAAGCTTTTAACACTTTGATAATAGGTTCACACGGATTGGGGGCGCACAGTGGAA 184
                                                                                                                                        154 GGTAGAGATTGCTAAGCGTAACGCTGAAGAAGTTGGGTTGTCTGATATTATTAAATTTAG
                                                                                                                                                                                                           214 TAAGATGGCTGATTATGATAAAGAAATCGAAGTATATGCTTCTGATATCGATCCAGAAAT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                    94 TGTAAAAGATGTCAATACATTAACAATTGATACAGAAGAACCGGTGGCGTTAATTGGAA
                                                                                                                                                                        66 TGTGGAAGAGTATGCGCTACTTGAAACAGGCGTAAGAGTGTTTTATCGGTGTGTAATCCC 125
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (213) 955-0440
TELEX: 67-3510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                                                 6 TAATATCAATGTCTTTGTTAATATATCTTGGCTGTATTTTTCAGGGATAGTTATGAAGAC
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                                                                                                                                                                                                                                                                                                  ocal Similarity
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                                                                                                                                                                                                                                                                                                  3.4%;
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ber 13, 1996
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Pred. No. 2.9;
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                                                                                                                                                                                                                                                                                 93;
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TITLE OF INVENTION: ES NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS:

KOSMOTKA,

ESTERASES

SWANSON, Ronald V. WARREN, Patrick V.

SOFTWARE:

PatentIn Release #1.0,

Version #1

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US-08-687-080-68/c

: Sequence 68, Application US/08687080

: Patent No. 5965427
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Best Local Similarity
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[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: """
STREET: """
CITY: LA JOLLA
CITY: CALIFORNIA
"""
TISA
                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                APPLICANT: Gregory Dolganov TITLE OF INVENTION: Human R.
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MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                  NUMBER OF SEQUENCES:
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TELECOMMUNICATION INFORMATION:
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NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               600
                                                                                                  STREET: 350 CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                          375 GCTAGGACACAGTATGGGCGGGCTGATAGCGCTCGGAACAGTTGC 419
                                                                                                                                                                                                                                                                                                                                                                                                          540 GGATGCCCGGGCTGTGGTGGGCTATGTCTCGGAGCGGTTCCCCGGCCGCCGGATAATATT 599
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                                                                  COUNTRY: U:
ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PS,
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                            GGTGGGGTTCAGTATGGGCGCGCGCTGTAGCGATCGTGGAGGGTGC 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58;
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                                                                                                                                350 Cambridge
                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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55.2%;
   compatible
PC-DOS/MS-DOS
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                                                                                                                               Avenue, Suite 250
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Pred. No. 2.7;
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RESULT 9
US-08-934-959-7
US-08-934-959-7
; Sequence 7, Application US/08934959
; Patent No. 5989867
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Best Local Similarity
Matches 73; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 324-09
INFORMATION FOR SEQ ID NO:
SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: US/08/934,959
                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                    APPLICANT: Fickenscher, Helmut
APPLICANT: Fleckenstein, Bernhard
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-7AN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                        APPLICANT: Knappe, Andrea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        546 TTATAACTTTTTACTAGGGGCACA 522
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                                                                                                                                                                             STREET: 901 Call
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 TCTTTGTTAATATATCTTGGCTGTATTTTTCAGGGATAGTTATGAAGACTGTGGAAGAGT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sholtz, Charles K
REGISTRATION NUMBER: 38
REFERENCE/DOCKET NUMBER:
                                                                                                                             ZIP: 94304-1104
                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDIVIDUAL ISOLATE:
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STRANDEDNESS: doub
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                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                California
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Pred. No. 8.7;
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                                      Version #1.30
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RESULT 10
US-08-448-170-7/c
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Best Local 9
APPLICATE:
FILING DATE:
CLASSIFICATION: 424
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,902
APPLICATION O1-JUNE-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Narva, Kennetn
APPLICANT: Stelman, Steve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 CAAGCGATAGAGAAAGAGGGTATGTGGAGGGCTTTCACAACTTCATAGAGGATATGAAGG 325
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                                                                                                                                                                                                                                                                      STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ching, Edwin P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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                                                                                                                                                                                                                                                                  Gainesville : Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Application US/08448170 5723758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 3.3%; Score 29.6; I
Similarity 30.3%; Pred. No. 2;
43; Conservative 30; Mismatches
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nucleic acid
                                                                                                                                                                                                                                                                                               E: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
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Best Local Similarity
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ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
                                                      APPLICATION UNMBER: US/08/9
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/0
FILING DATE: 01-JUNE-1993
CLASSIFICATION: 800
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,247
FILING DATE: 13-SEPT-1991
                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cannon, Raymond J. APPLICANT: Narva, Kenneth E.
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PRIOR APPLICATION DATA:
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ZIP: 32606
                                                                                                                                                                                                                                                                                                                                         CITY: Gainesville
STATE: Florida
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STREET: 2421 N.W. 41st St
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Encoding Lepidopteran-Active Toxins
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B.t. PS158C2, Active Against Lepidopteran
                                                                                           US 08/069,902
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Pred. No. 7;
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PRIOR APPLICATION DATA:

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US-08-727-034-5/c
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Sequence 5, App.-
Sequence 5, App.-
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: SAITO, YASHUSHI
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: IMAGENIA, KOJCHI
APPLICANT: YAMAZAKI, HIROYUKI
APPLICANT: YAMAZAKI, HIROYUKI
APPLICANT: YAMAZAKI NOVEL LDL RECEPTOR ANALOG PROTEIN AND
CODING THEREFOR
APPLICATION NUMBER: JP 102451/1996
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-079-0
                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 08-OCT-1996 CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (352) 375-8100
                                                                                                      APPLICATION NUMBER: JP 261440/1995
FILING DATE: 09-OCT-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 3684 base par
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUTTE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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Sanders, Jay M.
Sanders, Jay M.
MINBER: 39,355
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57.68;
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Pred. No. 7;
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Best Local
                                   APPLICATION NUMBER: JP 261440/1995
FILING DATE: 09-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: JP 102451/1996
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
RECISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-079-0
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/727,034 FILING DATE: 08-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy
                  TELECOMMUNICATION INFORMATION:
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APPLICANT: YAMAZAKI, HIROYUKI
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                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Local Similarity 50.7%;
les 71; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: ARLINGTON
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TELEPHONE:
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Pred. No. 10;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SENERAL INFORMATION:
                ATTORNEY/AGENT INFORMATION:

NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                  CLASSIFICATION: 800
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OTHER INFORMATION: encode the mature peptide"
OTHER INFORMATION: /note= "Identification Method: S"
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LOCATION:
                                                                                    APPLICATION NUMBER: FILING DATE: 27-DE
                                                                                                                                    SOFTWARE:
                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                         STATE: Washington
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OTHER INFORMATION:
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                                                                                                                                      PatentIn Release #1.0,
                                                                                                                                                                                                                                             USA
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81..6725
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165..6722
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NUMBER:
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GENE AND GENE PRODUCTS RELATED TO
WERNER'S SYNDROME
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                                                                                                  US/08/781,891
                                                                                                                                                                                                                                                                                             Center,
240052.419
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Pred. No. 10;
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                                                                                                                                                                                                                                                                                           701 Fifth Avenue
                                                                                                                                      Version #1.30
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31629 ACAGATGACATTAGAAAATAGAAGACATGGGATAAGTATAAAATGTTTGAAAGAGTTTAAAC 31688
                                                                                                                                                                                                    TELEFAX: 212-878-9655
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31689 ACATTCAAGGCAATATTAAGGGATTATTTTTTACTTCCAAGAAGCTCCTGGAAGCT 31744
                                  FEATURE:
                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 983 base pairs
                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 1-JUL-199
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58175000 No. 5817500disk of No.
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                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 4: TELECOMMUNICATION INFORMATION:
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OTTY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 AAAGGGGACATGGGAGAACGGCAAGCGATAGAGAAAGAGGGGTATGTGGAGGGCTTTCACA 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 ACTTCATAGAGGATATGAAGGCCTTCTCCGATTATGCCAAGTGGCGCGTGGGAGGT 360
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM COMPTON OPERATING SYSTEM: DOS COMPTWARE: FastSEQ for Windows Version 2.0 COMPTWARE: FASTSEQ FOR WINDOWS VERSION 2.0
                                                STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 10174
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les 62; Conserv
                 NAME/KEY:
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OCATION:
                                                                   ORGANISM:
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N: Animal Feed Additives
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Pred. No. 51;
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Perfect score:
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1099.363 Million cell updates/sec
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Human RING finger
Gene encoding a su
Aspergillus oryzae
Stealth virus nucl
Arabidopsis thalia
                                                                                                                                            DNA encoding Desul
Arabidopsis thalia
Polymorphic repeat
DNA sequence of th
Aspergillus oryzae
                                                                                                                                                                                                                                                                                                   Description
                                                                                                                          Chicory germacrene
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T79325
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Ovine Y-chromosoma	N90568	10	7960	3.4	30.2	٠.
Stealth virus nucl	X84332	20	5059	3.4	•	-
Arabidopsis thalia	C47636	21	2896	3.4	•	_
Ω3	A26867	21	1962	3.4	٠	
Homo sapiens clone	V32415	19	1939	3.4	30.2	
9	F11363	21	690	3.4	•	Ŭ
	V75148	18	433	3.4		_
	V78307	18	400	3.4	•	~
ç	V78600	18	322	3.4	•	-
psis t	C33998	21	898	3.4	٠	٠.
human reti	N90490	10	18177	3.4	•	٠.
0	N90489	10	5056	3.4	•	_
	Z88444	21	4839	3.4	•	_
	A29391	21	4839	3.4		
	X04501	20	4597	3.4	•	•
=	Q70536	15	4597	3.4	•	_
	N81369	9	4597	3.4	•	•
H	N81261	9	4579	3.4	٠	~
colon canc	C98275	21	551	3.4	٠	-
TBC-1 part	Z50905	21	99960	3.5		٠.
	A34844	21	22421	3.5	31	٠.
O .	F20966	21	22421	з. 5	31	_
ococcus faec	X13300	20	13932	3.5	31	_
th virus nu	X84323	20	9181		31	
	A34842	21	5561			
Human low adenosin	F20964	21	5561		31	Ŭ
Arabidopsis thalia	C4697	21	151	٠		_
Arabidopsis thalia	1 F22305	2	1082138		۲.	~
Human secreted pro	C69486	21	1879			-
đ	C34433	21	1121		۳	٠.
rococcus f	X12966	20	S		H	٠.
al yea	T456	17		3.6	31.8	_
lung cancer	C65752	21	694	3.6	۳	_
Human lung tumor a	Z245	20	694	3.6	31.8	

ALIGNMENTS

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Callen W,
                                                                                                                                                                                               Esterase; thermostable enzyme; ester; chiral compound; cheese; pulp; paper; lignin removal; sugar; lignocellulose; disease resistance; feedstuff; ss.
                 (RECO-) RECOMBINANT BIOCATALYSIS INC.
                                     16-FEB-1996;
                                                        11-FEB-1997;
                                                                                           WO9730160-A1.
                                                                                                                                                                             Desulfurococcus sp. strain M11TL
                                                                                                                                                                                                                                      DNA encoding Desulfurococcus sp. esterase M11TL.
                                                                                                                                                                                                                                                          16~FEB-1998
                                                                                                                                                                                                                                                                                              T79325 standard; DNA; 894
                                                                           21-AUG-1997
Kosmotka A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This DNA sequence codes for thermostable esterase Milt (W23072) CC of a new species of Desulfurococcus that grows heterotrophically by Grementation of different organic materials, optimally at 85-88 deg CC cand pH 7.0. It can be amplified from a pBluescript vector by PCR CC (see T79308-09). Claimed, newly identified polynucleotides (T79321-CC 30) encoding esterases (W23069-77, W2308) were recovered from genomic gene libraries. They can be used for recombinant production of the CC enzymes in host cells, and as probes to identify related sequences. The esterases are stable at high temperature and in organic solvents, making them superior for use in production of pure chiral CC compounds used in pharmaceutical, agricultural and other chemical industries. A method is claimed for transferring an amino group CC from an amino acid to an alpha-keto acid using a claimed esterase. The enzymes may also be useful as ripening starters in cheese making, in lignin removal in paper and pulp manufacture, in carbohydrate CC derivative synthesis, in fermentable sugar production from CC lignocallulosic waste, in the study of plant wall structure, plant cresistance to disease and organic matter decomposition and to select plants bred for production of highly degradable animal feeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                               GATCAAAGGGGACATGGGAGAACGGCAAGCGATAGAGAAAGAGGGGTATGTGGAGGGCTTT 300
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                                                                           acttataaagaaatcgccaagggagttatcgcgctagccccggccctccaaatcccctta
                                                                                                                                                     gacgaaataatattgctaggacacagtatgggcgggctgatagcgctcggaacagttgca
                                                                                                                                                                                                                                                                                                                                                                                   atcccggagaaagcttttaacactttgataataggttcacacggattggggggcgcacagt 180
                                                                                                                                                                                                                                                                                                      gatcaaaggggacatgggagaacggcaagcgatagagaaagagggtatgtggagggcttt
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Pred. No. 4.8
0; Mismatches
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1.8e-292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATGTCATACCTCCGGAGGCGAGCAAAAAAGCCTACCAATTAATACCTTCATTCCCTAAA
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990S-0126264.
990S-0126785.
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99US-0130077

99US-0130449

99US-0130891

99US-0131449

99US-0132484

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99US-0134253

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S-0128234.
S-0128714.
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R 08-0CT-1999 99US-011 R 13-0CT-1999 99US-011 R 13-0CT-1999 99US-011 R 13-0CT-1999 99US-011 R 14-0CT-1999 99US-011 R 12-0CT-1999 99US-011 R 12-0CT-1999 99US-011 R 21-0CT-1999 99US-011	02-AUG-1999 90 90 90 90 90 90 90 90 90 90 90 90 90 9	R 27-JUL-1999; 99US-014 R 27-JUL-1999; 99US-014 R 27-JUL-1999; 99US-014 R 28-JUL-1999; 99US-014 R 28-JUL-1999; 99US-014 R 02-AUG-1999; 99US-014 R 02-AUG-1999; 99US-014

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RESULT
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25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
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28-OCT-1999;
29-OCT-1999;
                                                                   Determining predisposition of humans to develop autoimmune disease involves detecting polymorphic microsatellite repeat sequence with human costimulatory receptor gene locus \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1218
                                              Disclosure; Page 128-142; 160pp; English.
                                                                                                                                                                                                                                                                                                                        Graves disease; autoimmune hypothyroidism; myasthenia gravis; thymomathyroiditis; postpartum thyroiditis; rheumatoid arthritis; Hashimoto's disease; coeliac disease; ss.
                                                                                                                                                                                                                                                                                                                                                         Autoimmune disease; polymorphic microsatellite repeat; PMR; CD28 gene; ICOS gene; CTLA4 gene; costimulatory receptor gene locus; CGRL; lupus; insulin-dependent diabetes mellitus; IDDM; Addison's disease; leprosy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1098
                                                                                                                                                Ling V,
                                                                                                                                                                       (GEMY ) GENETICS INST INC
                                                                                                                                                                                                25-MAR-1999;
                                                                                                                                                                                                                       24-MAR-2000; 2000WO-US07938.
                                                                                                                                                                                                                                                  28-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphic repeat microsatellite sequences present in the CTLA4 locus
                                                                                                                                                                                                                                                                                                                                                                                                                                     08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A96367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            691 CCCGTCCTGCTTATTCATGGGGAAAAAACAGAATGTCATACCTCCGGAGGCGAGCCAAAAAA 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACTTGTTTTTGAACCAGGCGCGCGGTGAAAATCGTCACAGACATTGTAGAGTGGGTTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttgtataatcaggcaccatcagttttcaaagacatcaaactctatgacggtttcttacac 1157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cctttctttgttctccatggtacagaggacaaagtcactgatccactagcttcccaagac 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98;
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                                                                                                                                                Wu P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       874
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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99US-0161369.
99US-0161359.
99US-0161361.
99US-0161361.
99US-0161992.
99US-0161992.
99US-0161992.
99US-0161993.
                                                                                                                                                                                                9905-0126215
                                                                                                                                               Gray
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Pred. No. 3.3e-05;
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                                                                                  repeat sequence within
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Two and

human bacterial artificial chromosome (BAC) clones that included flanked the human CTLA-4 locus were cloned and sequenced. The uence data was assembled into a contiguous sequence that is presented

sequence

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RESULT
245596/c
ID 2455
XX 2455
XX 06-A
XX DDR DNA
XX Huma
KW mentt
KW hypc
OX Homc
CXX Homc
FT exor
FT pron
FT pron
FT exor
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Best Local Similarity
Thes 76; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC in A96363-68. A96363-64 comprise BAC clone 22700, and A96365-68 comprise CBC BAC clone 22608. The sequences contain polymorphic microsatellite repeat CC (PMR) sequences. The specification describes a method for determining the predisposition of a human subject to develop autoimmune disease. The cCC CTLA4 gene of the human costimulatory receptor gene locus (hCGRL). PMR cCC certa4 gene of the human costimulatory receptor gene locus (hCGRL). PMR cCC sequences vary in length among individuals and can be amplified to compare the products that differ in size. These products can then be ccc detected by rapid and convenient high resolution processes. The method is useful for determining the predisposition of insulin-dependent cc diabetes mellitus (IDDM), Addison's disease, Graves disease, autoimmune hypothyroidism, myasthenia gravis, thymoma, lupus, thyroiditis, rheumatoid arthritis, Hashimoto's disease, coeliac disease and leprosy. PMR sequences within hCRGL are useful as markers in a variety of assays and in the field of forensic medicine, cc disease diagnosis and human genome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44057 ggcaacatttttgt 44071
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                                                                 exon
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                                                                                                                                                                                                                                                                                                                                                                                                           Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAGCCTACCAATTAATACCTTCATTCCCTAAAGAGTTGAAAAAATACCCCGATCTTGGA 807
                                                                                                                                                                                                                                                                                                                                                                      PCTG4 region; X chromosome; q13 region; polymorphism; retardation; autism; depression; bipolar affective disorder; yroidism; OPA gene; neuropsychiatric disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          of the wild type human PCTG4 region of
/number= 3
/note= "human
2649..2805
                                                                                                                                                                     /*tag= b
/note= "human OPA promoter"
complement (1565..1815)
                                                                2321..2512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                             /number= 2
/note= "human
                                                                                                                                                                                                                                                            number=
                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                               *tag=
                                                                                                                                               note- "unknown
                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                              398..1648
                                                                                                                                                                                                                                           note- "human OPA exon"
                                                                                                                                008..2112
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                                                                                                                                             promoter"
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               promoter"
                                                                               promoter'
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exon	FT exon	exon	FT exon	FT exon	FT exon	FT exon	exon	exon	FT exon	exon	FT FT EXON	FT exon	FT exon	FT exon	FT FT exon FT	FT exon	exon
7	/number= 20 /number= 20 /note= "human OPA promoter" 9973.10104 /*tag= w	9 7	/number= 18 /note= "human OPA promoter" 89799122	/number= 17 /note= "human OPA promoter" 8674.8792 /*tag= +	Ø 7	82 , 7	73	74	7 - T	Q	55 - 7	/*Lag= k . /number= 9 /note= "human OPA promoter" 53775513	5 7	49 1	_4.ª !	/number='5 /note="human OPA promoter" 3962.4072 /*taq= h	<pre>/*tag= f /number= 4 /note= "human OPA promoter" 3608.3787 /*tag= g</pre>
					,												
FT exon FT exon	FT exo	FT exon	FT exon	FT exon	FT exon	ET exon	ET EXON	FT exon	FT exon	FT exon	FT exon	FT exon	ET exon	FT exon	FT exon	FT exon	ET EXO

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Best Local
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                                                                    (NOVO)
                                                                                                                                                                                              Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon
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          Monitoring differential
                               WPI; 2000-594572/56
                                                                                                  22-MAR-1999;
                                                                                                                      22-MAR-2000; 2000WO-US07781
                                                                                                                                                            WO200056762-A2
                                                                                                                                                                              Aspergillus oryzae
                                                                                                                                                                                                                                                             Aspergillus
                                                                                                                                                                                                                                                                                13-MAR-2001
                                                                                                                                                                                                                                                                                                                      F13210 standard; cDNA; 724 BP
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toring differential expression of genes in filamentous fungal cells fluorescence-labeled nucleic acids isolated from the cells and a
                                                                                                                                                                                                                                                                                                                                                                                                            AGTGAGGGACAGGTGTGTGTGTGTGTGTAAGTGGATGTGGAAGTAGGGTGTG
                                                  RM,
                                                                                                                                                                                                                                                                                                                                                                      CAGGGGGATACGGGCGTGTGTAG 38147
                                                                                                                                                                                                                                                                                                                                                                                          CGATAGAGAAAGAGGGTATGTGG 292
                                                                                                                                                                                                                                                                                                                                                                                                                              TGCTAGGCACGGATTTGGATTCTGCATGCACGATCAAAGGGGACATGGGAGAACGGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACAGGTAAGAGTATATGTGTGTAGGGAAGGGGAATATTTGTTTGTGTTTCTGAGGAGAT 38230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76;
                                                                     NOVO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                     NORDISK BIOTECH INC. NORDISK AS.
                                                                                                                                                                                                                                                                               (first entry)
                                                 MW,
                                                                                                  99US-0273623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "human OPA promoter"
26123..26275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "probable NL-3 promoter"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "human OPA promoter"
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                                                  Shuster
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                                                 JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35.8;
Pred. No. 1
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                                                 Clausen
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                                                                                                                                                                                                                                                                                                                                                                        cc same genes in one or more second filamentous fungal cells. Monitoring cc the global expression of genes from FF cells allows the production cropation of the microorganisms to be improved. New genes may be consisted and gene copy number variation and stability can be consisted and gene copy number variation and stability can be consisted and gene copy number variation and stability can be consisted to changes in culture conditions, cenvironmental stress, spore complete to changes in culture conditions, cenvironmental stress, spore completesis, recombination, metabolic or catabolic pathway engineering. Cc using ESTs provides several advantages over genomic or random cDNA cc using ESTs provides several advantages over genomic or random cDNA cc using ESTs provides several advantages over genomic or random cDNA cc using ESTs provides several advantages over genomic or random cDNA cc equals one gene or open reading frame, and organisation of the canalysis of the results. F07478 to F11247 represents ESTs from Aspergillus niger: cc F11854 to F11248 to F12
                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the
                                                                                                                                                                                                                                                                                                                                                                        Sequence 724
                                                                                                                                                                                                                                                                                                                                                                                                                                   specifically claimed in the present invention.
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          463
                                                                           337
                                                                                                                                      403 GCGCTCGGAACAGTTGCAACTTATAAAGAAATCGCCAAGGGAGTTATCGCGCTAGCCCCG
                                                                                                                                                                                                                                         Local
                                                                    gcgcccaggacggtcgcgagttctactgcaagggcaatgataccgccaccgccacggcct
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                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                        BP;
                                                                                                                                                                                                                                                                                                                                                                        142 A;
                                                                                                                                                                                                                                      3.98;
53.78;
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                                                                                                                                                                                                                                                                                                                                                                        236 C;
                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                  Score 35.2; DB Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                        170 G; 176 T; 0 other;
                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                        DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                          Cichorium intybus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicory; long germacrene A synthase clone; germacrene sesquiterpene lactone biosynthesis; bitterness; pest r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chicory germacrene A synthase B cDNA.
     12-MAR-1999;
                                                                                               10-MAR-2000; 2000WO-EP02130.
                                                                                                                                                                                                    21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A97449;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nematode; micro-organism; flavour compound; fragrance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   457
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99EP-0870046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e A synthase resistance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a 558 amino acid chicory germacrene A synthase ("short") chicory germacrene A synthase ("short") chicory germacrene A synthase sto a 1755 nucleotide ("short") chicory germacrene A synthase cDNA (A97448) and to its encoded product, the 583 amino acid germacrene A synthase A (B23174). Germacrene A synthases plays a key role in the biosynthesis of sesquiterpene lactones, catalysing the formation of a germacrane biosynthetic precursor from farnesyl diphosphate (FDP). Sesquiterpene lactones are bitter-flavoured plant products which provide resistance against insects, nematodes, microorganisms and vertebrate herbispose and as nesets included in
                                                                       Human; RING finger; leucine rich repeat; LRR; zapop3; chromosome 9q34.11; retinitis pigmentosa-deafness syndrome 1; apoptosis inhibition; myocardial infarction; dilated myopathy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microorganisms and vertebrate herbivores, and are also involved in
                             Homo sapiens
                                                                                                                                                                                                                                             Human RING finger protein zapop3 degenerate nucleotide
                                                                                                                                                                                                                                                                                                        16-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                           A30203 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1953 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-638203/61.
DB; B23175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTGGATAAA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGGGAAAA 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTTCGTAATACTGTAAGTCAATCTTCTCGAAGAGTTTGTTGAGTTCGGCATCAATCTCA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTTGAACCAGGCGCGGTGAAAATCGTCACAGACATTGTAGAGTGGGTTAAGAATCTAC 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATTAATACCTTCATTCCCTAAAGAGTTGAAAAAATACCCCGATCTTGGACACAACTTGT 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTITATAACCATGGTGTCTGAAAACTTGAAATTGTACTGCAATAGTGTACAAATCAACT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RES INST AGROBIOLOGY & SOIL FERTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kodde
                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.8%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Α;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synthase genes useful for reducing bitterness and against insects, nematodes, microorganisms and in plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٦
                                                                                                                                                                                                                                                                                                                                                                                                                                           2169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      De Kraker J;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 2
Pred. No. 0.63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    540 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1953;
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                                                                                                                                                                                                                                                 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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pigmentosa-deafness syndrome 1. In addition to gene therapy for this disease, the protein, nucleic acid and antibodies can be used to diagnose and treat myocardial infarction, congestive heart failure, hypertrophic cardiomyopathy, dilated myopathy, to limit infarct size following a heart attack, to aid recovery after heart transplantation, to promote angiogenesis and wound healing, to develop coronary collateral circulation, for revascularisation in the eye, for
                                                                                                                                                                                                                                                                                      similar to proteins with a RING finger sequence, with the full length clone being obtained from a peripheral blood granulocyte library. BRCA is an example of a RING finger protein. The gene is found on chromosom 9q43.11, and its looms is assectional.
                                                         complications related to poor circulation, for stroke, induction of skeletal muscle neogenesis and/or hyperplasia, kidney regeneration and treatment of systemic and pulmonary hypertension. In addition to a RING finger domain, the protein also contains eight leucine rich repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotides encoding zapop3 polypeptides useful for detecting chromosomal abnormalities comprising a sequence identical to a specific amino acid sequence, identity being determined by a specific program -
Sequence
                                                                                                                                                                                                                                                                                  9q43.11, and its locus is associated with retinitis
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 96-97; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                     present sequence is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-387737/33
                                                                                                                                                                                                                                                                                                                                                                esent sequence is the human zapop3 gene degenerate sequence. The protein was isolated by searching an EST database for proteins
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2169 BP; 414 A; 222 C;
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311 G;
249 T; 973 other;
                                                           rich repeat
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RESULT
A10594
ID A1
XX
AC A1
XX
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 62
                                           A10594 standard;
                                                                                                                                                                                                                                                                                                                     352
                                                                                                                 262
                                                                                                                                                                                                       472
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                                                                                                                                                                         202
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                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                              ytncaygayaaycarytnacngcnytnccngaygayytng 301
                                                                                                                                                                                                                                                           ACAGTTGCAACTTATAAAGAAATCGCCAAGGGAGTTATCGCGCTAGCCCCCGGCCCTCCAA 471
                                                                                                                                                                                                                                                                                      gcnggngcngaygayathytngayathwsnaartgygarytnwsngarathccnttyggn 141
                                                                                                                                                                                                                                                                                                                  TCTAAGATCACCTTACAAAGGAGATTGCCGCAGAAACCAG 571
                                                                                                                                                                                                  ATCCCCTTAACCCCGGCTAGAAGACTTGTTCTAAGCCTCGCGTCAAGGCTTGCCCCGCAT
                                                                                                                                                                      acnwsnytnytnccnaarwsntgywsnytnytnwsnytngcnacnathaargtnytngay
                                                                                                                                                                                                                              gcnttygcnacntgyaargtnytncaraaraargtnytnathgtncayacnaaycayytn
                                                                                                                                                                                                                                                                                                                                                62;
                                                                                                                                                                                                                                                                                                                                                Conservative
                                           DNA;
                                                                                                                                                                                                                                                                                                                                                              3.8%;
                                           10732 BP
                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                                                                                                                                                                               Score 33.8; DB Pred. No. 0.78; B6; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                122;
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BXB

29-JUN-2000 (first entry)

A10594;

Gene encoding a subunit of cellulose synthase.

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RESULT 9
F12459/c
ID F12459 standard; cDNA; 687 BF
XX
AC F12459;
XX
DT 13-MAR-2001 (first entry)
XX
DE Aspergillus oryzae EST SEQ II
XX
KW Multiple gene expression; fil
KW Multiple gene expression; fil
KW Multiple gene; Trichoder
KW Aspergillus oryzae; Trichoder
KW Aspergillus oryzae; Trichoder
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10397
   Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; anora morphoroconic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MIZU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a gene encoding a subunit of the cellulose synthates complex of Vigna angularis. The invention relates to subunits cellulose synthetic equipment, that can be used to increase the amount cellulose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being produced by a plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10732 BP; 3149 A; 1212 C; 2074 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 14-21; 32pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A gene encoding a cellulose synthetic equipment \cdot in the amount of cellulose synthesised in a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-FEB-2000
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                                                                                                                                                                                                                                                                                                  674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                agrgysvaasngyvaysgyhsgasargasnthrasasnsraavara 10682
                                                                                                                                                                                                                                                                                                                                                                                               athrgnhasnthrvathrasnasnthraathrthrsrthrargaaasnvaasrsrrhsry 10576
                                                                                                                                                                                                                                                                                                                                                                                                                               GATTGCCGCAGAAACCAGAGGGTTTTCAAAGAGCAAAAGATATAGAATACAGTCTGAGTG 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACTTGTTCTAAGCCTCGCGTCAAGGCTTGCCCCGCATTCTAAGATCACCTTACAAAGGA 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCGCCAAGGGAGTTATCGCGCTAGCCCCGGCCCTCCAAATCCCCCTTAACCCCGGCTAGAA 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-342371/30
                                                                                                                                                                                                                                                                                                CAGGGGAAATTAATACTCCCGTCCTGCTTATTCATGGGGAAAAACA 719
                                                                                                                                                                                                                                                                                                                               svaysvaysthrargsrasgnmtaaasassrysaagnrysaasrasgyasnsrasnrgyv 10636
                                                                                                                                                                                                                                                                                                                                                             AAATATCAGTCAAGCTCGTGGACGAAATGATTAAAGCATCATCTATGTCTTGGACCATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               raaaasrgysaagcysgngthrasngyysgnysaamtaaaarysasaasrhassrvavaa 10516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ysgggaayscysggngngsrmtsrysgcyssryshsasasysasysrargasnastrgth 10456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 18.9
54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIZUNO K.
OJI PAPER CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cellulose production; increase yield; ds
                                                                                                                                                                                   ВP
                                                                                  ID NO:4982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33.2; D
Pred. No. 3.2;
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RESULT X84328 ID X84

10

X84328 standard;

DNA; 2287

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                                                                                                                                                                                                                                                                                   expression of genes in a first filamentous fungal (FF) cell relative to cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTS cere used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the cere same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production of the global expression of genes from FF cells allows the production of contential of the microorganisms to be improved. New genes may be cell dentified and gene copy number variation and stability can be cell dentified and gene copy number variation and stability can be cell consitored. The expression of genes can be used to study how FF cells capt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PA PA XX
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. F07478 to F11247 represents ESTs from Fusarium venenatum; F11248 to F11853 represents ESTs from Aspergillus niger; F11854 to F14878 represents ESTs from Aspergillus oryzae; and F14879 to F15337 represents ESTs from Trichoderma reesei, which are all
                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method for monitoring differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 88; Page 2096; 3161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monitoring differential expression of genes in filamentous fungal uses fluorescence-labeled nucleic acids isolated from the cells ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NOVO ) NOVO NORDISK BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus oryzae
                             407
                                                                                                                                  327
                                                                                                                                                   287 ATGTGGAGGGCTTTCACAACTTCATAGAGGATATGAAGGCCTTCTCCCGATTATGCCCAAGT
                                                                                                 347
                                                                                                                                                                                                                   Local
                             TCGGA 411
CGGGA
                                                                CCCTCGGGGGTGAGGGTAGTAGTAGTACTGCCACGAGAACTGGGTCTTGACATAGCCG
                                                                                               RM,
                                                                                                                                                                                                   67; Conserv
                                                                                                                                                                                                                                                                                   687
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203
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                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                   BP;
                                                                                                                                                                                                                                                                                                                 claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000WO-US07781
                                                                                                                                                                                                                                                                                 143 A;
                                                                                                                                                                                                                53.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shuster JR,
                                                                                                                                                                                                                                                                                   207 C;
                                                                                                                                                                                                  0;
                                                                                                                                                                                                                 Score 32.2;
Pred. No. 1
                                                                                                                                                                                                                                                                                   185 G; 152 T; 0 other;
                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                   58;
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                                                                208
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Matches 42
                                                                                                                                                                                                                                                                                               invention relates to a method of detecting and characterising a stealth virus by reacting a sample suspected of containing a stealth virus with a probe from a known stealth virus and sequencing the resultant isolated nucleotide. The method comprises the steps of: (a) isolating DNA or RNA from a sample suspected of containing a stealth virus, e.g. a culture of cells showing a viral cytopathic effect; (b) testing the reactivity of the isolated DNA or RNA with a molecular probe that contains at least 18 or more contiguous nucleotides identical to sequence previously identified from a stealth virus; and, optionally (c) sequencing the isolated DNA or RNA molecules that react with the probe. The method is used to detect stealth virus in a biological product, food or in the next of the probe of the probe of the probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers misc_difference 2167
                                                                       2091
                                                                                                                                                                                                                           Sequence 2287 BP; 531 A; 550 C; 548 G; 486 T; 172 other;
                                                                                                                                                                                                                                                  inhibitory or stimulatory effects on stealth virus replication and to determine capacity of the virus to recombine with and potentially alter the nucleic acid sequences of a cell or bacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 19; Page 59-60; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-405521/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Martin WJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MART/) MARTIN W J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stealth virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stealth virus; detection; diagnosis; infection; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stealth virus nucleic acid clone, SEQ ID NO: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X84328;
                                                                                                                   2031 vngnrmamhadataragrahntwhnmartndatnstathbcdcmbgtmsnwrmansymba 2090
                                                                                                                                                                                                                                                                                     environment. The method is also used to evaluate agents for their
                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a Stealth virus nucleic acid clone. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel strains of stealth virus
                                               702
                                                                                                                               582 AAGAGCAAAAGATATAGAATACAGTCTGAGTGAAATATCAGTCAAGCTCGTGGACGAAAT 641
762 AATACCTTCATTCCCTAAAGAGTTGAAAAAATACCCCGATCTTGGACACA 811
                                                                                GATTAAAGCATCTATGTCTTGGACCATAGCAGGGGAAATTAATACTCCCGTCCTGCT 701
                      dbbcttdgdanbcdaanrtntrywyvtabwrddcmntsmmarynrmatndcmntsmmary 2210
                                              TATTCATGGGGAAAAACAGAATGTCATACCTCCGGAGGCGAGCAAAAAAGCCTACCAATT 761
                                                                      rahbcwhnmartnwhnmartnhddtbcbwhnmartnnrmawhnmartnmcrstwrddhcc 2150
                                                                                                                                                                   42;
                                                                                                                                                                               Similarity
                                                                                                                                                                   Conservative
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/note= "this nucleotide is represented as a * in the
specification, and is included to maintain th
base numbering given in the specification"
                                                                                                                                                                               3.6%;
18.3%;
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AC C4
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25-MAY-1999;
27-MAY-1999;
28-MAY-1999;
01-JUN-1999;
04-JUN-1999;
04-JUN-1999;
07-JUN-1999;
10-JUN-1999;
10-JUN-1999;
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21-MAY-1999;
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07-MAY-1999;
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protein identification; signal transduction pathway;
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29-MAR-1999
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05-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  metabolic pathway; promoter; termination sequence;
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99US-0138540.
99US-0138847.
99US-0139119.
99US-0139452.
99US-0139453.
                                                                    99US-0137724
99US-0138094
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99US-0137502
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99US-0135353
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99US-0134941
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99US-0134218
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99US-0132486
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990S-0134221
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Best Local Similarity 51.0%;
Matches 104; Conservative
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20-AUG-1999
20-AUG-1999
20-AUG-1999
21-AUG-1999
23-AUG-1999
25-AUG-1999
27-AUG-1999
28-SEP-1999
29-SEP-1999
21-CCT-1999
22-CCT-1999
23-CCT-1999
24-CCT-1999
25-CCT-1999
26-CCT-1999
27-CCT-1999
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29-CCT-1999
21-CCT-1999
                    909
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                                   cgagaggg-----tcagggaggttagtaagagaagtgatggagatgttggaagagtacaa 1376
         TCTGAGTGAAATATCAGTCAAGCTCGTGGACGAAATGATTAAAGCATCATCTATGTCTTG
                                                                                                              990S-0149175.
990S-0149723.
990S-0149930.
990S-0149930.
990S-0151086.
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990S-0151086.
990S-0151333.
990S-015138.
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990S-015138.
990S-0154018.
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990S-0154018.
990S-0154648.
990S-0154648.
990S-0158331.
990S-0158332.
990S-0158331.
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990S-0159331.
990S-0159331.
990S-016081.
990S-016081.
990S-016081.
990S-0161105.
                                                                        Score 32; DB 2
Pred. No. 2.7;
0; Mismatches
                                                                                            21;
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                                                                                           Length 1648;
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                                      1321
                    665
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18-JUN-1999
18-JUN

990S-0139455 990S-0139459 990S-0139459 990S-0139461 990S-0139461 990S-0139461 990S-0139750 990S-0139753 990S-0140695 990S-0140695 990S-0140695 990S-0141287 990S-0141287 990S-0142803 990S-0142803 990S-0142803 990S-0142803 990S-0142803 990S-0142803 990S-0142803 990S-0142803 990S-0142803 990S-0142915 990S-0144332 990S-0144332 990S-0144333 990S-0147303 990S-0147303 990S-0147303 990S-0147303 990S-0147303 990S-0147303 990S-0147333 990S-0147333 990S-0147303 990S-0147303 990S-0147303 990S-0147335 990S-0147335 990S-0147335 990S-0147335 990S-0147335 990S-0147335 990S-0147335 990S-0147335 990S-0148341 990S-0148341 990S-0148341

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                                                                                                       Matches
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Best Local Similarity
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18-MAR-1998;
27-JUL-1998;
27-JUL-1998;
                                                                                                                                                                                           cancer. The polypeptides and monoclonal antibodies specific for the polypeptides can also be used to inhibit the development of lung cancer. Agents which bind the polypeptides can be used for detecting lung cancer and for monitoring the progression of lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1377
                                                                                                                                                                                                                                               cancer. The polypeptides and polynucleotides can be used to stimulate T cells or antigen presenting cells for use in the treatment of lung
                                                                                                                                                                                                                                                                         The invention provides isolated human lung tumor nucleic acids and polypeptides. The polypeptides can be used for the treatment of lun
                                                                                                                                                                                                                                                                                                                                                                                                                        Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1437
                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                 Claim 1; Page 65; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; lung tumor; lung cancer; T cell stimulation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lung tumor associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-DEC-1999
                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                   New
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                            559
                                                    479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
                                                                                                                                                                                                                                                                                                                                                  isolated lung tumor polynucleotides, used to develop products for treatment, prevention and monitoring the progression of lung cancer % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATACCTCCGGAGGCGAGCAAAAA 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACCATAGCAGGGGAAATTAATACTCCCGTCCTGCTTATTCATGGGGAAAAAACAGAATGT 725
CCTTCCCAACCAGAGGGTTCTGGAAGACCAAGATACTGAAGATACAG
                        CCGCAGAAACCAGAGGGTTTTCAAAGAGCAAAAGATATAGAATACAG
                                                  GTTCTTTCCATCTGTTAAAGTAGTACACTCCAAAGGGAAATGACCAGTAAAAAATGATCC 420
                                                                           GTTCTAAGCCTCGCGTCAAGGCTTGCCCCGCATTCTAAGATCACCTTACAAAGGAGATTG 558
                                                                                                                                                                                                                                                                                                                                                                                                                      SG,
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                                                                                                        60;
                                                                                                                                                                        694
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                                                                                                     3.6%;
nilarity 56.1%;
Conservative
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98US-0040984.
98US-0123912.
98US-0123933.
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                                                                                                    Score 31.8; DB Pred. No. 1.9; 0; Mismatches
                                                                                                     0;
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                                                                                                                                                                     222 T; 14 other;
                                                                                                                               DB
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                                                                                                                              20;
                                                                                                     47;
                                                                                                    Indels
                                                                                                                            Length
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373
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RESULT 13 C65752/c

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Best Local :
                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel isolated polypeptide (I) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polypucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are treated with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit development of cancer.
           07-FEB-1997
                                                              T45666 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-DEC-1999;
30-DEC-1999;
10-JAN-2000;
22-FEB-2000;
                                        T45666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in a
                                                                                                                                                                                                                                                                                                                            Sequence 694 BP; 173 A; 136 C; 148 G; 223 T; 14 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim la; Page 98; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polypeptide comprising an immunogenic portion of a lung tumor protein is used for detecting and monitoring progression of lung cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-APR-1999;
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vaccine; detection; ss.
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l Similarity 56.1%;
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                                                                   DNA;
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   vaccine;
                Enterococcus
                                        Enterococcus
                                                              19-MAR-1999
                                                                                                              X12966 standard; DNA; 7156 BP
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 6-10; 16pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA molecule involved in yeast flocculation - useful for if a sample yeast has a flocculation activity
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fermentation;
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ccus faecalls; contig; detection; Enterococ
attenuation; computer readable medium; ds.
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Pred. No. 4.4;
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Matches 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                               New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                         Sequence 7156
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Search completed: June 2, 2001, 22:15:36 Job time: 30434 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Result		Query		
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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Eukaryota; Viridiplantae; Embryophyta; ?
                                                                                                                                                                                                                                                                                                                                                                                                                       Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes and 5 can be viewed at: http://www.mips.blochem.mpg.de/pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (13-APR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: Bencke@mips.biochem.mpg.de,mayeremips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
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1 (bases 1 to 93205)
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                                             musculus,
                                                                                      complement(join(18058. .18417,18648.
/gene="T22P22_10"
                                           /note="similarity to MAP nusculus, EMBL:AF117340"
                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis
/variety="Columbia"
/product="putative protein"
                      codon_start=
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                                                                                                                                                                                                                                                                                         /db_xref="taxon:3702"
/chromosome="5"
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/number=3 21551. 21592 /gene="T22P22_30"	/number=3 2145621550 /gene="T22P22_30"	/number=2 21386. 21455 /gene="m22P22_30"	I	/number=1 21245. 21301 /gene="T2P22_30"	/number=1 21182. 21244 /gene="m222P22_30"	PDFYVDAAPSLPITKKLLCQHFELDRLLLDYINGT" 2099021181 /gene="T22P22_30"	/db_xref="G1:7573378" /translation="mekkregviegmsrivsdpyyflhfmaffsylpirssaapytsh /translation="mekkregviegmsrivsdpyyflhfmaffsylpirssaapytsh RLFDREIQAFLAFLMFSAIKMVREETWEAFVADSLLYAKIFLIAVSLIMDYRVAVWFS IIFSVIYLLAQQPAFSKLGTAKKLTPMQLEDLLSDGNTTKYWLIEFFACSSKCVRSS RCFPELSTTYSNNLLSFGTVDLGLFPNTAAKFGISLAGGMSOLPTYILFEKGVEVSRF	metanogaster and homo sapiens" /codon_start=1 /product="putative protein" /protein_id="CAB87682.1"		~ ` NI	/!mmber=2 2099022685 /dene="722P22 30"	19741 19891 /gene="122P22_20"	19658. 19740 /gene="122P22_20" /number=1	T = T	/ VI_ALCH GIT (1977) / UTANS ARTON ASSECT STATEMENT OF THE STATEMENT OF TH	/codon_start=1 /product="putative protein" /protein_id="CAB87681.1" /Ab rps="G1-7573377"	/yene="12722_20" /note="8imilarity to predicted proteins, Arabidopsis thaliana"	/gene="122P22_20" join(1927. 19657,1974119891)	Comptement(1804019109) /gene="122P22_10" /number=2 1957719891		ALL VICRAMPANNSSKNINVGUNNENCHGNCYLNLAPYVDEEVEDGVGTSQRPC" complement(1805818417) /gene="122P22_10" /number=1	NAGTFHVLGATCNVYTVTLMATPTCTCPDRKKPCKHILFVLIRVLGIPLDDKCLRQRR LRTCLLFHLFSAPTRPDCLASFRLQQRFLQLFPATTSQPGYTTNSSSSTSKMENEVDE EPATCPICLDDIIAIENVDGGNGGKEKETAVVKCRVCKNKVHDECMLAWRKSRGRRP	/protein_id="CAB87680.1" /db_xref="GI:7573376" /translation="MESVCSNOTSPYVSNRDORHFLAODVADRTLRALRHRIRLLHRP
intron	exon	intron	exon	intron	exon	intron					CDS	gene	exon	exon	intron	exon	intron	exon	intron	exon	intron	exon	intron
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                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (08-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Dec 7, 2000 this sequence version replaced q1:9838177.
Insert size: 177000; agarose-fp
Insert size: 192278; sum-of-contigs
Quality coverage: 6.09 in Q20 bases; agarose-fp
Quality coverage: 6.41 in Q20 bases; sum-of-contigs
                                                                              Sequencing vector: plasmid; 20%
Chemistry: Dye-primer ET; 48% of reads
Chemistry: Dye-terminator Big Dye; 30% of rea
Chemistry: Dye-terminator Big Dye; 30% of rea
Rosembly program: Phrap; version 0.990319
Consensus quality: 187685 bases at least Q40
Consensus quality: 188494 bases at least Q30
Consensus quality: 188988 bases at least Q20
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Summary Statistics

Sequencing vector: M13; 58%
                                                                                                                                                                                                                                                                                       Web site:http://genome.wustl.edu/gsc/index.shtml
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/gene="T22P22_40"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              748 AAAGCCTACCAATTAATACCTTCATTCCCTAAAGAGTTGAAAAAATACCCCGATCTTGGA 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
Allen, N., Allen, R., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Callins, S., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreita, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gyette, M., Graham, L., Garand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Grand-Pierre, N., Lieu, C., Liu, G., Locke, K., Landers, T., Lehoczky, J., Klein, J., LaRocque, K., Landerson, K., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murnhy, T., Navier, L., Norman, C. H., O'Connor, T., O'Donnell, P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAATCCTACCAAGTCATATTTTAAGTCCAGAAAAGAAATTTTAAACAACTGGATCTTCTG 66590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC055772 135978 bp DNA Mus musculus clone RP23-291K4, ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Similarity 76; Conserv
                                                                                                                                                                                                                                                                                                                                     Unpublished 2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 135978)
Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                              Mus musculus chromosome, clone RP23-291K4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC055772.4 GI:12658107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          be preserved
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                                                                                                                                                                                                                                                                                                                                  (bases 1 to 135978)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189667
189767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig11"
37556 c 39086 g 57696 t
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/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="RP11-388A17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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56.3%;
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189766: gap of unknown length
190159: contig of 393 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                         Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40.6;
Pred. No. 1.
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Musinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59;
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BASE COUNT
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                                                                                                                                                                                                                 35183 TATCTCTGAATTTGCTGATCTCTCGGGATATCAAATCTCTTTTGTCTTCTTCCATTTCAA 35242
                                                                                                       source
                                                      737
                                                                                                                                                                   677
                                                                                                                                                                                                                                                                       617 TATCAGTCAAGCTCGTGGACGAAATGATTAAAGCATCATCTATGTCTTGGACCATAGCAG 676
                                                                                                                                                                                                                                                                                                                                                          Local Similarity
AGAAAAATAACAAAATTTAGTATTTAATGCAAGTATTACAAATACATCTAAGTAAAAACCC
                                                   AGGCGAGCAAAAAAGCCTACCAATTAATACCTTCATTCCCTAAAGAGTTGAAAAAATACC
                                                                                                                                                             GGGAAATTAATACTCCCGTCCTGCTTATTCATGGGGAAAAAACAGAATGTCATACCTCCGG
                                                                                                                                                                                                                                                                                                                                   116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (18-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 3, 2001 this sequence version replaced gi:10800282
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40364 a
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Center clone name: 291_K_4
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128933 135978: contig of 7046 bp in length.
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108184 12883:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                Conservative
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82104 82203:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="Rep23-291K4"
/clone= "Rep23-23 Female Mouse BAC"
/clone lib="Rep21-23 Female Mouse BAC"
/28264 c 27650 g 38838 t 862 ot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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128832: contig of 20649 bp
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85587: contig of 3384 bp in length
687: gap of 100 bp
108083: contig of 22396 bp in length
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                                                                                                                                                                                                                                                                                                                          Score 40.4; DB Pred. No. 1.8; 0; Mismatches
                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                 DB 72;
                                                                                                                                                                                                                                                                                                                             126;
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KEYWORDS
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AC013530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 5, 2000 this sequence version replaced gi:8096882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 216493)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tesfaye,S., Tirrell,A., Vassıılev,H., vo
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
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                              Quality coverage: 6.3 in Q20 bases; agarose-fp Quality coverage: 5.6 in Q20 bas.

NOTE: This is a 'working draft' sequence. It currently consists of 46 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                              Summary Statistics
Sequencing vector: M13; M77815; 99% of reads
Sequencing vector: M13; M77815; 99% of reads
Sequencing vector: plasmid; n/a; 1% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 182913 bases at least Q40
Consensus quality: 197325 bases at least Q30
Consensus quality: 204893 bases at least Q30
Consensus quality: 204893 bases at least Q20
Insert size: 188000; agarose fp
Insert size: 211993; sum-of-contigs
arbitrary. Gaps between the contigs arruns of N, but the exact sizes of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L1950
                                                                                                                                                                                                                                                                                                                                                                                                            Center clone name: 114_M_7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seg.wi.mit.edu
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                    between the contigs are
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This record will be updated with the finished sequence as soon as it is available and the accession number will
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34443 75923: contig of 41481 bp
7594 76023: gap of 100 bp
76024 77521: contig of 1498 bp
77522 77621: gap of 100 bp
77522 77623: gap of 100 bp
79524 79623: gap of 100 bp
79524 79623: gap of 100 bp
81286 81385: gap of 100 bp
81286 8505: gap of 100 bp
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6258 6357: gap of 100 bp
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88776: contig of 10

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77 90854: contig of 10

75 90954: gap of 10

55 90354: gap of 10

35 9334: gap of 10

35 9334: gap of 10

36 9547: contig of 2
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9447: gap of 10
96799: contig of 10
1899: gap of 10
98898: contig of 10
1998: gap of 10
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Pred. No. 2.4;
0; Mismatches 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         elongation factor g; elongation factor tu; fus gene; ribosoma protein S7; rps7 gene; tuf gene.
Apple proliferation phytoplasma
Apple proliferation phytoplasma
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 226
99107774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chromosomal organization and nucleotide coding for the elongation factors G and proliferation phytoplasma Gene 226 (1), 103-109 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-SEP-1998) Seemueller E., im Obstbau, Biologische Bundesanstalt, Dossenheim, D-69221, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apple proliferation AJ011104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seemueller, E
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PIQLPIGSENEFKGITVLLEWTGVEFLGTSOBKFKTIEIPEXMKEPAQNKRIELIEKW
HNYDEELMMDYLNGKEITVEKLKNVIRQATLKADFFPVLGSAFKNKGVKKILDAIID
YLDSPHDVSSIVGCNFENKEIIRKTSONEPFTALAFKVWTDPYVGKLTFFRVYAGTIK
TGSYVTNATKQVKERLGRILQMHANSREEIKEVYAGDIVAAVGLKNITPGDTITSIND
DIILESMNFPEPVIEIAIEPKTKADQOKIGIALSKLSEEHPTFKIYTNRETAGTIIA
MGELHLEIILDRLKTEFKVEANVNQPQVAYRETLTKISTTEKFIRGSGRRQYGHVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Apple proliferation phytoplasma"
/strain="AT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                /product="elongation factor G"
/protein_id="CAA09487.1"
/db_xref="GI:4127381"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="lknimpelevrsrriggqkyqipsevrperkqslglrwlvqfaq
krnektmqqklakeiidaasgnglavkkreeihrmaeanksfahyrw"
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                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                       /gene="fus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               641 TGATTAAAGCATCATCTATGTCTTGGACCATAGCAGGGGAAATTAATACTCCCGTCCTGC 700
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                                                                                                                                                                             Plasmodium falciparum MAI3P7, complete sequence.
AL034559 AL008974 AL008975 AL008981 AL008983 AL009015 AL010138
AL010143 AL010146 AL010154 AL010157 AL010160 AL010165 AL010169
AL010187 AL010189 AL010207 AL010208 AL010214 AL021885 AL021888
AL139179 Z98556 Z98557 Z98558
AL139179 Z98556 Z98557 Z98558
AL034559.4 GI:8052273
HTG; 40S Ribosomal protein S3A; acyl transferase; acylaminoacyl-peptidase; ATP-dependent RNA Helicase; cyclophili elongation factor; F49C12.11-like protein; HesB-like domain protein; histone H2A variant; kinesin-related protein;
                                             Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                              N-acetylglucosamine-1-phosphate transferase; protein kinase; R-CG7 repeat; R-FA3 repeat; repl1; rep20; rifin; RNA-binding protein; stevor; T-complex protein 1 epsilon subunit; telomere; var.
                                                                     Plasmodium falciparum
                                                                                           malaria parasite P. falciparum.
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/gene="tuf"
2446. .3624
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YKFDQDKTPFVRGSALKALEGTDVEGINKLLEVLDEVIEDPIRDVEKPFLMPVEGVHT
ITGRCTVATGRVERGKIKISEEVEIIGLKETKKAIITGLEMFKKELDFAQAGONVGILL
LRGITRDQIERGQVLAKPGSLNAYHKELSQVYILTQQEGGRHTAFFSNYRPQFYFRTT
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  Basham,D.,
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  Brown, D.,
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Chillingworth, T.
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                                                                                                                                                                                                                                    cyclophilin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
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                                                       misc_feature
                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On May 24,
For more in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (17-DEC-1998) P.falciparum Genome Sequencing Con
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oliver, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The complete nucleotide sequence of chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 400 (6744),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 253305)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 253305)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           May 24, 2000 this sequence version replaced gi:4725992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"PFC0860w (MAL3P7.1), Kinesin-related protein, len: 1200 as: similarity: to kinesin-related protein.
D.melanogaster kinesin-like protein (TR:P91945) BLAST Score: 664, sum P(2) = 1.9e-67; 28% identity in 707 aa overlap, predicted using hexexon, Pfam: match to PF00225 kinesin, Kinesin motor domain Score 311.54"
                                                                                                                                                                                                                                                                                                                      GSYINGSLLALANČINSLASNRNISKVRVKYRDSKLTHLLKNSLEGNCLVVMIANING
SRTSFOESNNTLKYAFFARNIKLCATVGTNDNKESDIEK ILKKRENLOKEYDTLLGKY
TNLKEFFFILAVINGLYKKOLSCYKLIENISDNMSSNELKODITMYDGLYKMKSDSYR
KKVDSLKDLYQEEKQFLNNLFDTFLEKNLNYVINSKDVNDNNKSLLEEMIFFKHNENK
VNENFLVNEKVVDKNVVLNGNWYDENVMVDENVMVDENVMVDENVMVDENVMVDENVMVDENVMVDENVMVDENVMVDENVMVDENVMVDENVMVDENVMVDENVMVDENVMVSYNENITYVEKHKYGLS
AEGKSESHNKNNKDDIEDNDKDTIKDIHNNNNSSDNNDDEYQSANSPVESDIVKKEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYPNINGEPSTSVENITNGEHFINGQYDALKNMSLNYDHQHNNIMNISNKNKLFVL
NNNNNNNDVIENMNEYPTSKNIYDSIYIFQINIKNIINSKNKNLFVL
NYTNJHNNNNNSHPTSKYTSKNERNNLLTHLNAYSNYKVAVRIKPTGESEENIVS
IFNKNYVLIEKENEKECYLLSOKKKOSTYVFDSVFDVNATQEEVFFQTAKPLIPHVFK
GINCTYAYGAYGSGKTYTMLDDKNQNGTVQUSILELFTIINEKCRNIXVLMSFLEV
YNETJHBLLGKEKNKTLEVQEDVAFVKVSNLCEEIEVNNYBQAMLLINEGVKNRKMSFLEV
RANKVSSRSHAILQIYVYNEILDDNMNTISYKAKLCFVDLAGSERASATSNKGERFKE
4057. 4062
/note="potential splice donor indicate splicing"
                                                                                                                                                                                        DIHLTSIDTISKIHARDLLKENKRKLENFQENIKHEHKDEVSLYVKKKKIKKKM"
                                                                                                                                                                                                                    NNNNNNSSSSSGKVDGINILNNSNTNERLHTFSGVYSLNLNDEIKIEINKKDMEKN
                                                                                                                                                                                                                                                                    EKKGEYNPFHNNLTDMQNSTLYNTINNNVENSPHSPRMKKNVAKMLLKGNLNTANFTL
                                                                                 indicate
                                                                                                       /gene="PFC0860w, MAL3P7.1"
/note="potential splice do
                                                                                                                                                                                                                                                DDDT I KNMNSNK I SDKHNMKSNNI LNNENGK I NDKSKKCKNI NNNNNNNNNNNNNNNN
                                                                                                                                                                                                                                                                                                     KKIPINMETKKKRTMNGTKDPIHKTPYDINIVGILNKEDVSNKSNDYNTNKNIEKNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTNNILNYNDHTLKLICNITENNKAILHSNKSNLQKNNILMPSYMQKKGTHIRETIKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAB39023.
/db_xref="GI:4493964"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="kinesin-related/
protein_id="CAB39023.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         458. .4060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation-"MRKTKNLNDPFFLNNYYYNKEENNPIIICSDEKERKTKIYSTNH/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SPTREMBL:097277"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:5833"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Plasmodium
/strain="3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="PFC0860w, MAL3P7.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="PFC0860w,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'clone="MAL3P7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bowman,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253305
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                                                       splicing"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAL3P7.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         falciparum"
                                                                                                       donor
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                              at 3′
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                                                                                                             end
                              end
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                                                                                                          of
                           of PFCo860w may
                                                                                                             PFCo860w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Consortium,
on, Cambridge
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                                                      /db_xref="Sprewbl:097278"

//db_xref="Sprewbl:097278"

//db_xref="Sprewbl:097278"

//translatlon="MKDFLSYAENNDLNIFKLYNSEEDCLKNLKYAIELKSEDFKNVN

//translatlon="MKDFLSYAENNDLNIFKLYNSEEDCLKNLKYAIELKSEDFKNVN

//translatlon="MKDFLSYAENNDLNIFKLYNSEEDCLKNLKYAIELKSEDFKNVN

SLELNDDILNIHENDKNSLLY KLHTNI INIKSSEFNIKYEFYNFYKNNLVETKYSC

RPHILKYVKNTEFYKNE IKDI KNLKNENHYTQYFNDDRKKLFFYNNVYSKNLVETKYGNPHL

YYPYTLESDKK INEKNERNEKNERNEKNERNEKNEKNEKNEKNLLISSTUNNVYMK

NGIOSYHNNSINSNDDQKKKNNNNNYYYYNNPDGLITNVKYXIRVGDYALLNSNEK

YFFNDININLKQNFINFNTYDDLSFNIYFNSYYYESFFILVNYGYDEKGGKYKTELK

KNNLLTPRYDE INELNKERE ITMEYKTDEKEYQVNNEYINNVGYDEKGGKYKTELK

KNNLLTPRYDE INELNKERE ITMEYKTDEKEYQVNUEYINNICFDINKERKINIENFL

CCLKINKYYYYSWLLFYFILFFENITFNVVFLCVCLFIVNICFDINKERKINIENFL

CCLKINKYYYYSWLLFYFILFFENISHMLIICSIVSFVLLICLIYYIYYKRKMN

MLMTKYRGKSKSITNDKRKKSQQKTYEYGNINYDMSEKYPTHQLKDNSNDFMLEGSDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(7801. //240,0000...)

/gene-"PFC0870w, MAL3P7.3", putative elongation facto:
/note-"PFC0870w (MAL3P7.3), putative elongation facto:
len: 181 da; Similarity to P. falciparum elongation f.
len: 181 da; Similarity to P. fasta scores: opt: 366,
1.1e-15, 53.2% identity in 141 da overilap, revised:
shortened exon 2, Pfam: match to PF00736 EF1BD, EF-1
shortened exon 2, exchange domain Score 61.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MS580. .8585

MS580. .8585

/note-"potential splice donor sequence may indicate further splicing of PFC0870w"

join(11431. .20416,20578. .20690)

/gene-"PFC0875w, MAL397.4"

/note-"PFC0875w, MAL397.4"

/note-"PFC0875w (MAL397.4), hypothetical protein, le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identity in 297 aa overlap, predicted using hexexon, Pfarmatch to PF00076 rrm, RNA recognition motif. (a.k.a. RRM RBD, or RNP domain) Score 58.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VNTDELIETIENLGLDNEQLQKKKQMDDDEENYDEDDEIGGLVQSAEIISFNKL"8235. .8240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mantyDeLyvpLSyyILQNEGGNTSKIDQANTKKPKKEVINKS
SLIIDIKPYGENTDLDEVLKLVKNITMEGLTWGKAHKKTPFAFGLFKLQVSCVIVDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKDKKSHKRRHKHSYDKYSSRSRSYSTSSSTDR"
join(7801. .7928,8084. .8234,8392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MGLFDKIRNIEKLNEAELKNIGNNDSSWHDQYRDSSYIYIGNLD
NRLTEGDIVIYFSQYGEFIDVWLVRDWETGKSKGYCFLSYADQKSTILAVDWFNGYKL
LERPLVVDHILUYRLPKKYLKDADKWEYKPTGAEGGGIGVYNVVESEIKLKKVEPDKI
NKSNEEKKKKLLDEDELWALNFEKSIKKDIISPIGHDEKSRHNEGMKEEEEDEDDEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(5457. .5577,5689. .5787,5923. .6077,6189. .6743)
/gene="PFC0865w, MAL3P7.2"
join(5457. .5577,5689. .5787,5923. .6077,6189. .6743)
/gene="PFC0865w, MAL3P7.2"
/note="PFC0865w, (MAL3P7.2), RNA-binding protein, len
                                DDTCYELDTLHKKQVNSQMCLRIEKIRNDRRESNGHPYDIPMIPLRHNNNINNNINNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical
/protein_id="CAB39024.;
/db_xref="GI:8052275"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(7801. .7928,8084. .8234,8392.
/gene="PFC0870w, WAL3P7.3"
join(7801. .7928,8084. .8234,8392.
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/protein_id="CAB39067.1"
/db_xref="GI:4494008"
INNNINNNINNNINNNQHRNNQCYLIIQNVNKFYGKKHALKDVSLTLRSNRIFVLLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3032 aa, revised:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative elongation factor"
/protein_id="CAB39068.2"
/db_xref="01:8052274"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="revised splice donor sequence for exon 2 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      )DEDDDDDDSVDIKYKRHKEKRKSLTTKKYDKKEKHKRKSDHRDKHRRRENHSRHREK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TR:(218318) BLAST Score: 378, sum P(1) = 3.8e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'db_xref-"SPTREMBL:097319"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAL3P7.4), hypothetical protein,
added 3' exon, possibly spliced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L protein, PFC0875w<sup>1</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .8583)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spliced at 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor,
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Db 169851 ACAAGTATGAATATTCATGAAGAATATATACATTTTGTTAAAATATTAAAAGATATTCAT 169910
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 ATAGTTATGAAGACTGTGGAAGAGTATGCGCTACTTGAAACAGGCGTAAGAGTGTTTTAT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGCACAGTGGAATCTACATTAGTGTTGCTGAAGAATTTGCTA 214
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F., Boguslavkly,L., Boukhgalter,B., Brown,A., Castle,A., Colangelo,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC016984 162930 bp DNA Mus musculus clone RP23-48C4,
                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                   Mus musculus, clone RP23-48C4
                                                                                                                                                                                                                         Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC016984.4 GI:12718901,
                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                            (bases 1 to 162930)
                                                                                                              (bases 1 to 162930)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTGS_PHASE2.
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SFFNTSDFYFLLINCIIYLSIVFYKLLQIIFSKEFTDKKRESEKTINYEBIILINSYN
VGVQBKKEQKKNRYFFFLKNFYLSNEWYKQFKENYEKNRNPFFYFIQKILSHLIKRGNUY
DENNTTMGIYKYGEKYDSNNYISEDEININNQLNSEGYLKNDIYMNELNDNYNNDFDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FHEHFMRDFYINIYVFLSIVIFFCVFFERFKNEIENRKIFENFHVHQYIHYFQILLLE
YLYYFIYILCLFIVLYIFDYKEFLFMSFFCFLLLYGFNIFLSICLFSSLYLHSYILFL
FFNFIFCGIISIVIYVLVILSYAYNNEILINLSHVLVCIFRIFDSFALSHVLNIRSLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DILYYDYLYLFNKNKITYKNYTTNIKNNFKKFYSFQIKLKGIRDSKIIDYVHMFFSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KFDESNDISYTSNDVLKGDDDMLSLRRNTKESKRNKNKINKKKKENELILETYDIEK
TNMNQLGSNLSNSNYLECNISSNMNSVNEPIIHSFIKENILKIKEGIENEVIYTHIYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NTVDIEMQISEKSNIKEKMLYKETEIDKYYKGQSDDDNDEEKNFNKISQKYILKNLNI
KMRPYKIYTESSIFNNDLNILYFFKYFFCNNKDNLKGSLQTIAYGQNYEINNKFINKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSYNNNEEEEDINGNINYNDSNNIYITPKKNNKEEENNFLVKKLKKRIDTLNEPFNIK
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ETLETRNDTDVNKEVEININLFYNYTSIHSYAYYTNSLFNMLSDFQNILNKKSGNKNI
ILDGSTYDNIKVVEDVKGNCDMNTLLYDKENKYNYLIKDIDNKNIREECNANFRLSKN
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TKQDDNAEESHINNNDHNDNIKDILKLENNEYNYNKLIHENSFNYYNSTINSLLQKYC
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NFFTTYIKPTLLLKLKKDLGSSSFYWYKFIVPLFLLSFGLLIIKCVSLFGKVQNIDLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YCTYK INELESLKKLLCVLNKFKNILTYQLKTIDIYYTY IYITYLNEKKKLLKNIQDK
DIKYLIEIDPLFFLFFQNFKY FNELNNLLLMKNNHMQPISYNFAYLRDILVRGNENKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YYIFKTMKKKKYNSKKKKGNLISLCKFHKILLNLMIDKYSYLHSYLSRNKYISIFHLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KHAFARFEKVIKKMDDKNSKKPKKKKKKLISPKDMPSNSIILFLENNVKRNVLNVHNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VNLKCDIHINCNQLSGGMKKKVELMINLLRDDKIIFLYKLNDNIDFCSQIYINIILKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I I NSTNHDDNPYD I NMYNNHNKYGKYKNNNNNNSFYNMRDDTELTD I EEN I SSKKKKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNKNNSVDHIDHLFDILVTNINEFTNNRDIIKKNIIKFIKGTRNENKNCFIFFNENHI
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52.8%;
                                                                                                                                                                                                                                                                                                                                    Chordata;
                                                                                                                                                                                                                                                                                                  Rodentia;
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                                                                                                                                                                                                                             Nusbaum, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39.8; D
Pred. No. 2.8;
                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                             and Lander, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 253305,
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                                                                                                                                                                                                                                                                                                      Mus
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REFERENCE AUTHORS

TITLE

REFERENCE

AUTHORS JOURNAL SOURCE VERSION

ORGANISM

KEYWORDS ACCESSION

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RESULT 8 AC016984/c

DEFINITION

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Matches

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BASE COUNT
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AC010765
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  ACCESSION
                                                 DEFINITION
                                                                          LOCUS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                 10794 AGAAATAAATAAGTTTTTAAAGACTTTAAAGTTAAAGCAGGTAGTGCAGGTAAGAAATCAG 10735
                                                                                                                                                                                                    10674
                                                                                                                                                                                                                                                                                                 10734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                683 TT 684
                                                                                                                                                                                                 TT 10673
                                                                                                                                                                                                                                                                                                                                                TCAAGCTCGTGGACGAAATGATTAAAGCATCATCTATGTCTTGGACCATAGCAGGGGAAA 682
                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAAACCAGAGGGTTTTCAAAGAGCAAAAGATATAGAATACAGTCTGAGTGAAATATCAG
                                                                                                                                                                                                                                                                                                 TCAGGGCACTGCAAGAAGTGAAGTATAAAATATGCCCAGACTCTTCTCTGGGCCAC 10675
pieces.
AC010765
                                              Homo sapiens clone RP11-115N6, WORKING DRAFT SEQUENCE, 21 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 9, 2001 this sequence version replaced gi:11597083.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrin, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pierre, N., Pollara, V., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
                                                                          AC010765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collins,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 161780: contig of 161780 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        are represented
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161781 161880: gap of 161881 162930: conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: L5042 Center clone name: 48_C_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-23 Female 35471 c 36129 g 45563 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="RP23-48C4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                          155384 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collymore, A., Cooke, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.3%;
57.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .162930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a 'working draft' sequence. It currently contigs. Gaps between the contigs ed as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig of 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38.8;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (22-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 24, 2000 this sequence version replaced gi:8096878.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McGurk, A., McKarnan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
1 (bases 1 to 155384)
Birren,B., Linton,L., Nusbaum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Bogurna,A., Castle,A., Colangelo,M., Collins,S., CollymcCooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC010765.4 GI:9887724
HTG; HTGS_PHASE1; HTGS
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                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731
Consensus quality: 135849 bases at least Q40
Consensus quality: 144901 bases at least Q30
Consensus quality: 149193 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 163000; agarose-fp Insert size: 153384; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13; M77815;
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Center clone name: 115_N_6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
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                       86 6885: gap of 100 bp 1686 8549: contig of 1664 bp in le 168649: gap of 100 bp 1686 17004: contig of 4395 bp in le 17004: contig of 3860 bp in le 17104: gap of 100 bp 17104: ga
                                                                                                                                                                    04 9999; contig of 1796 b

00 4099; gap of 100 bp

00 6785; contig of 2686 b

00 6885; gap of 100 bp

00 8549; contig of 1664 b
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3: gap of 100 bp
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     contig of 4188
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1110898 124144; contig of 13247 t
124145 124244; gap of 100 bp
124245 138573; contig of 14329 t
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90378: contig of 8219
90478: gap of 100 b
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61986: contig of 6347 l
62086: gap of 100 bp
67833: contig of 5747 l
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49223: contig of 4754
49323: gap of 100 b
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44369: contig of 22977 bp in length
169: gap of 100 bn
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Best Local Similarity 55.1%;
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                                                                                                                                                                                                       Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 28% of reads
Sequencing vector: plasmid; L08752; 71% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 159926 bases at least Q40
Consensus quality: 160230 bases at least Q30
Consensus quality: 160230 bases at least Q30
Consensus quality: 160339 bases at least Q20
Insert size: 160541; sum-of-contigs
Insert size: 160541; sum-of-contigs
Quality: Coverage: 6.16% in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (21-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 30, 2000 this sequence version replaced gi:9796578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: bAll5N6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Sanger Centre
Center code: SC
                                                                                                          Draft Sequence Produced by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street,
                                                                                                                                                                                         coverage: 6.14x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome 10 clone RP11-115N6, PROCRESS ***, 4 unordered pieces. AL157781 AC010765
AL157781.5 GI:11042353
                                                                                    Genome Research, 320 Cha:
Cambridge, MA 02141, USA
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Mammalia; Eutheria; Primates;
http://www-seq.wi.mit.edu.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site:
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150784. .155384
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138674. .150683
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les 75; Conserv
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Direct Submission
Submitted (21-JAN-2001) Sanger Centre, Hinxton, Cambridgesh
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens chromosome 10 clone RP11-470P23, PROGRESS ***, 3 unordered pieces.
                                                                                                              Grafham,D.
                                                                                                                                                                                                                                                   Homo sapiens
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109947 160841: contig of 50895 bp in length
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Pred. No. 6.7;
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                                                                   2444 CTTTGTATCAATACATTTGAAGATCTAGCCAAAAATGGTCAATTCATTATAAATGTAGCT 2503
                                666 GACCATAGCAGGGGAA 681
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Insert size: 170828; 1.8% error; agarose-fp
Quality coverage: 7.71x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: plasmid; LO8752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 165727 bases at least Q40 Consensus quality: 165914 bases at least Q30 Consensus quality: 166002 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            requests: clonerequest@sanger.ac.uk
On Sep 6, 2000 this sequence version replaced gi:9955461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coverage: 8.28x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Sanger
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fragment_chain:1"
50930. .166315
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0 166315: contig of 115386 bp in length
Location/Qualifiers
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/clone="RP11-470P23"
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/db_xref="taxon:9606"
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Pred. No. 6.7;
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AUTHORS
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VERSION
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TITLE
JOURNAL
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DEFINITION
Homo sapiens chromosome RPCI-11 clone RP11-12C15, WORKING DRAFT
SEQUENCE, 19 unordered pieces.
CCESSION
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Chemistry: Dye-primer ET; 100% of reads Chemistry: Dye-terminator Big Dye; 0% of read Chemistry: Dye-terminator Big Dye; 0% of read Assembly program: Phrap; version of 0.990319 Consensus quality: 150364 bases at least Q30 Consensus quality: 154713 bases at least Q30 Consensus quality: 156776 bases at least Q20 Consensus quality: 156776 bases at least Q20 Center: Washington University Genome Center code: WUGSC Quality coverage: 4.80 in Q20 bases; agarose-fp Quality coverage: 5.08 in Q20 bases; sum-of-contigs Web site:http://genome.wustl.edu/gsc/index.shtml Insert size: 157000; agarose-fp Insert size: 160493; sum-of-contigs arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence. NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is as soon as it is available and the accession number will be preserved. vector: plasmid; gap of contig gap of contig gap of contig contig gap of contig contig of 3224 bp in length gap of unknown length contig of 3474 bp in length contig gap of contig gap of gap of contig gap of unknown of 9616 unknown of 5080 unknown of 5075 unknown of 5609 unknown unknown length of 29836 bp in length of 9761 unknown of 2588 unknown length bp in 1 length bp in length bp in length length bp in bp in length bp in length bp in length length length length reads length length length

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BASE COUNT
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26601. .56436
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38585 c 38757 g 42221 t
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/db_xref="taxon:9606"
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157559. .159409
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/clone="RP11-122C15"
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71578. .81193
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51717. .71477
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Pred. No. 10;
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contig of 1851 bp in length
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                                                                                                                                                                                                                                                                                                                                          Insert size: 128000; agarose-fp
Insert size: 171007; sum-of-contigs
Quality coverage: 3.91 in Q20 bases; agarose-fp
Quality coverage: 4.19 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: plasmid; 30% Chemistry: Dye-primer ET; 70% of reads Chemistry: Dye-terminator Big Dye; 30% of reads Chemistry: Dye-terminator Big Dye; 30% of reads Chemistry: Dye-terminator Big Dye; 30% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 16241 bases at least Q40 Consensus quality: 168345 bases at least Q20 Consensus quality: 168345 bases at least Q20
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------- Summary Statistics
Sequencing vector: M13; 70%
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Submitted (30-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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On Jul 16, 2000 this sequence version replaced gi:8568103
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Waterston, R.H.
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SEQUENCE, 19 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site:http://genome.wustl.edu/gsc/index.shtml
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                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                          as soon as it
be preserved.
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1196: contig of 1196 bp in length
1296: gap of unknown length
2419: contig of 1123 bp in length
2519: gap of unknown length
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          /note="assembly_name:Contig28"
87189. .102814
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                                                                                                              vector_side:right"
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21770. .27025
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11637. .16955
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50697. .60217
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17056. .21669
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/db_xref="taxon:9606"
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note="assembly_name:Contig29"
                                           note="assembly_name:Contig27"
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contig of 13415 bp in 1
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contig of 15626 bp in 1
gap of unknown length
contig of 16877 bp in 1
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contig of 24588 bp in 1
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contig of 28248 bp in 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 539 TCACCTTACAAAGGAGATTGCCGCAGAAACCAGAGGGTTTTCAAAGAGCAAAAGATATAG 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGCATTCCGGGTCTGATGACCCGCACGGTTTTCCCCAGATATGAGAAACTCATAGATGC 17722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAAT 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATACAGTCTGAGTGAAATATCAGTCAAGCTCGTGGACGAAATGATTAAAGCATCATCTA 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTCTTGGACCATAGCAGGGGAAATTAATACTCCCGTCCTGCTTATTCATGGGGAAAAAC 718
                                                                              Federspiel,N.A., Palm,C.J., Conway,A.B., Kurtz,D.B., Conway,A.R., Au,M., Araujo,R., Buehler,E., Dewar,K., Feng,J., Kim,C., Li,Y., Oji,O., Osborne,B.I., Shinn,P., Sun,H., Toriumi,M., Vyotskaia,V., Yu,G., Ecker,J., Theologis,A. and Davis,R.W. Direct Submission
Submitted (03-JUN-1998) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                       Submitted (04-FEB-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, 94304, USA
                                                                                                                                                                                                                                                                                                                                                            Federspiel, N.A., Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R., Au, M., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Oji, O., Osborne, B.I., Shinn, P., Sun, H., Toriumi, M., Vyotskala, V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Federspiel, N.A., Palm,C.J., Conway,A.B., Kurtz,D.B., Conway,A.R., Au,M., Araujo,R., Buehler,E., Dewar,K., Feng,J., Kim,C., Li,Y., Oji,O., Osborne,B.I., Shinn,P., Sun,H., Toriumi,M., Yysotskaia,Y.S., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93;
             4 (bases 1 to 67878)
Federspiel, N.A., Palm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 67878)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC004122 67878 bp
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                            Direct Submission
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Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC004122
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC004122.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 67878)
                                                                                                                                                                                                                                        (bases 1 to 67878)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
  Araujo, R.,
                                                                                                                                                                                                                                                                                                                                              Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vector_side:left"
144560, .172807
/note="assembly_name:Contig32"
a 38927 c 39034 g 47287 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_name:Contig30"
119892. .144459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_name:Contig31 clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:3176693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.2%;
                      Palm,C.J.,
  Buehler, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome I BAC T27I1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37.8; DI
Pred. No. 10;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
Conway, A.B., Kurtz, D.B., Conway, A.R., Dewar, K., Feng, J., Kim, C., Li, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1824 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 172807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                  CA
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e-mail for correspondence: arab@sequence.stanford.edu
Genes with similarity to proteins in the databases are described a
'putative', '-like' or 'similar to'. Genes that have EST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (04-SEP-1998) DNA Sequencing and Technology Center,
Submitted (nativersity, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), Fexa (V.Solovyev & A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/), and NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Jun 3, 1998 this sequence version replaced gi:3097845.
Bases 1-4933 of clone of clone T2771 overlap with bases
141573-146505 of 'IGF' clone F21M12, gb|AC006132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ecker, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Osborne,B.I., Shinn,P., Sun,H., Toriumi,M., Vyotskaia,V., Ecker,J., Theologis,A. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MLRRLGWLIGLSQRSRQTKSIDAEPYVARVKPVLMIDTVQEIAI
YIHREHNLDLFQQGWYQIKISMRWEDGDNNSCGIPSRVVQYEALDSTSNDSYGVWKID
DKDSSFLTQPFRIKYARQDVRLCMMVSFTMPLESATSAVLTOVSVHVSVWKSAXYKR
PVTHSDACAAAVHEFRIPPKALSGVH83YCPVHEDTFHAVLIDVSVHVSVWKSAAYKR
AILSSDASNGKNLTSGNIQSSKKAFTQLASADKKLVSEVKALLGARDTLLEEMQRLSK
AFTQLASADKKLVSEVKALLGARDTLLEEMQRLSK
LHFSSDASNGKNLTSGNIQSSKKAFTQLASADKKLVSEVKALLGARDTLLEEMQRLSK
LHFSSDASNGKNLTSGNIQSSKKAFTQLASADKKLVSEVKALLGARDTULEKLNGPFDLASDDW
LHFSKEHLSRFTHLLGTQLHYLMNTFLTLHRDNYTKLEYLDNIWTKDRRAEMSIMM
VYSKVEMPHREISGMEDISNHSSHKRVSTGLKLUDPAQVASTRAELHRRS IAQMRINN
RAIQDMHIFGDPMRVPIVIIERVWNAFRTFSDNSYMHHVDRIDSSGTKK
KHINPQHTGRELKIVFVHGFQASIFLMFSECGHHLDLRLIRNQWLLIDPKIEFLMSE
                                                                                                                                                                                                                                                                                                                                                                                                                       IADSLMDPYRKYFHTYISLSGPHLGYLYSSNSLFNSGLWLLKKLKSTQVIHQLTLTDD
PDLQNTFFYKLCKVEKDVNISSRSCTIVTNRPLFFGSEMLVLKLFSAKDVVQFQEYNS
PVFASARIESCQPASFDNSKRGVAFLEMLNNCMDQIRGPSPETPHHQRVFMRCDVNFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement()oin(1855...2132,2249...2605,2699...2957,
3162...3440,3522...3581,3668...3851,3951...4084,4179...4418,
4809....4863,4956...5209,5492...5646,5823...5908,6008...6180)
/gene="T2711.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(<1855. .2132,2249. .2605,2699. .2957, 3162. .3440,3522. .3581,3668. .3851,3951. .4084,4179. .4418,4809. .4863,4956. .5209,5492. .5646,5823. .5908,6008. .6347,
                                                                                                                                                                                                                                                                                                                complement(8064. .10102)
/gene="T2711.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(<1855. .>6834)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="overlap with bases 141573-146505 of 'IGF' clone F21M12, gb|AC000132"
                                                                                                                                                                                                                                                                               complement(join(8064. .8222,8378. .8410,8594. .8634
                                                                                                                                                                                                                                                                                                                                                                                         TTLYGRNLNSFIGRAAHIEFLESDVFARFIMWSFQDLFR*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANEERTHGDFREMGQRLAQEVVSFFKRKKDKHARYGRLKNIKLSFVGHSIGNVIIRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6642. .>6834))
/gene="T27I1.1"
MLFHCDFAAQVWNLAPLQLGHIPIGTPILEALNLLKKTIVLPPVGIHTATLFPWICWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAC34330.1"
/db_xref="GI:3540180"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Unknown protein; Location of EST gb|T04106"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="T2711.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="I"
/clone="T27I1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"
/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                          /protein_id="AAC34342.1"
                                                                                                                                                                            /note="Hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3702"
                                                                         'db_xref="GI:3540192"
                                    translation="MPKIKLFLWKAAAGALPVGAQLVRRHISSTWDCARCGAPETSTH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .67878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .6180))
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                                                                                                                                       CDS
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/product="putative amino acid permease"
/protein_id="AAC34329.1"
/db_xref="GI:3540179"
/translation="MaDYNNPSAVESGDAAVKSVDDDGREKRTGTFWTASAHIITAVI
/translation="MaDYNNPSAVESGDAAVKSVDDDGREKRTGTFWTASAHIITAVI
GSGVLSLAWAIAQLGWYAGTTVLVAFAIITYYTSTLLADCYRSDDSITGTRNYNYMGV
VRSYLGGKKVQLCGVAQYVNLVGVTIGYTITASISLVAIGKSNCYHDKGHKAKCSVSN
                                                                  complement(join(21422. .21493,21576. .21673,21751. .2188
21971. .22023,22196. .22221,22315. .22475,22646. .22900,
23079. .23149,23359. .23426,23504. .23778))
                                                                                                                                                                                                                   /note="Location of EST gb|T46432 and gb|AA404857.
splice junction at position 21576 is predicted fry
alignment with EST sequence gb|AA404857"
complement(21205. .23909)
                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(21205. .21493,21576. .21673,21751. .2188
21971. .22023,22196. .22221,22315. .22475,22646. .22900,
23079. .23149,23359. .23426,23504. .23909))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAC34343.1"
/db_xref="G1:3540193"
/db_xref="G1:3540193"
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RTFGVWTLLTCTLCFLCAFNLENKPLYLATFLSFIYALGHFLTEYLFYOTMTIANLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAC34331.1"
/db_xref="G1:3540181"
/tdb_xref="G1:3540181"
/translation="Mudecpetirlfighlalkyplaakttssyvhpssspcfckiklkn
/translation="Mudecpetirlfighlalkyplaakttssyvhpssspcfckiklkn
rppQftaAipyiplettToppEiQflaaffhlsssbiQrlaaktsittskpclkiliytgr
AGAACGVHSGRLLAKYSVPLDLSGTQSKPCVFHNGWISVGKGAGKSSSSAQFHLNVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Location of EST gb|T41885 and gb|AA395021" complement(14928. .17240) /gene="T2711.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"GC splice site at position 1256 is predicted fr
alignment and not confirmed experimentally. Highly
similar to Arabidopsis thaliana amino acid permease I
gi|404019, and other amino acid permeases."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIADAAAKLSLCISGNIGLDPDLSIYESVFRLALLTRLTIWLTLFSLEDIHCSIESYL
GRFQNLLRAGNMRYIQIMLILTRAFLKPLASDRNLKESNI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IWKARNQLIFQNSHFSVIETVTKAVQDALAWQSAQLALPKVRVATPRPNSTTTLTHDE
LCYVDAAWQQQSSLAGSGWVFQATSHSEKEITTFSAGCRRFPSPLAAEAWAIKSAMLH
ALQLERSDLLVLSDSKSIVDALNSNVSLNEIFGLLVEIRSIRNRFRSISFQFIPRLVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(15253. .16012,16421. .17046))
/gene="T2711.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(14928. .16012,16421. .17240))
/gene="T27I1.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YPYMAAFGIVQIIILSQLPNFHKLSFLSIIAAVMSFSYASIGIGLAIATVASGKIGKTE
LTGTYLGYDVTASEKVWKLFQAIGDIAFSYAFTTILIEIQDTLRSSPENKVNKRASL
VGVSTTTVFYILCGCIGYAAFGQNAFODFLTDFGFYEPFWLIDFANACIAHLIGSYQ
VYAQPFFQFVEENCNKKWPQSNFINKEYSSKVPLLGKCRVNLFRLVWRTCYVVLTTFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WLILRPGDCTWRPWGRLEAWRERGGATDGLGYRFELIPDGSSGAGIVLAESTISSHRG
GKFSIELGSSPSSSSPTSVVNRSRSRRGGSSGSGGGASPANSPRGGSGDYGYGLWPWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPDPRFVFQFDGEPECSPQVVQIQGNIRQPVFTCKFSCRHTGDRTQRSRSLPTETSVS
RSWLNSFGSERERPGKERKGWSITVHDLSGSPVAMASIVTPFVASPGTDRVSRSNPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb|AA395021"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMIFPFFNAILGLLGAFAFWPLTVYFPVAMHIAQAKVKKYSRRWLALNLLVLVCLIVS
ALAAVGSIIGLINSVKSYKPFKNLD"
                                                                                                                                                                                    /gene="T27I1.6"
                                                                                                                                                                                                                                                                                                                                                                            /gene="T27I1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGFFAGII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Unknown protein; Location of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(19286. .19400,20568.
/gene="T27I1.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="T27I1.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRKELCHESLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VYKGFVMSASVEGEGKCSKPCVEVSVQHVSCMEDAAAYVALSAAIDLSMDACRLFNQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13195. .13422,13615. .14040)
/gene="T27I1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="T27I1.
note="Unknown protein; Location of EST gb|T46432 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="Unknown protein; Location of EST gb|T41885 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oin(11290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .11611,12293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .20785)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .12386,12501. .12715,12814. .12956,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST gb|T45589"
                                                                                                                                                                                                                                                                                                         from
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RESULT 15
AC024007/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36379 AACCTGAAGCAACCGTTGATAGCTTTAA 36406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36319 CAAACCTTTGCCGGCAATACTCACTAAATAGAAGAGTGAGAAGGATTAACGGGATGGTGA 36378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AAGACTGTGGAAGAGTATGCGCTACTTGAAACAGGCGTAAGAGTGTTTTATCGGTGTGTA 120
                                                                       RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Rodarson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Pearellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M., Penestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gandyna, S., Ginde, S., Goyette, M., Graham, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Largocque, K., Leboczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Olivar, T.M., Peterson, K., Plerre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stoyanovic, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., W., Young, G., Zatnoun, J., Zimmer, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGTTTAATATCAATGTCTTTGTTAATATATCTTGGCTGTATTTTTCAGGGATAGTTATG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCCCGGAGAAAGCTTTTAACACTTTGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAGTAATATATATATATATATATATATACCTCGGCTGGATATTTCTGGAATATGGGCG 36318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 167374)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 1, clone RP11-157G15
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE, 4 unordered pieces. AC024007
Direct Submission
                                                                Wu,X., Wyman,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC024007.2 GI:7210066
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 167374)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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TKADRFKNLDMEEEMIRELTKLSWERVDVSFRGTLQRFLAHNTIQVKTKMINSAGADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKKKKKYMMGCLRABSDESGNUDLTUDFPGERTEPTHLVVMVNGLIGSAQNWRFAAKO
MLKKYPQDLLVHCSKRHSTQTFDGVDVMGERLAEEVHSLGKISFVGHSLG
GLIABYAIGRLYEQESREBLFHNSDDIGDKCSIEEPKARIAGLEPYFTISATPHLGS
RGHKQYPLFSGSYTLERLATRMSGCLGKTGKHLFLADSDGGKPPLLLRMVKDSRDLKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb|AA404857. Rare GC splice donor at position 21576 is predicted from alignment with EST sequence gb|AA404857"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(24584. .24921,25004. .25163,25600. .25946,26029. .26188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24584. . 28758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MEEEDSVIPKNTEGDGRVGSDLEGIRKPKKMKKMRSRKSDDKET/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GI:3540182"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria, Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167374 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67374 bp DNA HTG 08-MAR-2000 Chromosome 1 clone RP11-157615 map 1, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           id-"AAC34332.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37.6;
Pred. No. 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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REFERENCE AUTHORS

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                                                                                                   Matches
                                                                                                                                              Query Match
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  62256 AAAAAATGACTTAATGAATGAATGATACATCAGTCAAACTCTAGGGAAGGCAGTCAATTAT 62197
                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                            590 AAGATATAGAATACAGTCTGAGTGAAATATCAGTCAAGCTC-GTGGACGAAATGATTAAA 648
                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (20-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 8, 2000 this sequence version replaced gi:7008912. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                  46601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: Phrap; version 0.960731
Consensus quality: 162751 bases at least Q40
Consensus quality: 165494 bases at least Q30
Consensus quality: 16551 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 167074; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality coverage: 5.8 in Q20 bases; Quality coverage: 5.8 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: L'
Center clone name: 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 6557: contig of 6557 bp in length
6558 6657: gap of 100 bp
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15948 16047: gap of 100 bp
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/note="assembly_fragment"
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/clone_lib="RPCI-11 Human
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/chromosome="1"
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Pred. No. 11;
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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BF657575 OV2_23_H0
AV397710 AV397710
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AQ332328 HS_5007_A
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AQ332328 HS_5007_A
AQ335962 HS_5015_B
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AL107180 Droscophi1
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AU3038 12643 Lambd
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AA789157 ag41b12.s
AQ673914 HS_5460_A
AQ677914 HS_5460_A
AI164223 A057P53U
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                                                                                                                                                                                                                                                                                                  The University of Georgia
Plant Sciences Building, Rm.
Tel: 706 542 1805
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF657575
OV2_23_H05.
                                                                                                                                                                                                                                                             Email: mmpratt@uga.edu
Seq primer: JEN REV
                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
                                                                                                                                                                                                                          POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                            Department of Botany
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Cordonnier-Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                 An EST database from Sorghum:
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                   79
                                                                                                                                                                                                                                            quality sequence stop:
       /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/db_xref="taxon:4558"
/clone_lib="Ovary 2 (OV2)"
/clone_lib="Ovary 2 (OV2)"
/note="Organ: Mix of ovaries of varying immature stages
/note="Organ: Mi
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A1965512 sc73a07.y
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AW759075 sl34402.y
AW781953 s198901.y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A large scale structural analysis of cDNAs in a unicellular alga, Chlamydomonas reinhardtii. I. Generation of 3433 non-redundant expressed sequence tags DNA Res. 6 (6), 369-373 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota, Viridiplantae, Chloroph
Chlamydomonadaceae, Chlamydomonas.
1 (bases 1 to 456)
AZ517865 460
RPCI-11-89H18.TVB
                                                                                                                                                                                                                              69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The First Laboratory for Plant Gene Research Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV397710 456 bp mRNA EST 29-SEP-2000 AV397710 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii CDNA clone CL49bl1_r, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yasukazu Nakamura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332-3, Kisarazu, Chiba 292-0812, Japan
ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
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                                                                                                                                                                                                                                                                                                                                                     /Olyanasu
/Strain="C9"
/db_xref="taxon:3055"
/clone="C149b11_r"
/clone_11b="Chlamydomonas reinhardtii C9"
/dev_stage="photoautotrophic growth"
/dev_stage="photoautotrophic growth"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Chlamydomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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59.5%;
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RPCI-11 H
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Pred. No. 0.15
0; Mismatches
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Pred. No. 0.0016;
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Homo sapiens genomic clone RPCI-11-89H18,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAAAGGGATACAGATAAGAATCACCTACTTTAGTTGTCACATATCTTTTGGTGTT 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCAACTTGTGAAATGTCATTCGTCGTTTTTGACTTGCATGAACTTGATGAGTTTGAAGA
                                                                                               AQ332328 459 bp DNA
HS_5007_A2_H07_T7 RPCII1 Human |
genomic clone Plate=583 Col=14
AQ332328
AQ332328.1 GI:4129955
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75; Conservative
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
Homo
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Clones are derived from the human BAC library RPCI-11. For BAC

Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet cs (lnfo@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

This BAC end was generated during the R&D process and may have

higher chance of clone tracking errors.
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Other_GSSs: RPCIl1-89H18.TJ RPCIl1-89H18.
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Class: BAC end
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Mammalia; Eutheria;
1 (bases 1 to 460)
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AZ517865
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sapiens
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/note="Vector: pBACe3.6; Site_1:
/note="V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="RPCI-11-89H18"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="GDB:7533977"
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                                                                                                                                                                        Male BAC Library Homo sapiens Row=O, DNA sequence.
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                          GAAGGGAGTTTAATCCCCGCACT 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGAGGGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAAGGGATTGATAGGG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101;
                                                                                                                                                                                 AQ335962 465 bp DNA GSS HS_5015_B1_E07_SP6E RPCIll Human Male BAC Library Homo genomic clone Plate=591 Col=13 ROW=J, DNA sequence.
1 (bases 1 to 465)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                   GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics
BAC end Web Server: http://www.htsc.washington.
Plate: 583 row: O column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 Queen Anne Avenue North, Seattle, Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Mahairas GG, Wallace JC, High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Class: BAC ends
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                             Homo sapiens
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Location/Qualifiers
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/note="Vector: pBACe3.6; RPCIll Human Male
/8 c 74 g 159 t 1 others
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/db_xref="taxon:9606"
/clone="Plate=583 Col=14
/clone_lib="RPCI11 Human
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Male BAC Library"
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 Holzman, T., Adams, M.D.
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Contact: Mahairas GG, Wallace JC, High Throughput Sequencing Center
                                        scanning the human genome proc. Natl. Acad. Sci. U. S. A. 96 (17),
                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 510)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. a
                                                                                                                                                                                                                                                                                        AQ600815 510 bp DNA GSS 10-JUN-1999 HS_5318_A2_C09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=894 Col=18 Row=E, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (inf
BAC end Web Server: http://www.htsc.washington.edu
Plate: 591 row: J column: 13
Seq primer: SP6
Class: BAC ends
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/note="Vector: pBACe3.6; F
76 c 76 g 162
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/clone="Plate=591 Col=13
/clone_lib="RPCI11 Human
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Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.h
or from Resear h Genetics (info@resgen.com). BAC end Web Serve
http://www.htsc.washington.edu
Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part collaboration with the European Drosophila Genome Project (EDC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MF
                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS016TE 1010 bp DNA GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence SP6 end of BAC BACN16C05 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                              Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1010)
                                                                                                                                                                                                                                                                                                    fruit fly.
Plasmid Drosophila melanogaster
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Tel: (206) 616-3618
Fax: (206) 616-3887
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/db_xref="taxon:9606"
/clone="Plate=894 Col=18 Row=E"
/clone_lib="RPCI-11 Human Male i
/sex="male"
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Pred. No. 0.76;
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                                                                                                                                                                                                                                                                                                                                                                                                          TGACGGAGGTATA 477
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GSSBru0818 Sheared genomic library Bruce Abortus genomic clone B23, DNA sequence. AZ049266
                                                abortus genome
Unpublished (1999)
Contact: Zandomeni
                                                                                                                                                                                       Brucella melitensis biovar Abortus.
Brucella melitensis biovar Abortus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                         Sanchez, D.O., Zandomeni, R.,
                                                                                                                                                                                                                                                                                                 AZ049266
                                                                                                 Gene
                                                                                                                                                           Brucellaceae; Brucella.
                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                        AZ049266.1
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                                                                                              discovery through
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/note="end : SP6"
191 c 154 g
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/plasmid="pBeloBAC11"
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                                                                                                                         Rosetti,O.,
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TITLE
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Best Local
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source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCCGTTCGACCTCCTTTTCGACAAGGCGGATATCGTCATCGGCATCGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATACCTCTCGGAAGGGAGTTTAATCCCCGCACTTCTCGGCAGCTGTGCAATTCCCGGCA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGAAGACCTGAAAATTCCCATGACCATTACGGCGGTGGATTTTCATGGCGCGCGGGAGA
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Tel: 5411-4621-3316/1683
Fax: 5411-4481-1316
Email: zandomeni@inta.gov
            High quality sequence start: 6
High quality sequence stop: 88
Location/Qualifiers
                                                                       found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1068 row: f column: 08
                                                                                                                                                                                                               Tissue Procurement: CLONETECH Laboratories, Inc
                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1244)
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                            Unpublished (1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
                                                                                                                                CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Sheared genomic library"
/note="Vector: pBluescript SK(-) (STRATAGENE); Genomic
was mechanically sheared, blunt ended, and
size-fractionated by agarose gel electrophoresis.
Fragments between 1.5-3 Kb were recovered and ligated t
the ECORV site of the pBluescript SK (-) vector."

112 c 97 g 63 t 1 others
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/strain="s-2308"
/db_xref="taxon:235"
/clone="B23"
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47.8%;
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Catarrhini;
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i; Hominidae;
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                                                                           Determination of this BAC-en's sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library, or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
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1 (bases 1 to 1101)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
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                                                        found at http://bacpac.med.buffalo.edu/drosophila_bac.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence.
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                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:4248967"
/clone_1b="NHH_MGC_83"
/lab_host="DH1UB (T1 phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TTGAGATTGAGGAAATTTGAAGAGATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WKRGTDWRTWKRTWKGWGRKGDKGRKTAGRAGDGKDKKKGKDKDRTDDAKATDGKDTWRD
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                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; eudicots; Rosidae; eurosids II;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 508)
Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45;
                                                                                                                                                                                                      On Apr 14, 1993 this sequence version Contact: Thomas Newman MSU-DOE Plant Research Laboratory
                                                                                                                                                                                                                                                            Plant Physiol.
95148729
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                                                                                                                          Lansing, Mi
Tel: 517-353-0854
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12643 Lambda-PRL2
                                                                                                                                                                                                                                                                                large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241–1255 (1994)
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                                                                                                                                                                                      Michigan State University
                                                                      primer: T7 dye primer
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                                                                                         22313tcn@ibm.cl.msu.edu
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/note="end: TET3"
a 104 c 123 g
                                      1. .508
/organism="Arabidopsis thaliana"
/strain="var columbia"
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/db_xref="taxon:7227"
                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92;
                                                                                                                                              Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA
                                                                                                                                                                                                                                             Chen,J., Momiyama,M., Chan,E., Mooney,M., Carroon,B., Gilliland,D., Wang,X., Hillman,J., Guegler,K., Kim,C., Doyle,M., Brzoska,P., Goorgone,G., Burns,D., Griffin,J., Kim,C., Loua,M., Nguyen,D., Tan,R., Rose,M., Warren,B., Ton,B., Kastury,K., Borillo,C., Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S., Nobriga,A., Murry,L., Turner,C., Krikorian,S., Elder,L. and Hanson,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A1992658 569 bp
701558595 A. thaliana,
CDNA_clone 701558595, r
                                                                                                                                                                                              Contact: David Smoller, Ph.D.
                                                                                                                                                                                                                Arabidopsis thaliana Gene Expression MicroArray Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                 Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 569)
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314-427-3324
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                                                                             Location/Qualifiers
                             /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
             /clone="701558595"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3702"
/clone="164I14T7"
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Pred. No. 9.7;
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thaliana, Ohio State clone set"
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VERSION KEYWORDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGCGGCGGCGAAAATGGAAGATACCGCTTTGAGAGAAGCTGCTTCTGCAGGGATTCACG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGAAGAGGGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAAGGGATTGATA 255
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1 (bases 1 to 463)

Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray
                                                                                                                                                                                                                                                                 Tel: (626) 395-8421
Fax: (626) 793-3047
                                                                                                                                                                                                                                                                                                     Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strongylocentrotus purpuratus.
Strongylocentrotus purpuratus
Eukaryota, Metazoa, Echinodermata, Eleutherozoa,
Echinoidea, Euechinoidea, Echinacea, Echinoida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A2158907 463 bp DNA GSS 29-AUG-2000 SP_006_B2_A02_SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=61 Col=4 Row=B, DNA sequence.
                                                                                                                                                                                                Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                   Email: acameron@caltech.edu
Plate: 61 row: B column:
                                                                                                                                                                                                                                                                                                                                                            Contact: Cameron, RA,
                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U. S. A.
                                                                                                                                                                                                                                                                                                                                                                                                              additional resources
                                                                                                                                                                                                                                                                                                                                                                                                                              A sea urchin genome project: Sequence scan, virtual map, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strongylocentrotidae; Strongylocentrotus.
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                    /note="Organ: sperm;
DH10B"
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Arabidopsis thaliana Ohio State clone set."
a 119 c 163 g 131 t
                                                        urchin,
                                                 /clone="Plate=61 Col=4 Row=B"
/clone_lib="Strongylocentrotus purpuratus, purple
urchin, sperm genomic BAC library"
                                                                                                          /db_xref="taxon:7668"
                                                                                                                            /organism="Strongylocentrotus
                                                                                                                                                             Location/Qualifiers
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762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441 TTAAGATGGAGCCNCGATACAAGAGATTTATATGCATACAGAGTTTTATATGATTGTTAT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 TTAAGTTCAAGCCACCTCTGAAGGGATTGATAGGGTGGGAGAAGGCTATAAGATTCCTTG 283
                                       TTTACTGAAAGCGGAATCCTCCATTTCTCTGCACATCTACTGGCTTAAATTGTGGCAAAA 703
                                                                          TTTCAGGAAAGCGGTATTCCCACCGTTTGCGTTGATGTCCTTCCCATAGAGCCGGAAAAG 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK / Jia L
WashU-MGB/NHGRI EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jia, L., Robey, P., Young, M., Schuler, G., Powell, J., Yang, L., G., Hillier, L., Allen, M., Bowles, L., Geisel, S., Kucaba, T., M., Martin, J., Steptoe, M., Tan, F., Theising, B., Bowers, Y., T., Waterston, R., Wilson, R. and Francomano, C. Wash-MGB, MHGRIEST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ag41b12.s1 Jia bone marrow stroma Homo sapiens cDNA clone IMAGE:1119359 3' similar to gb:J03464 PROCOLLAGEN ALPHA 2(I) CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                             mRNA made from human bone marrow stroma, cDNA made by oligo-dT priming. Directionally cloned. Size-selected average insert size >0.5 kb. Library supplied by Dr. I
                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:1119359"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                        /note="Vector: pBluescript; Site_1: EcoRI; Site_2: XhoI;
                                                                                                                                                                                                                                                                                                                                           /dev_stage="mixed"
/lab_host="XL1-Blue MRF'/SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                    /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Jia bone marrow stroma"
                                                                                                                                                                                                                                                                                                                                                                                tissue_type="bone marrow stroma"
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131 c 1
                                                                                                                                  4.68;
46.18;
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                  ATTTGAAGAGATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGCATAGCCCACATAGG
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                                                                    61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                       Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                    library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seg primer: T?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
Other_GSSs: RPCI-11-346N21.TJ
Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
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RPCI-11-346N21.TV RPCI-11
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1 (bases 1 to 668)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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/note="Vector: pBACe3.6; Site_1:
/note="Vector: pBACe3.6; Site_1:
RPCI11 Human Male BAC Library"
125 c 153 g 179 t
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/db_xref="GDB:7632812"
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Homo sapiens genomic clone RPCI-11-346N21
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2: /cgn2_6/ptodata/2/pna/U

3: /cgn2_6/ptodata/2/pna/U

4: /cgn2_6/ptodata/2/pna/U

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6: /cgn2_6/ptodata/2/pna/U
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length: 2000000000
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US-09-688-337-197
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S US-09-103-840A-2
US-09-103-840A-2
US-09-103-840A-2
US-09-103-840A-1
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US-09-724-866A-7119
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52544, Ap
52544, Ap
5026, Ap
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; TYPE: DNA ; ORGANISM: Agrobacterium tumefaciens US-09-739-449-4665

PRIOR FILING DATE: 2000-02-NUMBER OF SEQ ID NOS: 13351 SEQ ID NO 4665 LENGTH: 858

CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23

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ALIGNMENTS

US-09-739-449-4665

Sequence 4665, Application US/09739449
GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens
FILE REFERENCE: 38-10(15490)C

Genome Sequences

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Sequence 213, Application US/09739449
GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Sqrobacterium tumefaciens
FILE REFERENCE: 38-10(1549)C
CURRENT APPLICATION NUMBER: US/09/739,449
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Best Local Similarity
Matches 113; Conserv
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CURRENT FILING DATE:

2000-12-19

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : NAME/KEY: unsure
: LOCATION: (1)..(300663)
: OTHER INFORMATION: unsure at all n locations
US-09-739-449-213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 111922 cctgatcgacggcgctcgtcaatcccgtgcccgtttccgtctgccggg 111971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 111862 gctgcgctccttcctacgcgctgcccggcatcttcgagcccgtgcaatgcaatggccgcac 111921
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PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 213
SEQ ID NO 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Best Local Similarity 49.1
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 197
                                                                                                                                                                                                                   APPLICANT:
                                  CURRENT APPLICATION NUMBER: US/09/668,337
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/156,565
PRIOR FILING DATE: 1999-09-28
                                                                                                                APPLICANT: Fong, Willy T.
TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION
FILE REFERENCE: PT-0086 US
                                                                                                                                                          APPLICANT:
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TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
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APPLICATION NUMBER: 60/168,197 FILING DATE: 1999-11-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCGGAAGGGAGTTTAATCCCCCGC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hodgson, David M.
                                                                                                                                                          Amshey, Stefan Fong, Willy T.
                                                                                                                                                                                             Liu, Tommy F.
Yap, Pierre E.
Stockdreher, Theresa K.
                                                                                                                                                                                                                                                          Chen, Wensheng
                                                                                                                                                                                                                                                                            Wright,
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Bratcher, Shawn R.
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Spiro, Peter A.
                                                                                                                                                                                                                                                                        Roseberry, Ann M.
Wright, Rachel J.
                                                                                                                                                                                                                                                                                                                                                              Yu, Jimmy Y.
                                                                                                                                                                                                                                                                                                                                                                                                   Hillman,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerard E.
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49.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stephen E
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                                                                                                                                      AND TREATMENT
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Query Match
Best Local Similarity
Thes 70; Conserve
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RESULT 5
US-09-103-840A-1
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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; OTHER INFORMATION: Incyte ID No: 246400.6.dec
US-09-668-337-197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2
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Best Local
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                                                                      370805 ctgcccgagttga 370817
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OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mycobacterium tuberculosis
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                                                                                                              464 TTGACGGAGGTATAGTTAACAACCTTCCCGTTGAGCCCTTTCAGGAAAGCGGTATTCCCA 523
                                                                                                                                                                                                                                                              404 TCGGCAGCTGTGCAATTCCCCGGCATATTTGAACCCCGTTGAGTATAAGAATTACTTGCTCG 463
                                                                                                           524 CCGTTTGCGTTGA 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            623 tgcccaggtgggcgttctcaaggccttggcggagtgcggcatccctgtggacatggtggg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 82; Conserv
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                                                                                                                                           gtgccggtgttgccgatgccaacgtttccgttgcccgagttgaaaaagccgatgtttccg 370804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn
                                                                                                                                                                                                                                                                                                Conservative
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52.6%;
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Pred. No. 39;
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                                                                                                                                                                                                                                                                                                Mismatches
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US-60-248-505-643
; Sequence 643, Application US/60248505
                                                                                                                                                                                                                                                             ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(27355)
; OTHER INFORMATION: n = A,T,C or
US-60-248-505-643
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ TD NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 370748 ctgcccgagttga 370760
                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
NUMBER OF SEO ID NOS: 1998
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 643
LENGTH: 27355
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Beasley, Ellen
                                                                                                                                                            Query Match 4.2%;
Best Local Similarity 52.7%;
Matches 68; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09103840A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR TITLE OF INVENTION: PROTEINS, AND USES THEREOF FILE REFERENCE: c1000918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FLEISCHMAN, ROBERT D. APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               404 TCGGCAGCTGTGCAATTCCCCGGCATATTTGAACCCGTTGAGTATAAGAATTACTTGCTCG 463
                                            650
                                                                                                       590 TGAGGAGCTTCTTTCTTGCGGTCCGCTCAAACTCCGAAAAGAGAAAGGAGTTTTTGTGACC 649
tggctatagattctgatcatgagatcatcagctgtagtgggttgaacagtgtgtccccaa 5557
                                        TCGTTATAGTTCCTGAGCTTGAGGAGTTCACACCCCTTGATGTTAGAAAAGCGGACCAAA 709
                                                                              tggagcgcttcctttttaaggactgtgaaaatgcaacaaagggtacgtggaaatttacc 5497
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Pred. No. 16;
0; Mismatches
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Pred. No. 39;
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; NAME/KEY: misc_feature
; LOCATION: (1)...(44239)
; OTHER INFORMATION: n =
US-60-248-505-102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature; ICCATION: (1)...(27785); OTHER INFORMATION: n = A,T,C or GUS-60-248-505-284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; SEQ ID NO 284
; LENGTH: 27785
; TYPE: DNA
; ORGANISM: human
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GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 102
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 102, Application US/60248505 GENERAL INFORMATION:
Query Match
Best Local Similarity
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Best Local
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CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 1998
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLA:
TITLE OF INVENTION: RECEI
TITLE OF INVENTION: PROFI
                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 1998
                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: c1000918
                                                                                                                                                    ORGANISM: human FEATURE:
                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                            LENGTH: 44239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5988 aaattcaca 5996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5558 aaattcaca 5566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5868 tggagcgcttcctttttaaggactgtgaaaaatgcaacaaagggtacgtggaaatttacc 5927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              590 TGAGGAGCTTCTTTCTTGCGGTCCGCTCAAACTCCGAAAAGAGAAAGGAGTTTTGTGACC 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       710 TAATGGAGA 718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Similarity 68; Conserv
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                                                                                                                                                                                                                                                                                                                                           ISOLATED HUMAN G-PROTEIN COUPLED RECEPTORS, NUCLEIC ACID MOLECULES PROTEINS, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISOLATED HUMAN G-PROTEIN COUPLED
RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
PROTEINS, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.2%;
 4.2%;
59.6%;
                                                                                               A,T,C
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Pred. No. 16;
 Score 31.4;
Pred. No. 1
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                   DВ
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18;

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; FEATURE:

, NAME/KEY: misc_feature

; LOCATION: (1)...(85729)

; OTHER INFORMATION: n = 1

US-60-248-505-429
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                                                                                                                                                                APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 215
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 215, Application US/09739449 GENERAL INFORMATION:
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Best Local
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NAME/KEY: unsure
LOCATION: (1)..(318095)
OTHER INFORMATION: unsure at all n locations
-09-739-449-215
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TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52894 atctccaggtgaccacaaagatttaaagtagaatggcggaccagccactagagggagcat 52953
                                                                                   ORGANISM: Agrobacterium tumefaciens FEATURE:
                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52954 taatacagtcttttgtattactgtgtcaa 52982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11464 taatacagtcttttgtattactgtgtcaa 11492
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                                                                                                                                                LENGTH: 318095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     665 AGCTTGAGGAGTTCACACCCCTTGATGTTAGAAAAGCGGACCAAATAATGGAGAGGGGAT 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       725 ACATANAGGCCTTAGAGGTACTTTCTGAA 753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atctccaggtgaccacaaagatttaaagtagaatggcggaccagccactagagggagcat 11463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCTTGAGGAGTTCACACCCCTTGATGTTAGAAAAGCGGACCAAATAATGGAGAGGGGAT 724
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Pred. No. 23;
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Query Match

4.28;

Score 31.4;

DB 5;

Length 318095;

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TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-724-866A-7119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 137196 GTGAGGCGGCGTCTGCGGAACGGTTGCGTCCGCCGCCGAGAATTTTTTGAGATCGAAGGTA 137137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δõ
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; ORGANISM: Homo sapiens US-09-801-833-7424
                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/801,833
CURRENT FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 09/371,168
PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/095,907
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/095,907
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/095,907
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                                                                 SOFTWARE: Fast
SEQ ID NO 7424
LENGTH: 4157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/171,432
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 24913
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 7119
                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Glucksma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7424, Application US/09801833
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Best Local
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                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM TITLE OF INVENTION: HUMAN BRAIN LIBRARY FILE REFERENCE: 1600.1037-005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/724,866A CURRENT FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Polynucleotides, Material Incorporating TITLE OF INVENTION: Them, and Methods for Using Them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 11000.1049BU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Havukkala, Ilkka
                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 CAGCCTTCTGAAGAGGGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 GAGCGCCGGGGCAATCGTTTCGGTCTTTTATGCCTCAGGCTACTCCCCTGAAGGGATGTT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 ataaagagaagttcaccaaggtggaccacgaaaaccgtgtgaa 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 CTGAAGGGATGTTCAGCCTTCTGAAGAGGGTAAACTGGCTGAA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 ctggaaggccagggcccgtcggcaccatcatcaagatcactttggccggaggtttctcct 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L Similarity
58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    Glucksmann, M. Alexandra
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                                                                                                                      for
                                                                                                                      Windows Version 4.0
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0; Mismatches
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; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(479874)

; OTHER INFORMATION: n = A

US-60-248-505-72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 407868 CCACCATGCTGTTCTCATGACAGTGAGTGAGTTCTCACAAAACCTGATGGTTTTAAAAGT 407809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 407928 AATCACAAGATGTCAAGGGAGGAGGAACCTGGTGGGGAGGTGATGGGATCATAAGGACAGTTT 407869
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                                                                                                                                                                                                                                                                                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 72, Application US/60248505
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
                                                                                                                                                                                                                                                                                           Sequence 2334, Application US/09739449 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 72
                                           SEQ ID NO 2334
LENGTH: 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.1%;
Best Local Similarity 52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.18;
Best Local Similarity 64.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                   APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR PILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 479874
TYPE: DNA
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: c1000918
CURRENT APPLICATION NUMBER: US/60/248,505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE:
ORGANISM: Agrobacterium tumefaciens
                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2634 AAAATAAATGC 2624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2694 GCACCAGCAAAAGCGATTTCCAACATATGTGTTTTGGAGGTAATTAAGTAACTCTGTATA 2635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 GGTGAGC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 AGGGTGAGGGC 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 ATTGAGGAAATTTGAAGAGATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGCATAGC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCACATAGGTGTTTTGAAAGCTATAAACGAGCTCGGTATAAGGGTGAGGGCTTTAAGCGG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31; DB Pred. No. 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 479874;
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Search completed: June Job time: 20249 sec

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2001, 01:53:50

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CURRENT APPLICATION NUMBER: US/09/833,381
CURRENT EILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1530
LENGTH: 543
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                                         밁
                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; LOCATION: (1)...(543)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-09-833-381-1530
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; LOCATION: (1)..(548)
; OTHER INFORMATION: unsure at all n locations
US-09-739-449-2334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1530, Application US/09833381 GENERAL INFORMATION:
                                                                                                                       Matches
                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Robison, Keith E. TITLE OF INVENTION: Novel Nucleic Acid and FILE REFERENCE: 5800-119
                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
532 GTTGATGTCCTTCCCATAGA 551
                                     105 ggtattctcaagatccatgccagggagatctttgactctcgcgggaatcccactgtagag 164
                                                                          472 GGTATAGTTAACAACCTTCCCGTTGAGCCCTTTCAGGAAAGCGGTATTCCCCACCGTTTGC 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 GGCATATTTGAACCCCGTTGAGTATAAGAATTACTTGCTCGTTGACGGAGGTATAGTTAAC 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 gctggagatcttgctcaggaattaacggatgatcttagtacccttttgcg 174
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                                                                                                           4.0%;
Local Similarity 61.2%;
les 49; Conserva+*...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 atacaggcagtggttccgtttcttgatctcgattgatccggcttatgcgcaggactcata 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.1%;
                                                                                                                   Score 30.4; DB Pred. No. 8.8; 0; Mismatches
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Pred. No. 6.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                        DB 5;
                                                                                                                     31;
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                                                                                                                                                          Length 543;
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM nucleic - nucleic search, using sw model
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1: /cgn2_6/ptodata/2/pna/US

2: /cgn2_6/ptodata/2/pna/US

3: /cgn2_6/ptodata/2/pna/US

4: /cgn2_6/ptodata/2/pna/US

5: /cgn2_6/ptodata/2/pna/US

6: /cgn2_6/ptodata/2/pna/US

7: /cgn2_6/ptodata/2/pna/US

8: /cgn2_6/ptodata/2/pna/US

8: /cgn2_6/ptodata/2/pna/US
Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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756
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cgn2_6/ptodata/2/pna/US08E_COMB.seq:*
cgn2_6/ptodata/2/pna/US08E_COMB.seq:*
cgn2_6/ptodata/2/pna/US09C_COMB.seq:*
cgn2_6/ptodata/2/pna/US091_COMB.seq:*
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cgn2_6/ptodata/2/pna/US095A_COMB.seq:*
cgn2_6/ptodata/2/pna/US095A_COMB.seq:*
cgn2_6/ptodata/2/pna/US095B_COMB.seq:*
cgn2_6/ptodata/2/pna/US095B_COMB.seq:*
cgn2_6/ptodata/2/pna/US096B_COMB.seq:*
cgn2_6/ptodata/2/pna/
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                                                                                      /cgn2_6/ptodata/2/pna/US6001_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6002_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6003_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6004_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6005_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6006_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6006_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6008_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US086_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US083_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US088
                                                                                                                                                                                                                                                                                                                                                         _6/ptodata/2/pna/US096E_COMB.seq:*
_6/ptodata/2/pna/US097A_COMB.seq:*
_6/ptodata/2/pna/US097B_COMB.seq:*
_6/ptodata/2/pna/US097C_COMB.seq:*
_6/ptodata/2/pna/US097C_COMB.seq:*
_6/ptodata/2/pna/US6000_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US6027_COMB.seq
               /cgn2_6/ptodata/2/pna/US6024_COMB.seq:
/cgn2_6/ptodata/2/pna/US6025_COMB.seq:
/cgn2_6/ptodata/2/pna/US6026_COMB.seq:
                                                                                                        /cgn2_6/ptodata/2/pna/US6018_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6019_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6020_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6021_COMB.seq:*
                                                                                                                                                                                                     /cgn2_6/ptodata/2/pna/US60
                                                                                                                                                                                                                          /cgn2_6/ptodata/2/pna/US60:
                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/pna/US6012_COMB.seq:*
                                                                     cgn2_6/ptodata/2/pna/US6022_COMB.seq:*
cgn2_6/ptodata/2/pna/US6023_COMB.seq:*
                                                                                                                                                                                     cgn2_6/ptodata/2/pna/US6017/
                                                                                                                                                                                                                                          cgn2_6/ptodata/2,
                                                                                                                                                                                                                                                           cgn2_6/ptodata/2/pna/US60
                                                                                                                                                                                     _COMB.seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Match Length DB Query H SUMMARIES Description

Result No.	Score	Query Match	Length	BCG	ID	Description
ນ 1	756 397 8		756 750	17	-242-2 -242-2	quence
ωı	ω.		2108	16	S-09-221-017	
4		7.	Ν	16	S-09-252-991A-118	Sequence 11
5	7.	•	S	16	S-09-252-991A-122	e e
6	7.	7.6	8	16	S-09-252-991A-	Œ
c 7	7	7.6	2616	16	S-09-252-991A-133	ce
	7.		ω	40	-60-082-302-692	nce
. 9	54	٠	915	18	-09-489-039A	nce
	52.4		48	26	-09-663-779-578	W
11	50		\mathbf{L}	17	9-328-352-1	w
	46.2	•	95	16	-09-252-691-372	10
13	46.2	6.1	954	16	9-252-6910	
14		6.1	-	16	-09-231-899-12	Sequence
_	•	5.9	574	48	-60-168-139-214	10
c 16		•	S	19	S-09-514-000-	w
17	Ñ	5.7	858	29	S-09-739-449-466	w
c 18	٠	5.7	037	19	S-09-514-000-31	10
19		•	300663	29	S-09-739-449-21	
27	ء د	л U	n u	1 2	-00-339-35	Sequence 281
22	40.4		ے د	30 t	-466-194-14	
N	9		\sim	21	S-09-540-236-102	Sequence
24		•	\circ	44	S-60-128-476-	Sequence
N	39.4	٠	6705	40	-60-082-116-20	
c 26	9	5.2	6	22	-09-596-002-4	
N	9	•	922	46	-60-140-121-41	W
28	7.	•	305	21	09-540-229-1374	Sequence
29	37.6	•	ıσ	21	-09-540-229-1156	w
3 2	٠.	٠	,		S-09-540-229-13	10
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ω (4	35.4	4.7	·ω	51	S-60-191-637-36	
35	35.4	4.7	5591	51	S-60-191-681-	Sequence 296
ω	5	4.7	343	49	-60-173-464-30	w
w	35.4	4.7	13437	51	S-60-191-637-36	10
w	5	4.7	34	51	-60-191-681-29	10
c 39	5	4.7	030	19	S-09-528-237A-286	
	35	4.6	6	52	-60-207-458-15236	,,,
41	35	. 4.6	621	25	-09-654-617-12335	Sequence
42	35	4.6	2	27	-09-684-016-12335	
4 ω			_	ŧ		
;	35	4.6		25	S-09-654-617-12335	
44	3 3 5 5	4.6	900	25	S-09-654-617-12 S-09-684-016-12	

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720 660 600

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; MOLECULE TYPE: US-09-382-242-26
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                                                                                                                                                                                                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 756; Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 619-678-5099 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
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LENGTH: 756 NUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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TOPOLOGY: LIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: LA JOLLA
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                          AGCGGGGTGAGCGCCGGGGCAATCGTTTTCGGTCTTTTATGCCTTCAGGCTACTCCCCTGAA 180
                                                                                                                               INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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REID, John
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                                                                                                                                                                                                                                                                  Score 756; DB 17;
Pred. No. 3.6e-227;
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                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH
COMPUTER: 1BM PS/2
OPERATING SYSTEM: MS-
                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
             ATTORNEY/AGENT INFORMATION: NAME: HAILE, LISA A.
                                                                                                                               SOFTWARE: WORD PERFECT 6.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                 STREET: 4225 EXECUCITY: LA JOLLA
STATE: CALIFORNIA
                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 92037
                                           FILING DATE:
                                                                                      CLASSIFICATION:
REGISTRATION NUMBER:
                                                                                                     FILING DATE:
                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                              ADDRESSEE:
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4225 EXECUTIVE SQUARE,
                                                                                                                                                                                                                                                                                                                            KOSMOTKA, Anna
KOSMOTKA, Anna
TON: ESTERASES
                                                                                                                                                                                                                                                                                                                                                                    SWANSON, Ronald V. WARREN, Patrick V.
                                                                                                                                                                                                                                                                                                                                                                                                   LINK,
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REID, John
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38,347
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RE, STE 1400
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RESULT 3
US-09-221-017B-305
; Sequence 305, Application US/09221017B
; GENERAL INFORMATION:
; APPLICANT: ROSS, Bruce C.
; APPLICANT: NOSS, Bruce C.
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TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 750 NUCLEOTIDES
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s 516; Conserv
                                                                                                                                                                        CCTGAGCTTGAGGAGTTCACACCCCTTGATGTTAGAAAAGCGGACCAAATAAT 713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCGGCATATTTGAACCCGTTGAGTATAAGAATTACTTGCTCGTTGACGGAGGTATAGTT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGGCTCTATACCTCTCGGAAGGGAGTTTAATCCCCGCACTTCTCGGCAGCTGTGCAATT 420
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                                                                                                                                                      CCTCCCCTTGAAGAGTTCTCTCCTCTGGACGTAAATAAGGCGGACGAGATATT
                                                                                                                                                                                                                        TTTCTGGCGGTTCGTTCCAATTCGGAAAAGAGAAAGGAGTTCTGCAACGTAGTTATAGAA
                                                                                                                                                                                                                                                      TTTCTTGCGGTCCGCTCAAACTCCGAAAAGAGAAAGGAGTTTTGTGACCTCGTTATAGTT 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGATGTTAAAACTCCTGAAAGAGGTAAACTGGCTCAAACTTTTTAAGTTCAAAACACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCGCCCATATAGGTGTTTTAAAAGCTCTGGAAGAGCTCGGTATAAAGGTAAAGAGGCTC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGAAATTGAAGAGGTTTGAAGAGGTTAACTTAGTTCTTTCGGGAGGGGCTGCCAAGGGT 72
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N: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
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72.4%;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: MODITOY, Gladys H
27340-2007
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 338; Conserv
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                                                                                                                                                                                                             1247
 1427
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
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FRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PP2911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                   204
                                                                                                                                                               84 AGCTATAAACGAGCTCGGTATAAGGGTGAGGGCTTTAAGCGGGGTGAGCGCCGGGGCAAT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PP11 FILING DATE: 31-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: Windows SOFTWARD -
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CITY: Palo Alto
                                                                                                                                                                                                                                              24 GATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGCATAGCCCACATAGGTGTTTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
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CAAAAATTTCAGATTCCTAACAGAGTGGCAAATACCACAAAGAGGTGTATTCAGCATCCA 1486
                                 GGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAAGGGATTGATAGGGTGGGA 263
                                                                                                                                                                                                             GATAGGCTTGGCTCTTAGCGGCGGAGCGGCCAAAGGCTTTGCACATTCGGGAGTACTCCA 1306
                                                                    GGTAGCTGCACTCTATGCCGATGGATACAGGCCCGAAGAGATTCCACAATTATTCCGAGG
                                                                                                     CGTTTCGGTCTTTTATGCCTCAGGCTACTCCCCTGAAGGGATGTTCAGCCTTCTGAAGAG 203
                                                                                                                                        TGCTCTTGAGGACAATGGGATTCGTCCCGACATCATAGCAGGTACGAGTGCAGGAGCGTT
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                                                                                                                                                                                                                                                                                   Conservative
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Pred. No. 5.4e-18;
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1180
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US-09-252-991A-1180
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                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 1180
                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                         LENGTH: 825
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143 TCGTTTCGGTCTTTTATGCCTCAGGCTACTCCCCTGAAGGGATGTTCAGCCTTCTGAAGA 202
                                                                               83
                                                                                                                                                                                                                   Match 7.6%;
Local Similarity 53.0%;
                                                                                                                                                        23 AGATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGCATAGCCCACATAGGTGTTTTGA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGTTTAATCCCCGCACTTCTCGGCAGCTGTGCAATTCCCGGCATATTTGAACCCGTTGA 443
                                    aggccctcgacgaacagggcatccagatcgacgccatcgccggcaccagcatgggcgcgg
                                                                           AAGCTATAAACGAGCTCGGTATAAGGGTGAGGGCTTTAAGCGGGGGTGAGCGCCGGGGCAA 142
                                                                                                               agatcggtctggtcctctccggcggtgccgcccgcggcctggcccatatcggcgtgctca 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTTCTT 1973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTACTT 747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAAAAGAGAAAGGAGTTTTGTGACCTCGTTATAGTTCCT---GAGCTTGAGGAGTTCAC 680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAGGAAAGCGGTATTCCCCACCGTTTGCGTTGATGTCCTTCCCATAGAGCCGGAAAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTATAAGAATTACTTGCTCGTTGACGGAGGTATAGTTAACAACCTTCCCGTTGAGCCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCCCTTGATGTTAGAAAAGCGGACCAAATAATGGAGAGGGGATACATAAAGGCCTTAGA 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCGTGAAGACTGCCGTTATCTCATAGGAGTACACCTCAATCCCAAAGAGCCTTCCGACTA 1786
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                                                                                                                                                                                                                   Score 57.2; DB 16; Pred. No. 9.3e-07;
                                                                                                                                                                                              Mismatches 108;
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US-09-252-991A-1225
                                                                                                                                NUMBER OF SEQ ID NOS:
SEQ ID NO 1270
LENGTH: 2280
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LENGTH: 1257
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Best Local Similarity 53.6
Matches 122; Conservative
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TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
-09-252-991A-1270
                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788
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                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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TITLE OF INVENTION:
FILE REFERENCE: 107
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TITLE OF INVENTION:
FILE REFERENCE: 107
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ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 agatggactggcagcaggcgctgtccgacgcgccgccgcgcaaggacgtg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agatcggtctggtcctctccggcggtgccgcccgcggcctggcccatatcggcgtgctca 161
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VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING

VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

ENCE: 107196.136
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VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING

VENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING

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Pred. No. 1.1e-06;
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1336
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                                                                                       Sequence 692, Application US/60082302 GENERAL INFORMATION:
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LENGTH: 2616
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TITLE OF INVENTION:
FILE REFERENCE: 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 53.0 nes 122; Conservative
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                                                                                                                                                                                                                                     GGGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAAGGGATTG
                                                                                                                                                                                                                                                                         TGGTCGGCGGCCTGTACGCCTCCGGCTACACCCCCGCCGAACTGGA&CGCATCGCCCTGG 195
                                                                                                                                                                                                                                                                                                                                              AGGCCCTCGACGAACAGGGCATCCAGATCGACGCCATCGCCGGCACCAGCATGGGCGCGG
                                                                                                                                                                                                                                                                                                                                                                                  AAGCTATAAACGAGCTCGGTATAAGGGTGAGGGCTTTAAGCGGGGGTGAGCGCCGGGGCAA 142
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                                                                                                                                                                                                                                                                                                        TCGTTTCGGTCTTTTATGCCTCAGGCTACTCCCCTGAAGGGATGTTCAGCCTTCTGAAGA 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marc J. Rubenfield et al.
         CORLEY, NEIL C.
RUSSO, FRANK D.
HANN, AMY L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                    LAGACE, ROBERT E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UN: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS ON: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS 107196.136
JOE .D
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53.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 57.2; DB 16; Pred. No. 1.6e-06;
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US-09-489-039A-3153; Sequence 3153, Application US/09489039A
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                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Gary Br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 53.0 Matches 122; Conservative
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-77
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR EILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                     APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 65
SEQUENCE CHARACTERISTICS:
LENGTH: 26737 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25536 AGATCGGTCTGGTCCTCCCGGCGGTGCCGCCGCGGCCTGGCCCATATCGGCGTGCTCA 25595
                                                                                                                                                                                                                                                                                                          25716 AGATGGACTGGCAGCAGGCGCTGTCCGACGCGCCGCCGCGCAAGGACGTG
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TOPOLOGY: cir
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PM
TELECOMMUNICATION INFORMATION:
TELECHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: FINNEY, GREGORY L.

APPLICANT: BROOKS, JACQUELINE
TITLE OF INVENTION: NUCLECTIDE SEQUENCES OF PSEUDOMONAS AERUGINOSA
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                      143
                                                                                                                                                                                                                                                                                                                                                   203 GGGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAAGGGATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: HEREW
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PALO ALTO
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Pred. No. 4.4e-06;
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; NUMBER OF SEQ ID NOS:
; SEQ ID NO 3153
; LENGTH: 915
; TYPE: DNA
; ORGANISM: Klebsiella p
US-09-489-039A-3153
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US-09-663-779-578/c
Sequence 578, Application US/09663779
GENERAL INFORMATION:
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; SEQ ID NO 578
; LENGTH: 1486
; TYPE: DNA
; ORGANISM: Bacillus thuringiensis
US-09-663-779-578
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                                                                                                                                                                                                                                                                       Query Match 6.9%;
Best Local Similarity 46.6%;
Matches 167; Conservative
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Best Local Similarity
Matches 147; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/663,779
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/154,678
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEC. 1999-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Corbin, David R. APPLICANT: Malvar, Thomas M. APPLICANT: Shukla, Hridayabhiranjan TITLE OF INVENTION: THEREOF TITLE OF INVENTION: THEREOF 38-21(51376)B
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                                                                                                                                                                                                              2 TGAGATTGAGGAAATTTGAAGAGATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGCA 61
                                                                                                                         TAGCCCACATAGGTGTTTTGAAAGCTATAAACGAGCTCGGTATAAGGGTGAGGGCTTTAA 121
                                                        GCGGGGTGAGCGCCGGGGCAATCGTTTCGGTCTTTTATGCCTCAGGCTACTCCCCTGAAG 181
                                                                                                TTGCTCATATTGGTGTAATAAAGGTTTTAAGGGAAGCGGGTATCCCTATTCACATGATTG 243
                                                                                                                                                                                      TGAGAAAAATGAAAGAACCAAAGATTGGTTTAGCGCTTTGGGTCTGGAGGAGCGAAAGGGT 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gctgttgccaccaatttaagcaccggtagggagctgtggtttaccgaaggcgatctacat 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATATGCGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCGGAAGGGAGTTTAATC 393
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                                                                                                                                                                                                                                                                       Score 52.4; DB 26;
Pred. No. 4e-05;
0; Mismatches 191;
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Pred. No. 1e-05;
0; Mismatches 155; Indels
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                                                                                                                                                                                                                                                                                                                 Length 1486;
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RESULT 12
US-09-252-691-372
~~uence 372, Application
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-1258
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US-09-328-352-1258
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1258
SEQ ID NO 1258
LENGTH: 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1258, Application US/09328352
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                           632
                                                                                                                                                                                                                                                  392 TCCCCGCACTTCTCGGCAGCTGTGCAATTCCCCGGCATATTTGAACCCGTTGAGTATAAGA 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 TGAAGGGATTGATAGGGTGGGAGAAGGCTATAAGATTCCTTGAGGAAGTTCTCCCTTACA 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 TAAGATTCCTTGAGGAAGTTCTCCCTTACAGGAGAATAGAAAAACTTGAGATACCGACGT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 TCGTTCTTTCGGGAGGTGCAAAGGGCATAGCCCCACATAGGTGTTTTGAAAGCTATAA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 206; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 AAAATTTAGAAGAGTTAGATATCCCGACGGCTGTTGTGGCTACTGACATATTGAAGGG
                                                                                                                                           aatctgaatatgtagatggtggtttagttagtccagtacctgttga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAAGGGATTGATAGGGTGGGAGAAGGCTA 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTTTTATGCCTCAGGCTACTCCCCTGAAGGGATGTTCAGCCTTCTGAAGAGGGTAAACT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGAATAGAAAAACTTGAGATACCGACGTATATATGCGCGACGGATTTATACTCGGG
                                                                                                                                                                    ATTACTTGCTCGTTGACGGAGGTATAGTTAACAACCTTCCCGTTGA 497
                                                                                                                                                                                                                            ggcaagccgtgagagcatcagcctcaataccaagcatgtttgtgccgactaaaattggta
                                                                                                                                                                                                                                                                                                                 atgtggtggcaacagagctaaagcatggcaccaaaactgtatttaattatggcaatacgg 571
                                                                                                                                                                                                                                                                                                                                                            ATATATGCGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCGGAAGGGAGTTTAA 391
                                                                                                                                                                                                                                                                                                                                                                                                       aagactatgtaaaccagcaagtaaataacttgccgctcgaaaaaatgaaaattccgatgt 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cggcagatgttcgtgacatcagtattggtttaaaaggtttctttgatggcaaaaagttg
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ilarity 44.2%;
Conservative
                                 US/09252691B
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Pred. No. 0.00019;
0; Mismatches 260
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; SEQ ID NO 372
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Enterobacter cloacae
US-09-252-691-372
RESULT 14
US-09-231-899-12
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/074,787
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 11326
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CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                  448
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                                                                                                                        460 CTCGTTGACGGAGGTATAGTTAACAACCTTCCCGT 494
                                                                                                                                                                                                                                                                                      340 GCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCGGAAGGGAGTTTAATCCCCGCA 399
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                                                                               ctcgttgacggtggcgtagtgaatcctgtccctgt 542
                                                                                                                                                              gttcgtgcatcctgtagtatgcctgggttaatggcgcctgtgcctcacaacggctactgg
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56.1%;
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Pred. No. 0.0029;
Pred. No. 0.0029;

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Pred. No. 0.0029;
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: SEQ ID NO 2142

: LENGTH: 5742

: TYPE: DNA

: ORGANISM: Agrobacterium tumefaciens

US-60-168-139-2142
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Best Local Similarity
Matches 99; Conserv
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GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequence And Uses Thereof
FILE REFERENCE: 38-21(15490)A
CURRENT APPLICATION NUMBER: US/60/168,139
CURRENT FILING DATE: 1999-12-01
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                                                                                                                        Query Match
Best Local Similarity
Matches 114; Conserv
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APPLICANT: Mett, James G
APPLICANT: Mett, James G
APPLICANT: Facciotti, Daniel
TITLE OF INVENTION: SCHIZOCHYTRIUM PKS GENES
FILE REFERENCE: CGNE 131.02US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1997-06-04
EARLIER APPLICATION NUMBER: 09//
EARLIER FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 86
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339 CGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCGGAAGGGAGTTTAATCCCCGC 398
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                                           CATGCAGGAGCATCTGGAAGGCCTGCGCGTCGAAAACCTCGAGCACCCCTTCATCGCTGT 4387
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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                  APPLICANT:
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  LINK, Steven
SWANSON, Ronald V.
WARREN, Patrick V.
KOSMOTKA, Anna
TAVENTION: ESTERASES
          INVENTION:
SEQUENCES:
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                                                          MURPHY, Den
REID, John
MAFFIA, Ant
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                                                           Anthony
                                                                                Dennis
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NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEPAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 29:
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LENGTH: 750 NUCLEOTIDES
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ADDRESSEE: FISH & RICHARDSON P
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ZIP: 920
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                                                                                                                                AGGGCTCTATACCTCTCGGAAGGGAGTTTAATCCCCGGACTTCTCGGCAGCTGTGCAATT
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AACAACCTTCCCGTTGAGCCCTTTCAGGAAAGCGGTATTCCCCACCGTTTGCGTTGATGTC
                                      CCCGGGATTTTTGAACCAGTTGAGTACGAGAATTTTCTACTTGTTGACGGAGGTATAGTG
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; ORGANISM: Vibrio marinus
US-09-090-793-12
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                                                                                                                                                                                     Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 12
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Calgene, LLC
TITLE OF INVENTION: Production of polyunsaturated fatty acids by
TITLE OF INVENTION: of polyketide-like synthesis genes in plants
FILE REFERENCE: CGNE.131.01US
CURRENT APPLICATION NUMBER: US/09/090,793
CURRENT FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,650
EARLIER FILING DATE: 1997-06-04
NUMBER OF SEQ. ID NOS: 66
                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
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                                                                                      APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT
                                                     CORRESPONDENCE ADDRESS:
                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                         203
                                                                                                                                                                                                                                                                                                                                                                                                            143 TCGTTTCGGTCTTTTATGCCTCAGGCTACTCCCCTGAAGGGATGTTCAGCCTTCTGAAGA 202
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STREET:
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                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGCATAGCCCACATAGGTGTTTTGA 82
                                                                                                                                                                                                                                                                                                                                       GGGTAAA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                    aatacctgttagagcaagatataagaccgaatgtaattgcgggtacaagtgctggctcta 14936
                                                                                                                                                                                                                                                                                                                                                                           tggttggtgcactttattgctcaggacttgagattgatgacattttacaattcttcatcg 14996
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 Alexandria
               E: Foley & Lardner
1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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52.9%;
                 Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46.2; DB 4;
Pred. No. 7.1e-05;
0; Mismatches 88;
                 Suite
                                                                                          FOWLPOX VIRUS
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Best Local :
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TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
1034 GGAATTAATT 1025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                         123 CGGGGTGAGCGCCGGGGCAATCGTTTCGGTCTTTTATGCCTCAGGCTACTCCCCTGAAGG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 5.3%; Score 40.4; DB 1; Local Similarity 7.4%; Pred. No. 0.0024; hes 32; Conservative 206; Mismatches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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ZIP: 22313-0299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                    CGGCATATTT 432
                                                                                                                                             GAGAATAGAAAAACTTGAGATACCGACGTATATATGCGCGACGGATTTATACTCGGGAAG 362
                                                                                                                                                                                                                   GAAGGGATTGATAGGGTGGGAGAAGGCTATAAGATTCCTTGAGGAAGTTCTCCCTTACAG 302
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                                                                       RRRRRRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCTCGACCTGCAGCCAAGCTC
                                                                                                        GGCTCTATACCTCTCGGAAGGGAGTTTAATCCCCGCACTTCTCGGCAGCTGTGCAATTCC
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RESULT 6
US-08-747-574-3/c
; Sequence 3, Application US/08747574
; Patent No. 6015939
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Best Local Similarity
Matches 62; Conserva
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GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 97-1140
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2901-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                               481
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                               493 GTTGAGCCCTTTCAGGAAAGCGGTATTCCCACCGTTTGCGTTGATGTCCTTCC 545
                                                                                                                                                                                                    541 GAAGCCCTTGAGAAGGCAAATATAAGACCCGTTGCGGACGTATTCCTTGAAAAACTTGAG 482
                                                                                                                                                                                                                                         433 GAACCCGTTGAGTATAAGAATTACTTGCTCGTTGACGGAGGTATAGTTAACAACCTTCCC 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2057 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                             GTAAATGAGGAAGAGGGAAGCGTAAAATACACCGTTAGCTTTGAAGTCGCTCC 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
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RYU, JAE RYEON
CHOI, IN GEOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAN, YE SUN
YU, GYU YU
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SUPEROXIDE DISMUTASE AND PROTEIN EXPRESSED IN ESCHERICHIA
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                                                                                                                                                                                                                                                                           Score 31.4; DB 3;
pred. No. 1.2;
0; Mismatches 51;
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                                                                                                                                                                                                                                                                               51;
                                                                                                                                                                                                                                                                                                                Length 2057;
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RESULT 7
US-08-607-509-3
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                                                                                                                                                                                   Sequence 3, Application US/08607509 Patent No. 5876735
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (916) 753-15
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,
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CORRESPONDENCE ADDRESS:
                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                           642 TTGTGACCTCGTTATAGTTCCTGAGCTTGAGGAGTTCACACCCCTTGATGTTAGAAAAGC 701
                                                                                                                                                                                                                                                                                       251 TCCTGACCTGAATGCAGATAAAGGACGTGAGGATCTCCCACCAGTTGTTCTGAGATCAGC
                                                                                                                                                                                                                                                                                                                                                         311 CAGCTCTTTCAGCTCATTCTTTGATGGTAATGGCACAATGTCAAATATCCCCCTTAGAGAA 252
                                                                                                                                                                                                                                                                                                                                                                                        582 CATCCTTTTGAGGAGCTTCTTTCTTGCGGTCCGCTCAAACTCCGAAAAGGAGAAAGGAGTT 641
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                                 CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/023, FILING DATE: August 6, 1996
            COUNTRY:
                                                              STREET:
                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Calgene, Inc. STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                           64;
98104-7092
                             Washington
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                                                                6300 Columbia
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                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                 SEED and BERRY LLP
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                                                                                                                                    METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES
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L5939ember 7,
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                                                                  Center, 701 Fifth Avenue
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Pred. No. 2.3;
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COMPUTER READABLE FORM:

TYPE:

Floppy disk

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US-08-634-642-3
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Best Local Similarity
Matches 82; Conserv
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NAME/KEY:
                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1867 base pairs
                ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                    SOFTWARE: PatentIn Rele
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 GGTGAGCGCCGGGGCAATCGTTTCGGTCTTTTATGCCTCAGGCTACTCCCCTGAAGGGAT 185
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                                               APPLICATION NUMBER: FILING DATE: 18-APR-CLASSIFICATION: 424
                                                                                                                                                                                                                                                               STREET: 6300 CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1: CLASSIFICATION:
                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGATTGATAGGGTGGGAGAAGGCTATAAGATTCCTTGAGGAAGTTCTC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTCCGCTTCCTGCCGAAGGACATCCAGGTCGCGCTCTTCTCCGCCACGATGCCGGAGGA 760
                                                                                                                                                                                                                 98104-7092
                                                                                                                                                                                                                                                  Washington
                                                                                                                                                                                                                                                                                   E: SEED and BERRY LLP 6300 Columbia Center,
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TO NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                          Reed, Steven G.
                                                                                                                         PatentIn Release #1.0,
                                                                                                                                                                                                                                   USA
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                                                                  18-APR-1996
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                                                                                                                                                                                                                                                                                                                                                                         METHODS FOR ENHANCEMENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.9%;
                                                                                                                                                                                                                                                                                                                                                       PROTECTIVE IMMUNE RESPONSES
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                                                                                      US/08/634,642
31,392
                                                                                                                                                                                                                                                                                     Center,
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                                                                                                                                                                                                                                                                                     701 Fifth Avenue
                                                                                                                         Version #1.30
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US-08-989-370-3
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                                                                                                                        TELEFAX: (206)682-6031 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                      FILING CLASSICATION:
CLASSICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
NAME: Maki, David J.
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
OPERATING SYSTEM: FC-DOS/MS-DOS
                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reed, St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 GGTGAGCGCCGGGGCAATCGTTTCGGTCTTTTATGCCTCAGGCTACTCCCCTGAAGGGAT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        701 CTTCCGCTTCCTGCCGAAGGACATCCAGGTCGCGCTCTTCTCCGCCACGATGCCGGAGGA 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 GTTCAGCCTTCTGAAGAGGGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             641 GGTGCTCGACGACGATGATGAGATGCTGTCTCAGGGCTTCGCGGACCAGATTTACGAGAT 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    761 GGTACTGGAGCTGACGAAGAAGTTCATGCGCGACCCCGTGCGTATTCTC 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                             REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 12-DEC-1997
NAME/KEY:
                                 TOPOLOGY:
                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGATTGATAGGGTGGGAGAAGGCTATAAGATTCCTTGAGGAAGTTCTC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                               98104-7092
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                                                nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
                                                                                 1867 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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117..1325
                                 linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES
                                                                                                                                                                                                                                                                                                    US/08/989,370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ω
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Pred. No. 4.
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                              TOPOLOGY: L:
                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 756 NUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,359A
FILING DATE: February 16, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: HAILE, LISA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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OPERATING SYSTEM: MS-L-.

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                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: HAILE, LISA A. REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26, 55, 30
5942430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCCGCTTCCTGCCGAAGGACATCCAGGTCGCGCTCTTCTCCGCCACGATGCCGGAGGA 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KOSMOTKA, AULICANTON: ESTERASES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAFFIA, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROBERTSON, Daniel E
                                                                                                                                                                                                                  LINEAR
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                                                                                                                                                                              GENOMIC DNA
                                                                                                                                                                                                                                                  SINGLE
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   Score 29.6; D. Pred. No. 2.8;
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Pred. No. 4.1;
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                                       Length 756;
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Fanucci A., Allan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                    OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                  EATURE:
                                                                                              EATURE:
                                                                                                                                                                                                                                                                                                                                                                  OLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            571 TCTTTATATCCTTTTCCGGCTCTATGGGAAGGACATCAACGCAAACGGTGGGAATA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          576 TCTTCACATCCTTTTGAGGAGCTTCTTTCTTGCGGTCCGCTCAAACTCCGAAAAGA 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        631 TCTTTTCGGAGTTTGAGCGGACCGCAAGAAAGAAGCTCCTCAAAAGGATGTGAAGAATGT 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      516 TATTCCCACCGTTTGCGTTGATGTCCTTCCCATAGAGCCGGAAAAGGATATAAAGAACAT 575
                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
SOFTWARE: PatentI
                                                          NAME/KEY: CDS
NAME/KEY: 4051.4731
                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 2547..3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: EP 95201669.9 FILING DATE: 20-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                OTHER INFORMATION:
                                                                                                           OTHER INFORMATION:
                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                      OTHER INFORMATION:
                                                                                                                                                                                                                                                                     NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 352.
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
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                   NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
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CDS
4898..5854
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                                                                                                                           CDS
3249..3995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                 /product- "epsA"
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                                                                                                           /product= "epsD"
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                                                                                                                                                                        /product= "epsC"
                                                                                                                                                                                                                                      /product- "epsB"
                                               /product= "epsE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Release #1.0, Version #1.30
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                                                                                                                                                 RESULT 12
US-08-746-682A-1
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; LOCATION:
US-08-597-236-1
                                                                                                                    Sequence 1, Application US/08746682A Patent No. 5786184
                                                                                                                                                                                                                                                                                                                                                    Query Match 3.8%;
Best Local Similarity 55.4%;
                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                      GENERAL INFORMATION:
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OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: FEATURE:
                                           TITLE OF INVENTION: LACTIC BACTERIA PRODUCING TITLE OF INVENTION: EXOPOLYSACCHARIDES
                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: FEATURE:
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OTHER INFORMATION: /product= "epsK"
FEATURE:
                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                          602 TTCTTGCGGTCCGCTCAAACTCCGAAAAGAAAGAAAGGAGTTT 642
                                                                                                                                                                                                                                                                                                       542 TTCCCATAGAGCCGGAAAAGGATATAAAGAACATTCTTCACATCCTTTTGAGGAGCTTCT 601
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                                                                                                                                                                                                               246 TCTTATTTTTTGAAAAAAGAATGACAATTGAAATGAGGTT 286
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LOCATION: 11302.12222
OTHER INFORMATION: /product= "CDS (eps L)
OTHER INFORMATION: (eps k) on nucleotides
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LOCATION:
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LOCATION: 12233..1
OTHER INFORMATION:
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INCATION: 10392..11339
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OTHER INFORMATION: /product= "epsJ"
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LOCATION: 7736..8212
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 ADDRESSEE:
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8221..9192
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MOLLET, Beat
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13732..14305
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12233..13651
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RMATION: /product= "epsG"
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Pennie & Edmonds
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                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                  Score 29; DB
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                     Mismatches
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10392-11339"
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/746,682A
FILING DATE: 14-NOV-1996
CLASSIFICATION DATA:
APPLICATION UMBER: 08/597,236
FILING DATE: 20-JUN-1995
APPLICATION NUMBER: EP 95201669.9
FILING DATE: 20-JUN-1995
APPLICATION NUMBER: 30256
INFORMENT ARBOIT NUMBER: 30256
INFORMENT CHARACTER CHAR
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MEDIUM TYPE: Floppy disk
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CITY: N
NAME/KEY: CDS
LOCATION: 10392..11339
OTHER INFORMATION: /pro
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LOCATION:
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LOCATION: 1807..2535
OTHER INFORMATION: /product= "epsB"
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                                                                                                                           LOCATION: 9285..10364
OTHER INFORMATION: /product= "epsJ"
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LOCATION: 7736..8212
OTHER INFORMATION: /product= "epsh"
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OTHER INFORMATION:
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TOPOLOGY: li
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LOCATION: 352..1803
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6425..7540
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4051..4731
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2547..3239
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4898..5854
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3249..3995
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   /product= "epsK"
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RESULT 13
US-08-761-258-1
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US-08-746-682A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08761258 Patent No. 5756087
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Best Local Similarity
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LOCATION: 11302..12222
OTHER INFORMATION: /production: /production: /production: /eps k
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                     NUMBER OF SEQUENCE ADDRESS:

CORRESPONDENCE ADDRESS:

AnnRESSEE: Clba-Gelgy Corporation

AnnRESSEE: Thire Plains Road, P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY:
ATTORNEY/AGENT INFORMATION:
RAME: Welgs, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                            IIILE OF INVENTION: Genetically Modified Pseudomonas Strains
IIILE OF INVENTION: with Enhanced Biocontrol Activity
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                                                                                                                                                                                                                                          STREET: 520 wiit.
CITY: Tarrytown
                                                                                                                                                                                                                                                    ADDRESSEE: Clpa vega
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LOCATION:
                                                             CLASSIFICATION: 424
                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /function= "CDS on the OTHER INFORMATION: complementary strand" OTHER INFORMATION: /product= "orfz"
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OTHER INFORMATION:
                                                                               FILING DATE:
                                                                                            APPLICATION NUMBER:
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13732..14305
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340..345
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(eps k) on nucleotides 10392-11339"
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Pred. No.
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Best Local Similarity
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IMMEDIATE SOURCE:
CLONE: Plasmic
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HYPOTHETICAL:
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                                                                440 TTGAGTATAAGAATTACTTGCTCGTTGACGGAGGTATAGTTAACAACCTTCCCGTTGAGC 499
500 CCTTTCAGGAAAGCGGTATT 519
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LOCATION:
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OTHER INFORMATION: /product-
OTHER INFORMATION: "CDP-diacylgly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: complement (4616..4691)
OTHER INFORMATION: /product= "tRNA"
OTHER INFORMATION: /note= "(complementary DNA strand) Homology to glyW from OTHER INFORMATION: Coli."
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LOCATION:
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210..1688
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1906..3633
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                                                                                                                3.8%;
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/note= "Coding sequence for
CDP-diacylglycerol-glycerol-3-phosphate-3-phosphatidyltran
has homology to pgsA."
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                                                                                                                                                                                              nt (7400..8041)

/function= "response
regulator/transcription activator"
/product= "gacA (aka gafA)"
/note= "Coding sequence for gacA (aka gafA) has homology t
uvrY and gacA genes of E. coli and Ps. fluorescens,
respectively."
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/note= "coding sequence for sensor kinase rcsC, frzE, and bvgS genes of E. coli, M. Borditella pertussis, respectively."
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"CDP-diacylglycerol-glycerol-3-phosphate-3-phosph
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product= "UVR exonuclease subunit
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Pred. No. 24;
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Xanthus, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA
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COMPUTER READABLE FORM:
TIM TYPE: Floppy disk
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NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,
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                    OTHER INFORMATION: OTHER INFORMATION:
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SOFTWARE: PatentI
                                                        NAME/KEY: misc_RNA
LOCATION: compleme
                                                                                                              OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN: CGA267356 (aka MOCG134 and aka BL915)
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Hill, Dwight S.
Gaffney, Thomas D.
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Stafford, Jill M.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas fluorescens
complement (4616..4691)
WATION: /product= "tRNA"
WATION: /note= "(compleme
WATION: Coli."
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/note= "Coding sequence for methyltransferase has homology t
the cher and frzF genes from E. coli and Myxococcus xanthus,
respectively."
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Best Local Similarity
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                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19-OCT-19
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: RETITLE OF INVENTION: TO NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                 ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A
REGISTRATION NUMBER: 36,
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TELECOMMUNICATION INFORMATION:
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               REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 7112-0037.00
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ZIP: 20006-1812
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CITY: Washington
STATE: DC
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/product= "gacA (aka gafA)"
/note= "Coding sequence for gacA (aka gafA) has homology
uvrY and gacA genes of E. coli and Ps. fluorescens,
respectively."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atidyltrans."
/note= "Coding sequence for
CDP-diacylglycerol-glycerol-3-phosphate-3-phosphatidyltran
se has homology to pgsA."
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                                                                                                                           US/08/326,117B
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"CDP-diacylglycerol-glycerol-3-phosphate-3-phosph
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/function= "response
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Pred. No. 24;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5577 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
INFEATURE: TYPE: CDN
FEATURE: CDN
FEATURE: CDN
FEATURE: CDN
LOCATION: 197.4780

US-08-326-117B-1

Query Match
Best Local Similarity 52.0%; Pred. NO. 19;
MANE/KEY: CDS
MANE/KEY
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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                                                                                                                    752.8
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2: /SIDS2/gcgdata,

3: /SIDS2/gcgdata,

4: /SIDS2/gcgdata,

5: /SIDS2/gcgdata,

6: /SIDS2/gcgdata,

7: /SIDS2/gcgdata,

8: /SIDS2/gcgdata,
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length: 2000000000
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11:
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13:
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/SIDS2/gcgdata/geneseq/geneseqn/Na1981.DAT:*
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Gapop 10.0 , Gapext 1.0
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(without alignments)
929.662 Million cell updates/sec
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(c) 1993 - 2000 Com
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DNA encoding Aquif
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Neisseria meningit
Neisseria meningit
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V. marinus PKS-lik
V. marinus PKS-lik
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disease
                                                                                                                                                                                                                                         Key
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                                                                                                                                                                                                                                                                                                                                                                          DNA encoding Aquifex pyrophilus esterase 28LC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T79324 standard; DNA;
                                                                                     16-FEB-1996;
                                                                                                                    11-FEB-1997;
                                                                                                                                                  21-AUG-1997.
                                                                                                                                                                              WO9730160-A1.
                                                                                                                                                                                                                                                                                                                                              Esterase; thermostable enzyme; ester; chiral compound; cheese;
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                                                                                                                                                                                                                                                                                                                 paper; lignin removal; si
se resistance; feedstuff;
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29.2	29.2	29.2	29.2	29.4	29.4	29.6	29.6	29.6	29.8	30	30	30.2	30.2	30.2	30.4	30.6	30.6	30.6	30.8	31	31	31	31.4	31.6	32	32	33.2	34	34.4	35	35	39	42.6
3.9	3.9	3.9	3.9	3.9	٠,	٠,	٠,	. 9	3.9						4.0		4.0	4.0	4.1	4.1	4.1	4.1	4.2	N	4.2	'n		5	4.6		o	5.2	5.6
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X84327	A37056	F12050	C41802	A70213	X02828	V52237	T79324	C35689	T80385	A10225	C48117	220986	A31191	A31221	T66243	X20248	X20249	Z12004	N70513	V21209	2									_	_	X18	A81390
Stealth virus nucl	Human PRO1311 (UNQ		Arabidopsis thalia	Plasmodium falcipa	WO9905287 Seq ID 3	Streptococcus pneu		4		Human PCTA-1 genom	Zea mays DNA fragm	Human semaphorin Z	Plant microsatelli	Plant microsatelli	Arabidopsis violax	Borrelia burgdorfe	Borrelia burgdorfe	Neisseria gonorrho		Methanococcus jann	hypoxia:	Human secreted pro	nan OX2RH1.2 d	N. tabacum NIM1 ho		Arabidopsis thalia	Thermococcus 9N-2	Polynucleotide seq					N. meningitidis Me

ALIGNMENTS

ВP

sugar; lignocellulose;
f; ss.

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Callen W, Kosmotka A, Link S, Maffia AM, M
Reid J, Robertson DE, Swanson RV, Warren PV;
                                                                                                                                                                                                                                                                                                                                                                                            Aquifex pyrophilus strain KO1 5a.
                                                             (RECO-) RECOMBINANT BIOCATALYSIS INC.
                                                                                                        96US-0602359
                                                                                                                                                   97WO-US02039
                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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/transl_except= (pos: 742..746, aa:Val)
                    Murphy
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rigino-07). Claimed, newly identified polynucleotides (T79321-30)
cencoding esterases (W23069-77, W23088) were recovered from genomic
gene libraries. They can be used for recombinant production of the
cenzymes in host cells, and as probes to identify related sequences.
The esterases are stable at high temperature and in organic
solvents, making them superior for use in production of pure chiral
compounds used in pharmaceutical, agricultural and other chemical
industries. A method is claimed for transferring an amino group
from an amino acid to an alpha-keto acid using a claimed esterase.
The enzymes may also be useful as ripening starters in cheese making,
in lignin removal in paper and pulp manufacture, in carbohydrate
derivative synthesis, in fermentable sugar production from
lignocellulosic waste, in the study of plant wall structure, plant
resistance to disease and organic matter decomposition and to select
plants bred for production of highly degradable animal feeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 44-45; 113pp; English.
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CTTCCCATAGAGCCGGAAAAGGATATAAAGAACATTCTTCACATCCTTTTGAGGAGCTTC
                                              aacaaccttcccgttgagccctttcaggaaagcggtattcccaccgtttgcgttgatgtc
                                                                          AACAACCTTCCCGTTGAGCCCTTTCAGGAAAGCGGTATTCCCACCGTTTGCGTTGATGTC
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                                                                                                                                                       cccggcatatttgaacccgttgagtataagaattacttgctcgttgacggaggtatagtt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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This DNA sequence codes for thermostable esterase VF5-23LC (M23074) of Aquifex VF5, a marine strictly chemolithoautotrophic knall gas bacterium that grows optimally at 85 deg C and pH 6.8. It can be amplified from a pBluescript vector by PCR (see T79312-13). Claimed, newly identified polynucleotides (T79321-30) encoding esterases (W23069-77, W23089) were recovered from genomic libraries. They can be used for recombinant production of the enzymes in host cells, and as probes to identify related sequences. The esterases are stable at high temperature and in organic solvents, making them superior for use in production of pure chiral compounds used in pharmaceutical, agricultural and other chemical industries. A pharmaceutical, agricultural and other chemical industries. A method is claimed for transferring an amino group from an amino acid to an alpha-keto acid using a claimed esterase. The enzymes may also be useful as ripening starters in cheese making, in lignin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T79327;
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                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                paper manufacture, and to study plant resistance
                                                                                                                                                                                                                                                                                 Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in cheese
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disease resistance; feedstuff;
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                                                                                                                                                                                                                                      Page 48-49; 113pp; English
                                                                                                                                                                                                                                                                                                                                                                            Robertson DE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strain VF5.
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                                                                08-OCT-1999
                                                                                                Z12214;
                                                                                                                            Z12214 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 750 BP;
 Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
                               Neisseria meningitidis strain A complete ORF137 sequence
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                                                                                                                                                                                                                                                                                                                                                     CTTCCCATAGAGCCGGAAAAGGATATAAAGAACATTCTTCACATCCTTTTGAGGAGCTTC
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14-NOV-1997;
18-NOV-1997;
27-NOV-1997;
10-DEC-1997;
14-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequences Z11972-Z12358 represent open reading frames (ORFs) of Neisseria meningitidis and N. gonorrhoeae which encode antigenic proteins (see Y38499-Y38944). The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteins from Neisseria meningitidis and N. gonorrhoeae diagnosis, treatment and prevention of infection
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                     GAAGGGAGTTTAATCCCCGCACTTCTCGGCAGCTGTGCAATTCCCGGCATATTTGAACCC
                                                              GAGATACCGACGTATATATGCGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCG
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                                                cccatcaaatttgccgccgttgctactgattttgaaaccggcaaggccgtcgctttcaat
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Best Local Similarity
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences, A81453 to A82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; A8126 to A81303 and B25620 to B25663 represent Neisseria DNA sequences and their corresponding proteins; A81254 to A81259 and A81304 to A81321 represent PCR primers used in the isolation of Neisseria meningitidis MenB sequences; and A81322 to A81452 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the
                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleotide sequences of Neisseria meningitidis which can used in the diagnosis and treatment of N. meningitidis infection \epsilon other Neisserial infections, for example, N.gonorrhoea -
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                                                                                                                                                                                                                                                                                                                                               Page 471-498; 1760pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pizza M;
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infection; antibacterial; identification;
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Ratti G, Scarselli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identified proteins could be components of vaccines against Meningococcus B; against all serotypes; and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly sequences facilitate production of make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more
09-NOV-2000
                                      WO200066791-A1
                                                                         Neisseria meningitidis
                                                                                                                                   Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine;
diagnosis; antigen; detection; infection; gene therapy; antibacterial;
                                                                                                                                                                                            Neisseria meningitidis B nucleotide sequence SEQ ID NO:114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGGGAATGCCGGGCAGGCTGTGCGCGCCTTCCGCCGCCATTCCCAATGTGTTCCAACCC
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Pred. No. 5.5e-06;
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GAGATACCGACGTATATATGCGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes the full length genome of CC Nelsseria meningitidis B (NMB). The sequences in F21544 and F21607 to CC F21613 represent fragments of the NMB genomic sequence, as the sequence CC was too long to go in a record on its own it was split into 8 sequences CC which overlap each other at the beginning and end of each sequence by 4980 bp (i.e. the last 49980 bp of F21544 is repeated at the beginning CC of F21607, the last 49980 bp of F21547 are repeated at the beginning of F21608, and so on). F21545 to F21588 encode the Nelsseria proteins given CC in B58550 to B58593, and F21589 to F21606 represent PCR primers which CC are used in the exemplification of the present invention. The NMB genome CC and fragments from it have antibacterial activity, and can be used in CC cantibodies which binds to the proteins can be used in compositions for CC treating or preventing infection due to Neisserial bacteria or as a CC diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised to Neisserial bacteria. Computer memory, CC computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                            Matches 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 172325 BP; 43072 A; 47583 C; 41465 G; 40205 T; 0 other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Appendix A; 692pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections - {\sf T}
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Frazer CM, Grandi G;
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08-OCT-1999;
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GAAATTTTAGGCAAAACCGATTTGGTCGATTTAACCTTGTCCACCAGTGGTTTTATCAAA 153561
                                                                                                                                                                     ATTAAGGTTTTGAAAGAAAACGGTATTCCTGTGAAGGTGGTTACCGGCACATCGGCAGGT 153681
                                                                                                                                                                                                           TTGAAAGCTATAAACGAGCTCGGTATAAGGGTGAGGGCTTTAAGCGGGGGTGAGCGCCGGG 138
                                                                                                                                                                                                                                                                                               GAAGAGATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGCATAGCCCCACATAGGTGTT 78
                                     AAGAGGGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAAGGGATTGATAGGG 258
                                                                                TCGATTGTCGGCAGCCTTTTTGCATCGGGTATGTCGCCCGACCGCCTCGAATTGGAAGCC
                                                                                                                          GCAATCGTTTCGGTCTTTTATGCCTCAGGCTACTCCCCTGAAGGGATGTTCAGCCTTCTG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the outer membrane proteins currently used.
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C, Mora M,
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99WO-US23573
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Pred. No. 7.7e-06;
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Scarlato V,
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                                                                                                 The present invention describes methods of obtaining immunogenic CC proteins from Neisseria genomic sequences. A8143 to A82414 represent CC specifically claimed Neisseria meningitidis genomic DNA sequences; A81260 CC to A81303 and B25620 to B2563 represent Neisseria DNA sequences and CC represent PCR primers used in the isolation of Neisseria meningitidis DNA Sequences and A81322 to A81452 represent Neisseria meningitidis DNA CC sequences; and A81322 to A81452 represent Neisseria meningitidis DNA CC polynucleotide ORF sequences, which are all used in the exemplification CC of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a CC composition. The composition can be used as a medicament (or in the CC manufacture of a medicament) for treating, preventing or diagnosing CC infection due to Neisserial bacteria. For example, some of the identified CC proteins could be components of vaccines against Meningococcus B; against CC all serotypes; and/or against all pathogenic Neissariae. Identification CC sequences from the bacterium will also facilitate production of Diological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to CC make efficacious Meningococcus B vaccines have failed mainly due to CC make efficacious meningococcus B vaccines have failed mainly due to CC make efficacious meningococcus B vaccines have failed mainly due to CC make efficacious meningococcus B vaccines have failed mainly due to CC make efficacious meningococcus B vaccines have failed mainly due to CC make efficacious meningococcus B vaccines have failed mainly due to CC make efficacious meningococcus B vaccines have failed mainly due to CC make efficacious meningococcus B vaccines have also been tried but none
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                    further, complete sequences may provide an opportunity to secreted or surface exposed proteins that may be presumed immune system and which are not antigenically variable or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleotide sequences of Neisseria meningitidis which used in the diagnosis and treatment of N. meningitidis infectiother Neisserial infections, for example, N.gonorrhoea -
    conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 629-865; 1760pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rappuoli R,
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Masignani V,
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30-APR-1999;
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                                                                                     successfully overcome antigenic variability. The provision
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    other more variable
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Ratti G, Scarselli
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Grandi G,
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10-DEC-1997
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06-NOV-1997;
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                                                         CHIRON
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Masignani V,
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97GB-0024190.
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  Pizza M,
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Pred. No. 1.8e-05;
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Rappuoli R,
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  Scarlato
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RESULT V81946 ID V8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequences Z11972-Z12358 represent open reading frames (ORFs) of Neisseria meningitidis and N. gonorrhoeae which encode antigenic proteins (see Y38499-Y38944). The antigenic proteins,
                              V. marinus PKS-like cluster comprising ORFs 6,7,8 and
Polyketide-like synthesis; PKS; PKS-like gene; PUFA; DHA; transgenic;
                                                                    19-OCT-1999
                                                                                                     V81946;
                                                                                                                                    V81946 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 903 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page 324-325; 524pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteins from Neisseria meningitidis and N. gonorrhoeae useful diagnosis, treatment and prevention of infection % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as hybridisation probes and antisense reagents.
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DB; Y38780.
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                                                                                                                                                                                                                                                                                   gtcatcatcggcaggcacaaatatgttgacggcggtctgtcgcagcccgtgcccgtcagt 609
                                                                                                                                                                                                                                                                                                                  GTTGAGTATAAGAATTACTTGCTCGTTGACGGAGGTATAGTTAACAACCTTCCCGTTGAG
                                                                                                                                                                                                                                                                                                                                                   caagggaatgccggccagtcggttcgtgcttccgccgccattcccaatgtgttccagcca
                                                                                                                                                                                                                                                                                                                                                                                                                  cccatcaaatttgccgccgttgccactgattttgaaaccggcaaggccgtcgctttcaat
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGATACCGACGTATATATGCGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGAGAAGGCTATAAGATTCCTTGAGGAAGTTCTCCCTTACAGGAGAATAGAAAAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gagattttaggtaaaaccgatttagtcgatttaaccttgtccaccagtggttttatcaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tcgatagtcggcagccttttggcatcgggtatgtcgcccgaccgcctcgaattggaagcc
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Pred. No. 1.5e-05;
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CDS
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                                                                                                                                            Vibrio marinus
                                                                                                         Location/Qualifiers
17394..25352
                                                                                                                                                                            anti-inflammatory;
                                                                                                                                                                                     malnutrition,
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CDS CDS /product= "ORF 34454..36118 /product= "ORF 25509..28160 /product= "ORF 9" /product= "ORF /*tag= /*tag= 8209..34265 O 8, 6

10-DEC-1998

04-JUN-1998; 98WO-US11639

04-JUN-1997; 97US-0048650

(CALJ) CALGENE LLC

Facciotti D, Lassner M, Metz JG;

WPI; 1999-070271/06

New nucleic acid encoding polyketide-like synthesis enzymes of Vibrio marinus – and transformed plants and microbes that produced polyunsaturated fatty acids, useful as pharmaceuticals and foo

Example 1; Fig 5; 153pp; English.

generate transgenic plants that can express transgenes encoding PRS-like genes associated with PUFA production. The PRS-like genes are used to transform plants and microbial cells to give recombinants having altered contents of PUFA (specifically DHA and EPA). Oils from these plants are useful as dietary supplements (in infant feeeding formulations, to give a PUFA profile closer to that of human milk; for treating malnutrition; in intravenous feeding formulations; in cooking oils, fats etc.), also as anti-inflammatory agents and for reducing cholesterol levels. Fragments from the genes are useful as probes to isolate related molecules or to detect organisms that express PKS-like genes. The method facilitates large scale production of PUFA by providing new pathways for their synthesis or suppressing interfering pathways. Expression of PUFA in seeds allows simple recovery, as oil which can be engineered to have a marticular purp profile. particular PUFA profile. Expression in microbes also allows simple recovery and control of PUFA profile and is not subject to external variables such as weather or food supply. The present sequence represents an approximately 40 kb PKS-like cluster DNA fragment from V. marinus comprising open reading frames (ORFs) 6, 7, 8 and 9. The invention provides polyketide-like synthesis (PKS)-like genes that are used for the production of long chain poly-unsaturated fatty acid (PUFA) productions. Genes responsible for elcosapentenoic acid (EPA) production in Shewanella putrefaciens and novel genes associated with the production of docosahexanoic acid (DHA) in Vibrio marinus are used to

Sequence 40138 BP; 11845 A; 7635 C; 8758 G; 11900 T; 0 other;

Query Match
Best Local Similarity Matches Conservative 52.98; 0, Score 46.2; DB 20; Pred. No. 0.00029; Pred. No. 0.00029; Length 40138; Indels 0; Gaps

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                             normal use the recipient receives a desired amount of poly-unsaturated long chain fatty acids. The nucleic acids are also useful in large scale production of docosahexenoic acid and elcosapentenoic acid, and for the modification of the fatty acid profile of host cells and edible plant tissues and/or plant parts. Transgenic production of polyunsaturated fatty acids in particular host cells allows quicker purification from
                                                                                                                                            This invention describes novel DNA sequences encoding for polyketide (PK)-like synthesis (PKS-like) pathway genes from Shewanella, Vibrio and Schizochtrium. The nucleic acids are useful for isolating related molecules or in methods to detect organisms expressing the PKS-like genes. They are also useful for creating transgenic plants that express poly-unsaturated long chain fatty acids. The poly-unsaturated long chain fatty acids produced recombinantly are useful as dietary supplements for patients undergoing intravenous feeding or for preventing or treating malnutrition. The poly-unsaturated long chain fatty acids can also be incorporated into cooking oils, fats of margarine formulated so that in
                                                                                                                                                                                                                                                                                                                                                                                                                    New DNA sequences encoding for polyketide (PK)-like synthesis pathway genes from Shewanella, Vibrio and Schizochtrium, useful for creating transgenic plants that express poly-unsaturated long chain fatty acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PKS pathway; polyunsaturated long chain fatty acid; plant; transgenic; polyketide-like synthesis; PUFA; dietary supplement; intravenous feedi mainutrition; cooking oil; cooking fat; wargarine; docosahexenoic acid production; eicosapentenoic acid production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V. marinus PKS-like
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 Vibrio marinus DNA
                     natural sources such as fish or plants. This
                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 5; 302pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CALJ ) CALGENE LLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9908-0231899
   fragment encoding the PKS gene cluster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lassner
                     sequence represents a
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Best Local
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                     (ORPs) of Neisseria meningitidis and N. gonorrhoeae which encode antigenic proteins (see Y38499-Y38944). The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections,
                                                                                                                                                                                                                                                                                                                                                                                   Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-SEP-1998;
06-NOV-1997;
                                                                                                                           Nucleotide sequences Z11972-Z12358 represent open reading
                                                                                                                                                                                                                                                       Proteins from Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212212 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 40138 BP; 11845 A; 7634 C; 8759 G; 11900 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis partial ORF137 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
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DB; Y38777.
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  as meningitis, septicaemia and
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99; Conser
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                                                                                                                                                                           Page 322;
                                                                                                                                                                                                                                                                                                                                                                                   Masignani V,
                                                                                                                                                                                                                               treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria infection;
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97GB-0026147
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97GB-0024190.
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                                                                                                                                                                        524pp; English
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Pred. No. 0.00029;
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                                                                                                                                                                                                                                                                                                                                                                                   Rappuoli R,
gonorrhea.
                                                                                                                                                                                                                               s and N. gonorrhoeae useful of infection
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                                                                                                                                                                                                                                                                                                                                                                                        Scarlato
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RESULT 12
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Best Local
specifically claimed Neisseria meningitidis genomic DNA sequences; A81260 to A81303 and B35620 to B25663 represent Neisseria DNA sequences and their corresponding proteins; A81254 to A81259 and A81304 to A81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and A81322 to A81452 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the
                                                                                                                                                                                                   Isolated nucleotide sequences of Neisseria meningitidis which used in the diagnosis and treatment of N. meningitidis infectiother Neisserial infections, for example, N.gonorrhoea -
                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are closely related. Fragments of the as hybridisation probes and antisense
                                                                                                                             The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. A01453 to A02414 represent
                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                         Rappuoli R,
                                                                                                                                                                                                                                                                                                    Frazer CM, F
Masignani V,
                                                                                                                                                                                                                                                                                                                                               (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                           09-OCT-1998;
30-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis; Neisseria gonorrheae; genome; immunogenic; antigen; vaccine; diagnosis; infection; antibacterial; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N. meningitidis MenB polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2000
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                                                                                                                                                                                                                                                                                                      Hickey E,
Galeotti
                                                                                                                                                                        Page 216; 1760pp; English.
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                                                                                                                                                                                                                                                                                       Pizza M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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99US-0132068
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54.0%;
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C, Mora
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Pred. No. 0.00041;
0; Mismatches 74;
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Ratti G,
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Scarselli
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                                                                                                                                                                                                         s infection and
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RESULT 13
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Query Match
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Matches 87
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                                                                                                                                                       P-PSDB;
                                                                                                                                                                                                                                                                                                                                             Alcaligenes sp
                                                                                                                                                                                                                                                                                                                                                                         PoxI; aromatic;
drug; ds.
                                                                                                                                                                                                                                                                                                                                                                                                       Alcaligenes; PoxR; PoxA; PoxB; PoxC;
                                                                                                                                                                                                                                                                                                                                                                                                                               Alcaligenes sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X18867 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved than other more variable regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the iden
                                                                                                                                                                                                                             25-JUL-1997;
                                                                                                                                                                                                                                                                                      16-FEB-1999
                                                                                                                                                                                                                                                                                                                 JP11042088-A
                                                                                                                                                                                                 (TOFU ) TONEN CORP.
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                                                                                                                                         1999-197820/17.
IDB; W98969, W98970, W98971, W98972, W98973, W98974, W98975, W98976, W98977, W98978.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGAGATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGCATAGCCCACATAGGTGTT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tcgattgtcggcaacctttttgcatcgggtatgtcgcccga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity
87; Conserv
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                                                                                                                                                                                                                                                          97JP-0200625
                                                                                                                                                                                                                                                                                                                                                                                       oxidative; petroleum
                                                                                                                                                                                                                                                                                                                                                                                                                                Pox proteins R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA;
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Pred. No. 0.00041;
0; Mismatches 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                А, В,
                                                                                                                                                                                                                                                                                                                                                                                       purification;
                                                                                                                                                                                                                                                                                                                                                                                                      PoxD;
                                                                                                                                                                                                                                                                                                                                                                                                                                c,
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                                                                                                                                                                                                                                                                                                                                                                                                      POXE; POXF; POXG;
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                                                                                                                                                                                                                                                                                                                                                                                        chemical industry;
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POXC, POXD, POXE, POXF, POXG, POXH and POXI. The proteins at the fields of petroleum purification, chemical industry and industry related to the synthesis, conversion and decomposit

The present sequence encodes Alcaligenes sp. proteins PoxR, PoxA, PoxPoxC, PoxD, PoxE, PoxF, PoxG, PoxH and PoxI. The proteins are useful

encoding an aromatic cpd. oxidative decompsn. efficids of petroleum purification, chemical and

enzyme drug

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGTCGTGCTGTCCGGCAGCCTGGTCGATGCGGTGCTGGCCAGCGCCGCCATCCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCTTCCCGTT 495
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1 Similarity 50.3%;
96; Conservative
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Pred. No. 0.038;
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Best Local Similarity 49.2%;
Matches 92; Conservative
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25-MAR-1999

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Pred. No. 0.26;
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                                                                                                                                                                                                                                                                                                                                    /gene≃"nuoK2"
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                                                                 TTTCTGGCCGGTTCGTTCCAATTCGGAAAAGAGAAAGGAGTTCTGCAACGTAGTTATAGAA 13002
                                                                                                                                                    CTTCCCATAACTCAAGAAAGAAGAATTAAAAATATACTCCACATCCTTATAAGGAGCTTC
                                                                                                                                                                                             CTTCCCATAGAGCCGGAAAAGGATATAAAGAACATTCTTCACATCCTTTTGAGGAGCTTC
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FTRALLFLAAGAVTTAFHHHLYDIFKNGGLKKYMPVTYVAFMIGALSLAGVPPPSGFW
SKDRIVASMYEMSGVLGVLGTUAFITAYAGREGFLVPHGRERREIYDKDVBUEG
VMTVPMGLLGFLTVLTGLFGLMLEHMYVGLIGGEKGIHLSVALVSLGVAIAGIMLAW
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DGFINALYKYFFKFVKFLMKYLDIKIIDVLIHETVLTAFRLGRLSRRLQTGLVNHYIL
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ATKASFEAFYMNRIGDWLFIFGIIYSFYLFKTLEITQIFPKYEEYDKYALGYATMLLF
GGAYGKSGQFPLHTWLPNAMAGPTPYSALLHAATMVAAGYYMYARLYPMFEATPQTLK
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stover.C.K., Pham.X.Q., Erwin,A.L., Mizoguchi,S.D., Warrener,P., Hickey,M.J., Brinkman,F.S., Hufnagle,W.O., Kowalik,D.J., Lagrou,M., Garber,R.L., Goltry,L., Tolentino,E., Westbrock-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lim,R., Smith,K., Spencer,D., Wong,G.K., Wu,Z. and Paulsen,I.T. Complete genome sequence of Pseudomonas aeruginosa PA01, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Washington Genome
Box 352145, Seattle, WA 98195,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University Of Washington,
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Stover, C.K., Pham, X.Q., Erwin, A.L.,
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AE004756.1 GI:9949466
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406 (6799), 959-964 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="PA3335"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain-"PAO1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          translation="msQnmDLTIGTHRESAFYELEFGPRTIMTLANFPDDVLPLLQME"
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                                                                                                                                                                                                                                                 -"PA3336"
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3558. .
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AAMVAFALFGQVPAVAVAALVVIGLTGVSMNPALVTRGARVGHNNMLVNSVHTACIML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEYDSGYINAASLMIGFDTPLGPLTFSYGINDENFKAFYLNLGQNF" complement(5752...7800)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RQIANNGEIRLGAVQAYGKADVRIGDPSLPDIDFTEGYYELKYSFDTVDDVNFPHEGE
EIGLTMRRYDKSLGSDDSYRQWDLRLNKALSFGADTWVFGGGYGRTLDDAEVVTSSFT
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ESGLLGYREFPESLRARYQSHTCADLELLREAGYRDDFQSLEEGVAGYCRWLARSA"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                     AGATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGCATAGCCCCACATAGGTGTTTTGA 82
                                                                                                                                                         GGGTAAACTGGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAAGGGATTG 252
                                                                                                                                                                                                       TGGTCGGCGGCCTGTACGCCTCCGGCTACACCCCCGCCGAACTGGAGCGCATCGCCCTGG 3807
                                                                                                                                                                                                                                                    TCGTTTCGGTCTTTTATGCCTCAGGCTACTCCCCTGAAGGGATGTTCAGCCTTCTGAAGA 202
                                                                                                                                                                                                                                                                                              AGGCCCTCGACGAACAGGGCATCCAGATCGACGCCATCGCCAGCACCAGCATGGGCGCGG 3747
                                                                                                                                                                                                                                                                                                                                      AAGCTATAAACGAGCTCGGTATAAGGGTGAGGGCTTTAAGCGGGGGTGAGCGCCGGGGCAA 142
                                                                                                                                                                                                                                                                                                                                                                                      AGATCGGTCTGGTCCTCTCCGGCGGTGCCGCCCGCCGGCCTGGCCCATATCGGCGTGCTCA 3687
                                                                                                                 AGATGGACTGGCAGCAGGCGCTGTCCGACGCGCCGCCGCGCAAGGACGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVMADHDSLTGLHNRRSFNQHLDRLWRQAQREQKTLALLLCDVDHFKAYNDRYGHQAG
DAVLQRIGAVFEANARRPLDMAVRLGGEEFALLLYGANEHEARLRAEALRAQVQALRM
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LSGEADGLRVGLNLSCGVNETSFTENCYWLDGELLKVDSVRFDFDRDQPLRPWTIRSY
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LIADIEAlAASVRNDVLTGIDESEQALCQQVLLRILANLENR"
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Submitted (13-MAR-1998) Andersson R.A.,
University of Agricultural Sciences, Boy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erwinia carotovora subsp. carotovora and acts negat sigma factor RpoS (sigma s)
Mol. Plant Microbe Interact. 12 (7), 575-584 (1999)
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Erwinia carotovora subsp.
Erwinia carotovora subsp.
Bacteria; Proteobacteria;
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Andersson, R.A.
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Andersson, R.A., Palva, E.T. and Pirhonen, M.
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                                                                                                                                                                                             /db_xref="Sptremb::086197"
/translation="meoplagkhilviddeaversylagyltsigasyreaingidal
/translation="meoplagkhilviddeaversylagyltsigasyreaingidal
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SULLKPIRDYTRIRDAVMSCLYPDMFTSQLMBLDQLMODMSLNQSPEAITKLLAQL
OPPVQQTLARCRVNYRQLTTAEOPGLVLDIAALSETELAFYCLDVTQGVNNNGTLAAL
LLRTLENGLLGEHLVDQOHRLPYLPTLLKQVNQLLRQASLDGERPLLVGYYHRPIKQL
LLRTLENGLLGEHLVDQOHRLPYLPTLLKQVNQLLRQASLDGERPLLVGYYHRPIKQL
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LVGAAYATNNLSSMEQWVRGFGYWDVIRLMDLSWQRGSLLRGDRVFNSVKHLLHTTQI
EDCAIKYGVVTTNLSTGRELWLTEGDLHQAMRASCSMPGLLSPVRFNDYWLVDGAVVN
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353. .1264
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1381. .2397
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RLLRGRRQSAESSPTAMEIMSTSIQILENRLKMTRMAGDPPDVLLQPYCPQIATLDFH
                                                                                       /gene="galU"
2593. .2797
                                                                                                                                                                                                                                                                                                                                    /product="ExpM protein"
/protein_id="CAA11942.1"
/db_xref="GI:3319928"
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/protein_id="CAA11941.1"
/db_xref="GI:3319927"
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/strain="SCC3193"
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?604 . .>2797
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|370. .2397
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'function="regulation
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                     'gene="galU"
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Best Local Similarity 54.4%;
Matches 111; Conservative
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                            TCGATAGTCGGCAGCCTTTTTGCATCGGGTATGTCGCCCGACCGCCTCGAATTGGAAGCC
                                                                                        ATTAAGGTTTTGAAAGAAACGGTATTCCTGTGAAGGTGGTTACCGGCACATCGGCAGGT 249
                                                                                                                     TTGAAAGCTATAAACGAGCTCGGTATAAGGGTGAGGGCTTTAAGCGGGGTGAGCGCCGGG 138
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Pizza M., Scarlato, V., Rappuoli, R., Grandi, G. and Masign Neisserial antigens
Patent: WO 9924578-A 561 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAPPUOL: CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA (IT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unidentified
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VVNECIAAGINEIILVTHSS"
                                                                                                                                                                                                                                                                                                    /organism="unidentified"
/db_xref="taxon:32644"
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Pred. No. 3.3e-05;
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Pred. No. 8.2e-05;
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 GAAATTTTAGGTAAAACCGATTTGGTCGATTTAACCTTGTCCACCAGTGGTTTTATCAAA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGGGAGTTTAATCCCCGCACTTCTCGGCAGCTGTGCAATTCCCGGCATATTTGAACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTATCATCGGCAGGCATACATATGTTGACGGCGGTCTGTCGCAGCCCGTGCCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGATACCGACGTATATATGCGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL162752.2 GI.7977
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                                                                                                                                                                                                                                                                                                                                                                           Details of N. meningitidis sequencing at the Sanger Centre available on the World Wide Web. (URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (30-MAR-2000) Submitted on behalf of the Neisseria sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: parkhill@sanger.ac.uk
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seament 1/7
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Neisseria meningitidis Z2491
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
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AL162752 AL1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature
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/translation="mSnTQTIRSADFTTSRAWGALDIANMNGTTVRLHWTDQPYKWHV
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/protein_id="CAB83321.1"
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                                                                                                                                                                   /gene="NMA0001"
                                                                                                                                                                                                                    /note="serogroup: A"
complement(38. .358)
/gene="NMA0001"
                                        /db_xref="SPTREMBL:Q9JX93"
                                                                                                                    /transl_table=11
                                                                                                                                             /codon_start=:
                                                                                                                                                       /note="NMA0001, unknown,
                                                                                                                                                                                                                                                                                                  /organism="Neisseria meningitidis Z2491"
/strain="Z2491"
                                                                                                                                                                                                                                                                               db_xref="taxon:122587"
                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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                                                                                                  NMA0001
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                 /note-"NMA0004, unknown, len: 191 aa; similar to hypothetical proteins e.g. Y977 HAEIN HI0977 (191 aa), fasta scores; E(): 0; 80:58 identity in 190 aa overlap, and to proteins involved in cell cycle e.g. TR:054679 (EMBL:AF036487) Lactococcus lactis plasmid px24000 putative mobilization protein (200 aa), fasta scores; E(): 0, 55:18 identity in 167 aa overlap, and FIC_ECOLI cell filmentation protein FIC (200 aa), fasta scores; E():
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"NMA0002, nuoL, NADH dehydrogenase I chain L, len: 674 aa; similar to many e.g. NUOL_RHOCA NADH dehydrogenase I chain L (EC 16.5.3) (700 aa). Contains Pfam match to entry PF00361 oxidored_q1, NADH-Ubiquinone/plastoquinone (complex I), various chains, and to entry PF00662
                                                                                                                                                                                                                                                                                                             complement(2833. .2837)
complement(2952. .3527)
/gene="NMA0004"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NADH-Ubiquinone/plastoquinone (complex I), various chains, score 351.80, E-value 7.3e-102" complement(2061. .2243)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1116. .2030)
/gene="nuoL"
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LFFGYUWSLITVTCLLLFVGAMGKSAQFPLHVWLDDSMEGPPPLSALIHAATUTAGL
FMVSRMSPIYEMSSTALSVINVIGATTALFMGFLGVIQNDIKRŸVAYFXLSQIGVTMV
ALGASAYSVAMFHVMTHAFFKALLFLAAGSAIIGMHDQDMRHMGNLKKYMPITWLTM
LIGNLSLIGTPFFSGFYSKDSIIEAAKYSTLFGSGFAYFAVLASVFVTAFYAFFQQYFM
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EAADKLLSTGEKKTQTGFTELiLSGGGVHALKYSMEYLVLQKPWCDLFTEEQLAVARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2487. .2828)
/gene="NMA0003"
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/gene="NMA0003"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mnDmTLYLIIALVPLAGSLIAGLEGNKIGRAGAHTVTILGVAVS
AVLSAYVLWGELNGSRAKFDENVYTWLTMGGLDESVGFLVDTMTAMMVVVVTGVSLMV
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                                                                                                                                                                                                                                                                                     complement(2952. .3527)
                                                                                                                                                                                                                                                                                                                                                                                                         RLERVGFVSPK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein NMA0003"
/protein_id="CABB3323.1"
/db_xref="GI:7378781"
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                                                                                                                                                                                                                                                             /gene="NMA0004"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="nuoL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Pfam match to entry PF00361 oxidored_q1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SWISS-PROT:Q9JX92"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="NMA0003, unknown,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EC_number="1.6.5.3"
29.4% identity in 126 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _table=11
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                                                                                                                                         gene
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/note-"NMA0006, nuoJ, NADH dehydrogenase I chain J, len: 223 aa; similar to many e.g. NUOJ_RHOCA NADH dehydrogenase I chain J (EC 16.5.3) (202 aa), fatsa scores; E(): 9.7e-21; 41.3% identity in 201 aa overlap. Contains Pfammatch to entry PF00499 oxidored_q3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="NMA0005, nuoK, NADH dehydrogenase I chain K, len: 101 aa; simlar to many e.g. NUOK_RHOCA NADH dehydrogenase I chain K (EC 1.6.5.3) (102 aa), fasta scores; E(): 1.1e-24; 65.0% identity in 100 aa overlap. Contains Pfam match to entry PF00420 oxidored_q2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKDNLTDDVDNREIIFKGIEQSYYYEGYEKG" complement(3516. .3525) /gene="NMA0004"
                                                                                                                                                                                                                            NADH-ubiquinone/plastoquinone oxidoreductase chain score 77.90, E-value 2e-19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NADH-ubiquinone/plastoquinone oxidoreductase chain 4L, score 141.50, E-value 1.5e-38" complement(3863. .4534)
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complement(3564. .3863)
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/gene="nuok"
                                                                                                                                                                                                                                                                                                                                               complement(4034. .4525)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="sptrembl:Q9JX90"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(3863. .4534)
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/gene="nuoK"
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MNIAHPFLEGNGRSTRIWLDLVLKKNLKKVVNWQNVSKTLYLQAMERSPVNDLELRFL
                                                                                                               complement(4570. .5277)
/gene="NMA0007"
                                                                                                                                                                                                  complement(4570.
                                                                                                                                                                                                                                                                                                                                                                                                    complement(3874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="NADH dehydrogenase I chain J"
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/protein_id="CAB83325.1"
/db_xref="GI:7378783"
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/protein_id="CAB83324.1
/db_xref="GI:7378782"
/product="hypothetical protein NMA0007"
                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                               /gene="nuoJ"
                                                                                                                                                                                                                                                                                                                                                                       /gene="nuoJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA I ALVHRKTVNPKRMDPADQVKVRADQGRMRLVKMEAVKPQTESAEESEVSDDLKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NADH-ubiquinone/plastoquinone oxidoreductase chain
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                                transl_table=11/
                                                                                  note-"NMA0007,
                                                                                                                                                                          'gene="NMA0007"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MITLTHYLVLGALLFGISAMGIFMNRKNVLVLLMSIELMLLAVN/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transl_table=11
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                                                                                                                                                                                                                                                                                       'note="Pfam match to entry PF00499 oxidored_q3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'EC_number="1.6.5.3"
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GCAGTGGTCGGTTTGGCACTCGGTGGCGGCGCATCTAAAGGATTTGCCCCATGTAGGTATT 189
                            GAAGAGATAAACCTCGTTCTTTCGGGAGGAGCTGCAAAGGGCATAGCCCACATAGGTGTT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTATCATCGGCAGGCATACATATGTTGACGGCGGTCTGTCGCAGCCCGTGCCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGATACCGACGTATATATGCGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCG 378
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                                                               211;
                                                                                                                                                                                                                     Patent: WO 9924578-A 559 20-MAY-1999;
PATENT: WO 9924578-A 559 20-MAY-1999;
PIZZA MARIAGRAZIA (IT); SCARLATO VINCENZO (IT); RAF
CHIRON SPA (IT); GRANDI GUIDO (IT); MASIGNANI VEGA
LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                  1 (bases 1 to 903)
Pizza,M., Scarlato,V., Rappuoli,R., Grandi,G.
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Bacteria;
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Neisseria meningitidis
of the complete genome.
                                                                                                                     Submitted (17-MAR-2000) The Institute f Medical Center Dr. Rockville, MD 20850,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete genome sequence of Neisseria
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                          /organism="Neisseria
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GEMANGHY KASAAIRWY GYYLLIGKHII YDGGGYGY YYYAAKKUJANE Y AYDIISKK PGKNISQGFFSYLDQTLNYMSYSALQNELGQADYVIKPQYLDIGAYGGFDQKKRAIRL GEEAARAALPEIKRKLAAYRY" gene 55666015 /gene="NMB2140"	/transl_table=11 /product="conserved hypothetical protein" /protein_id="aAF42447.1" /db_xref="GI:7227396" /translation="MVTFSKIRPLLAIAAAALLAACGTAGNNAVRKPVQTAKPAAVVG /translation="MVTFSKIRPLLAIAAAALLAACGTAGNNAVRKPVQTAKPAAVVG LALGGGASKGFAHVGIIKVLKENGIPVKVVTGTSAGSIVGSLFASGMSPDRLELEAEI LGKTDLVDLTLSTSGFIKGEKLQNYINRKVGGRQIQFFIKFAAVATDFETGKAVAFN OGNAGAAVBASAA TONVEONVITGERTVVTGGTSODDVGAABVGANTATGAB	IKDLRTGYEVGNTKAVLDGDLDGFIEASLKQGV" complement(43285221) /gene="NMB2139" CDS complement(43285221) /gene="NMB2139" /note="conserved hypothetical prot Glimmer?; putative" /codon start=1	/transl_table=11 /transl_table=11 /product="peptide chain release factor 2" /protein_id="AAF42446.1" /protein_id="AAF42446.1" /db_xref="G1:7227395" /db_xref="G1:7227395" /translation="MEAEVINQLNWTLNDLEKRSEDIRVYMDYQGKKDRLEEVIGLSE /translation="MEAEVINQLNVTLNDLASGIEDNRMLIEMTVEENDEEGFAAVQ DPELMNDFKRAQEIGKERKILEGIVLTILDNIAGGIEDNRMLIEMTVSERMYSRYAER EDVAGLEKOMADLEFKNEMVOPADPNNCFTDTTGAGGCTEAEDMAGMLFRMYSRYAERF KGFRIEILEEDDGEIAGINRATIRVEGEYAYGLLRTETGVHRLVRYSPFDSNNKHHTS FASVFVYPEIDDSIELEINFADLRIDTYRASGAGGQHLMKTDSAVRITHEPTGIVYQC GNDBGONAKFA AMMEN KGT YET FADEV BUREFYAN FEGGGTENDEGGTESGTENDEGGTESGTENDEGGTESGTENDEGGTESGTENDEGGTESGTENDEGGTESGTESGTENDEGGTESGTESGTENDEGGTESGTESGTENDEGGTESGTESGTENDEGGTESGTESGTESGTENDEGGTESGTESGTENDEGGTESGTESGTENDEGGTESGTESGTENDEGGTESGTESGTESGTENDEGGTESGTESGTENDEGGTESGTESGTENDEGGTESGTESGTENDEGGTESGTESGTESGTENDEGGTESGTESGTENDEGGTESGTESGTESGTESGTESGTESGTESGTESGTESGT	JGGQRH APGR")) 38590 Lfied	/gene="NMB2137" /gene="NMB2137" /note="hypothetical protein; putative" /codon_start=1 /transl_table=11 /product="hypothetical protein /protein_id="ARP42445.1"	GINTULAAARGUIGULIGLIE INAGGUILGGGVILGGGVILGGGVILGGGVILGGGVILGGGVILGGGGVILAGGGVILGGGGVILAGGGFUNG GGGVILGGGGVILAGGGGVILGGGGVILAGGGGVILAGGGGGAAAVGAAAYGAAATGGAGAAAGGAAATGAAAGGAAATGAAAAGGAAGG	CDS 7722229 /gene="NMB2136" /note="similar to GB:AL009126 percent identity: 59.41; identified by sequence similarity; putative" /codon_start=1 /trans1_table=11 /product="peptide transporter" /protein_id="AAR42444.1" /trans1ation="NSSRHPAPTGEKTFEGHPPQLSTLPHIELWERFSFYGMQGILLIY
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AX044035
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                                                                                                                                                                    Neisseria
Bacteria;
                                                           Pizza,M., Hickey,E., Peterson,J., Tettelin,H., Venter,J.C., Masignani,V., Galeotti,C., Mora,M., Ratti,G., Scarselli,M., Scarlato,V., Rappuoll,R., Frazer,C.M. and Grandi,G. Neisseria genomic sequences and methods of their use Patent: WO 0066791-A 114 09-NOV-2000;
CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARC!
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Masul,N., Fuji,F., Takaki,Y., Inoue,A. and Horikoshi,K
Sequencing of three lambda clones from the genome of a
Bacillus sp. strain C-125
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Bacillus halodurans
Bacteria; Firmicutes; Bacillus/Clostridium
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                                                                                                                                                                                                                                                                                                               Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and Technology Center, Deep-sea Microorganisms Research Group; 2-15 Technology Cycles (Kanagawa 237-0061, Japan Yokosuka, Kanagawa 237-0061, Japan Yokosuka, Kanagawa 237-0061, Japan
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Analysis of the genome of an alkaliphilic Bacillus strain industrial point of view
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                                                                                                                                                                                                                                                           URL:http://www.jamstec.go.jp/jamstec-e/bio/DEEPSTAR/FResearch.html,
Tel:81-468-67-3895, Fax:81-468-66-6364)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takami, H., Takaki, Y., Nakasone, K., Hirama, C.,
                                                                                                                                                                                                                                                                                                    (E-mail:takamih@jamstec.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249-284; Springer-Verlag (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HORIKOSHI,
                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 300950)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (sites)
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                                                                                                                                         complement(179. .2113)
                                                                                                   complement(179.
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                                                                                                                                                             /note="alkaliphile"
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/db_xref="taxon:86665"
/product="stage V sporulation protein (soprulation
                                                                                                                                                                                                                          . .300950
                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    Takaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of facultatively alkalihilic Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. 63,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakamura, Y., Ogasawara, N., Kuhara, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp. C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Masui, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
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YPKHTYASHLIGYTDRDMGESRMGLERSLDEYLRGEDGEIRFKKDGQGIPLPRPSEQI
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TIMNHSLQYLNISPSVEELKDEEEEGYELADFIGESARSAREELEQAGMKVYVLGEGD
TVEGQQPYSGHKLLEGERVILRTESESYTLPSMIGWSLRDVLKVANVLDVNVNLFGQG
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KGGHGSQTFLEVVENSCNPGFVVLGERLGKDRLFDYIEAFGFGQKTGIDLQGEAKGII
FNRDRIGPLEQATTAFGQGVSVTPIQQVAAVSAAVNGGYLYEPYVAKDWVDPYTGEVV
   complement(5901.
                                                                                                   TLKLITKKPIVPTAEEIELNNRARSAKLRIAEKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(4939.
/gene="BH2575"
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AKSLGMKLEDENVKVVQN"
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LENNHIVSFIGFAPADDPQIVVYVAIDNPKDTVQFGGVVAAPIVGKIIGDSLQALGIE
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DRQKAYELITKRESIVRLNPEGRKISKDKANEVRKLRLPGVYIAEDSKRHYPFGSYLS
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/protein_id="BAB06291.1"
                                  /gene="BH2576"
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/note="BH2573"
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                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BAB06293.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RENQIEKERKWNDEPLYEVPDLYGRTKRDLHESYYELKIDADGKGDYYVAQAPEPGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="BH2575
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.6332)
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Best Local (
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                                                             512 GCGG 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 TCGTTCTTTCGGGAGGTGCAAAGGGCATAGCCCACATAGGTGTTTTGAAAGCTATAA 91
                                                                                                                                                                                                                                                                                                                                                     GAATTGTAGCGGCTGATTTGCTTAAAGGCGAGCGGGTTATTTTGCAAGAAGGGGACGTTG 15728
                                                                                                                                                                                                                                                                                                                                                                                                            ATATATGCGCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCGGAAGGGAGTTTAA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGAGCTTATCCGTGTCCTTGCAAAAAAGAAGCGAGTGGAAGAGTTAGACCCACCTGTGC 15788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAAATATTATTTGGATTTTACGGTCCCGAAAATGGGGTTTATCGCTGGCCATCGCGTGG 15848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTGAAGCTGTTTAAGTTCAAGCCACCTCTGAAGGGATTGATAGGGTGGGAGAAGGCTA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGAGCTCGGTATAAGGGTGAGGGCTTTAAGCGGGGTGAGCGCCGGGGCAATCGTTTCGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGCTTTAGGGTCAGGTGGAGCTCGTGGGGTATGCACATATCGGTGTGTTGAAAGTATTAG 16028
                                                                                                                   ACCGACTGCTCATTGACGGCGGCGTTATTGACCGTGTACCTGTCTCTGTCGTCAAGGAGA 15608
                                                                                                                                                                       ATTACTTGCTCGTTGACGGAGGTATAGTTAACAACCTTCCCGTTGAGCCCCTTTCAGGAAA 511
                                                                                                                                                                                                                                                                                     TCCCCGCACTTCTCGGCAGCTGTGCAATTCCCCGGCATATTTGAACCCCGTTGAGTATAAGA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAAGATTCCTTGAGGAAGTTCTCCCTTACAGGAGAATAGAAAAACTTGAGATACCGACGT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTTGTACGGAGCCGGTCATCCAACGGAACATCTGATTCGTTTTGCCAATCTGTTTAAAC 15908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACAGGAAAAGATACCGATAGACTATCTCGCCGGTAGTAGTATGGGAGCCCTTGTGGCCT 15968
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CVVIVSNRVEJWSKELWEEYFAESEESFSEIAENIVDFDL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKLANKNWSITESOLREMERRMKRHVRERFEHELSKFDEAERWLKPNGLLOERHDHVI
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complement(8180. .8566)
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RKRIASEAGLNKETLAKWLATVFRSLPETEHTLPLYERVKTLAGRSNTYTDFFAELLL
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/gene="BH2577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VMQDALFPVLAFVAGPGEISYWATLKRVFHECGMKMSPVVPRISATCVPSAVQKWFAE
KQYSYEEAIAHGLEKEKEGWLEEQTPWPIDQVVEEAITQIRHSHKPIKDLAEQIGETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EETNAHLFYVEEGSRYRIDYTGENYELNGKNQTFSREELLEHLTLHPERFSNNVVTRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown conserved
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/db_xref="GI:10175197"
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Pred. No. 0.00063;
0; M1smatches 270; Indels
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
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Nature 409 (6819), 529-533 (2001)

2 (bases 1 to 10410)
Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D.,
Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A.,
Posfai, G., Hackett, J., Kink, S., Boutin, A., Shao, Y., Miller, L.,
Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K.,
Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C.,
Welch, R.A. and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli O157:H7
AE005340 AE005174
AE005340.1 GI:12514944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli 0157:H7. Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Welch, R.A. and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE005340
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IVRSTIGATION TO THE TOTAL TO THE TOTAL TO THE TOTAL TOTAL TOTAL TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Residues 1 to 1247 of 1247 are 99.91 pct identical to residues 1 to 1247 of 1247 from Escherichia coli K-12 Strain MG1655: B1224"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="
227. .3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="nitrate reductase
/protein_id="AAG56084.1"
/db_xref="GI:12514945"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             respiration"
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/strain="EDL933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MSKFLDRFRYFKQKGETFADGHGQLLNTNRDWEDGYRQRWQHDH/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /serotype="0157:H7"
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                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="nitrate reductase 1, beta subunit"
/protein_id="AAG56085.1"
/protein_id="AAG56085.1"
/db_xref=="Gi:12514946"
/translation="MKIRSQVGMVLNLDKCIGCHTCSYTCKNVWTSREGVEYAWFNNV
ETKEGGEFTDWENQEKYKGGWIRKINGKLQPRMGNRAMLLGKIFANPHLPGIDDYVG
PEDETVQNLHTAPEGSKSQPIARPRSLITGEBENKIEKFGPWEDDLGGEFDKLAKDK
PDNIQKANYSQFENTFMYLPRLCEHCLNPACVATCPSGAIYKREEDGIVLIDQDKCR
GWRMCITGCPYKKIYFWWKSGKSEKGIFCYPRIEAGQPTVCSETCVGRIRYLGVLLYD
                                                                                                                                                                         /translation="MQFLNMFFFDIYPYIAGAVFLIGSWLRYDYGQYTWRAASSQMLD
RKGMNLASNLFHIGILGIFYGHFFGMLTPHWMYEAWLPIEVKQKMAMFAGGASGVLCL
IGGVLLLKRRLFSPRVRATTTGADILILSLLVIQCALGLLTIPFSAQHNDGSEMMKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Z2004"
6212. .6889
                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="enzyme; Energy metabolism, carbon: Anaerobic
respiration"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MIELVIVSRLLEYPDAALWOHOOEMFEAIAASKNLPKEDAHALG IFLROLTTMDPLDAQAQYSELFDRGRATSLLLFEHVHGESRDRGQAWDLLAQYEQHG LQLMSRELPHLPLYLEYLAQLPQSEAVEGLKDIAPILALLSARLQQRESRYAVLFDL LLKLANTAIDSDKVAEKIADEARDDTPQALDAVWEEEQVKFFADKGCGDSAITAHXRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADAIERAASTENEKDLYQRQLEVFLDPNDPKVIEQAIKDGIPLSVIEAAQQSPVYKMA
MEWKLALPLHPEYRTLPMVWYVPPLSPIQSAADAGELGSNGILPDVESLRIPVQYLAN
LLTAGDTKPVLRALKRMLAMRHYKRAETVDGKVDTRALEEVGLTEAQAQEMYRYLAIA
  7247...7816

72ene="22005"

/function="orf; Unknown function"

/functe="Residues 2 to 67 of 189 are 86.36 pct identical
                                                                                                                                    QLVRARH"
                                                                                                                                                         GWAQSVVTFHGGASQHLDGVAFIFRLHLVLGMTLFLLFPFSRLVHIWSVPVEYLTRKY
                                                                                                                                                                                                                                                                                             subunit"
                                                                                                                                                                                                                                                                                                                                                                               MG1655: B1227"
                                                                                                                                                                                                                                                                                                                                                                                                    /note="Residues 1 residues 1 to 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6212.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Residues 1 residues 1 to 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="enzyme; Energy metabolism, carbon: Anaerobic
respiration"
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residues 1 to 512
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                                                                    /gene="Z2005"
7247. .7816
                                                                                                                                                                                                                                             /protein_id="AAG56087.1"
/db_xref="GI:12514948"
                                                                                                                                                                                                                                                                                                               /product="nitrate reductase
                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAG56086.1"
/db_xref="GI:12514947"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5212. .6889
/gene="narI"
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/gene="narJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="narJ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'function="enzyme; Energy metabolism, carbon: Anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'qene="narH"
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                                                                                                               .7816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to 236 of 236 are 99.57 pct identical to of 236 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to 512 of 512 are 99.80 pct identical to of 512 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                    to 225 of 225 are 99.55 pct identical to of 225 from Escherichia coli K-12 Strain
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CCCACCGTTTGCGTTGATGTCCTTC 544
                                           CTGGTTGATGGGGCAGTCGTTAACCCAATTCCTATTTCGCTCACGCGTGCATTGGGTGCT
                                                                                      CTCGTTGACGGAGGTATAGTTAACAACCTTCCCGTTGAGCCCCTTTCAGGAAAGCGGTATT
                                                                                                                                      ATTCGCGCATCATGCAGTATTCCAGGACTAATGGCACCCGTTGCGCATAACGGCTACTGG
                                                                                                                                                                                 CTTCTCGGCAGCTGTGCAATTCCCGGCATATTTGAACCCGTTGAGTATAAGAATTACTTG
                                                                                                                                                                                                                               GCCACCAATTTAAGTACTGGGCGTGAATTATGGTTTACTGAAGGCGATCTCCATCTTGCT 9825
                                                                                                                                                                                                                                                                          GCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCGGAAGGGAGTTTAATCCCCGCA
                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                            complement(8859. .9317)
/gene="ychJ"
/function="orf; Unknown function"
/note="Residues 1 to 152 of 152 are 99.34 pct identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"formyltetrahydrofolate
purT-dependent FGAR synthesis"
/protein_id-"AAG56089.1"
/db_xref-"GI:12514950"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Translation="MHSLQRKVLRTICPDQKGLIARITNICYKHELNIVQNNEFYDHR TGRFFMRTELEGIFNDSTLLADXDSALPEGSVBELNPAGRRRIVILVTKBAHCLGDLL MKANYGGLDVEIAAVIGHDTLRSVLERFDIPFELVSHEGLSRKEHDQKAWADAIDAV DKOW PDYVLAKYMRVLTPEFVSRFPNKIINIHHSFLPAFIGARPYHQAYERGVKIIGATAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mmvvgegllsaarfalqvvacgnalslalesnlsrsfssfsawa
Eylftdslessgtfesdggggrirtfevddgrftvcslwplgnptrgnsnfevmlema
VGKGLFVASLLTLRAVACENVLSLSLESNLSRRFSPFPDECKLSQSHRSYHIAVVNHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="enzyme; Nucleotide biosynthesis: Purine ribonucleotide biosynthesis" ribonucleotide biosynthesis" to 280 of 280 are 98.92 pct iden residues 1 to 280 of 280 from Escherichia coli K-I:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(7967.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="RNA; complement(7723.
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complement(7429. .7513)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGRIRTFEVDDGRFTVCSLWPLGNPTTG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="ychJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YVNDNLDEGPIIMQDVIHVDHTYTAEDMMRAGRDVEKNVLSRALYKVLAQRVFVYGNF
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="tRNA-Tyr"
/function="""
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/product="tRNA-Tyr"
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52.7%;
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                                                                                                                                                                                                                                                                                                                        Score 49.8; DB 1;
Pred. No. 0.0016;
0; Mismatches 97;
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                                                                                                                                                                                                                                                                                                                                                                     Length 10410;
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                                                                        GATATTGTGATAGCGGTTGACCTGC 1476
                                                                                                                   CCCACCGTTTGCGTTGATGTCCTTC 544
                                                                                                                                                                                                             CTCGTTGACGGAGGTATAGTTAACAACCTTCCCGTTGAGCCCCTTTCAGGAAAGCGGTATT
                                                                                                                                                                                                                                                        ATTCGCGCATCATGCAGTATTCCAGGACTCATGGCACCTGTTGCACATAACGGCTACTGG 1561
                                                                                                                                                                                                                                                                                                      CTTCTCGGCAGCTGTGCAATTCCCCGGCATATTTGAACCCGTTGAGTATAAGAATTACTTG 459
                                                                                                                                                                                                                                                                                                                                                    GCCACCAATTTAAGTACGGGACGTGAATTATGGTTTACTGAAGGCGATCTCCATCTTGCT 1621
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                                                                                                                                                                 CTGGTTGATGGAGCAGTCGTTAACCCAATTCCTATTTCCCTCACGCGTGCATTGGGGGGCT 150:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  107;
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J. Bacteriol. 17
94110230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bosl, M. and Kersten, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia.
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07; Conservative
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/codon_start=2
/codon_start=2
/transl_table=11
/protein_id-"aaA16860.1"
/protein_id-"aAA16860.1"
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/translation-"GLLARITNICYKHELNIVONNEFVDHRTGRFFMRTELEGIFNDS
/translation-"GLLARITNICHORMADAIDAFQPDYVVLAKYMRVLTPEF
/translation-"GLLARITNICHORMADAIDAFQPDYVVLAKYMRVLTPEF
NDTURSLYERDIFFELVSHEGITRNEHDGKMADAIDAFQPDYVVLAKYMRVLTPEF
VARFDKKIINIHHSFLPAFIGARPYHDAYERGYKIIGATAHYVNDLDEGPIIMQDVI
HVDHTYTAEDMMRAGRDVEKNVLSGRALYKVLAQRVFVYGNRTIIL"

916 c 843 g 946 t
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<2687.
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/strain="K-12"
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/gene="tgs"
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/gene="tgs"
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52.2%;
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  protein_bind
                                                                                                                   source
                                                                                                                                                                           Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Web Site (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein or RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez as gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (13-OCT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
This sequence was determined by the E. coll Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from E. coll K12 strain MG1655, Predicted open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
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Direct Submission
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3 (bases 1 t
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Blattner, F.R.
Direct Submission
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Escherichia coli K12
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Direct Submission
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/db_xref="taxon:83333"
33..49
                                                                                                                                         Location/Qualifiers
                                           /sub_strain="MG1655"
                                                                      /strain="Kl2
                                                                                           /organism="Escherichia
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                                                                                                                                                                     /product="nitrate reductase 1, beta subunit"
/protein_id="AAC74309.1"
/protein_id="AAC74309.1"
/db_xref="GI:1787478"
/translation="MKIRSQVEMYLINLDKCIGCHTCSVTCKNYWTSREGVEYAWFNNV
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PFDFDYQNLHTAPEGSKSQPIARPRSLITGERWAKIEKGPNWEDLGGEFDKLAKDKN
FDNIDKAMYSQFENTFEWMYLPRICEHGLNPACVATCPSGATYKREEDGIVLDODKGF
GWRMCITGCPYKKIYFNWKSGKSEKCIFCYPRIEAGQPTVCSETCVGRIRYLGVLYD
ADAIERAASTENEKDLYQROLDVFLDPNDFKYIEQAIKGGIPLSVIERAAQGSFVYKM
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VLLHKLPVKRLOLADGSTALVTTVYDLTLANVGLERGLNDVKCATSYDDVKAVTPAWA
EQITGVSRSQIIRIAREFADNADKTHGRSMIIVGAGLNHVLDMNYGLINMLIFCG
CVGQSGGWAHFVGQEKLRPOTGWOPLAFALDWQRPARHMNSTSYFYNHSSQWRYETV
TAEELLSPMADKSRYTGHLIDFNVRAERMGWLPSAPQLGTNPLTIAGEAEKAGMNPVD
TTVKSLKEGSIRFAAEQPENGKNHPRNLFIWRSNLLGSSGKGHEFMLKYLLGTEHGIQ
GKDLGQOGGVKPEEVDWQDNGLEGKLDLVFTLDFRLSTCLYSDIILFATWYEKDDM
NTSDMHPFIHPLSAAVDPAWEAKSDWEIYKAIAKKFSEVCVGHLGKETDIVTLPIQHD
SAAELAQPLDVKDWKKGECDLIPGKTAPHIMVVERDYPATYERFTSIGPLMEKIGNGG
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at1279037"
                                                                                       MEWKLALPLHPEYRTLPMVWYVPPLSPIQSAADAGELGSNGILPDVESLRIPVQYLAN
LLTAGDTKPYLRALKRMLAMRHYKRAETVDGKVDTRALEEVGLTEAQAQEMYRYLAIA
NYEDRFVVPSSHRELAREAFPEKNGCGFTFGDGCHGSDTKFNLFNSRRIDAIDVTSKT
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LAYGFNYYGTVGSNRDEFVVVRKMKNIDWLDGEGNDQVQESVK"
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AALSEFTGRDHTHLALNKEDEKIRFRDIQAQPRKIISSPTWSGLEDEHVSYNAGYTNV
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SSWQEVNELIAASNVYTIKNYGPDRVAGFSPIPAMSMVSYASGARYLSLIGGTCLSFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="enzyme;
respiration"
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/protein_id="AAC74308.1"
/db_xref="GI:1787477"
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/bound_moiety="CynR predicted site"
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/bound_moiety="Narr documented site"
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/function="enzyme; Energy metabolism, carbon: Anaerobic
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/transl_table=11
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'gene="narH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="o512; 100 pct identical to NARH_ECOLI SW: P11349"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EC_number="1.7.99.4"
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10065 ATTCGCGCATCATGCAGTATTCCAGGACTCATGGCACCTGTTGCACATAACGGCTACTGG
520 CCCACCGTTTGCGTTGATGTCCTTC 544
                                                                                                                                                                               CTTCTCGGCAGCTGTGCAATTCCCGGCATATTTGAACCCGTTGAGTATAAGAATTACTTG 459
                                               CTGGTTGATGGAGCAGTCGTTAACCCAATTCCTATTTCCCTCACGCGTGCATTGGGGGCT 10184
                                                                              CTCGTTGACGGAGGTATAGTTAACAACCTTCCCGTTGAGCCCTTTCAGGAAAGCGGTATT
                                                                                                                                                                                                                                                   GCCACCAATTTAAGTACGGGACGTGAATTATGGTTTACTGAAGGCGATCTCCATCTTGCT 10064
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107; Conservative
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/db_xref="GI:1787480"
/db_xref="GI:1787480"
/translation="MOFLNMFFFDIYPYIAGAVFLIGSWLRYDYGQYTWRAASSOMLD
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IGGVLLLKRRLFSPRVRATTTGADILLISLLYIQCALGLLTIPFSAQHHDGSEMMKLV
GWAQSVYTFHGGASQHLDGVAFIFRLHLVLGMTLFLLFPFSRLIHIWSVPVEYLTRKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="orf; Unknown"
/note="091; 35 pct identical (3 gaps) to 54 residues
approx. 1040 aa protein BGAL_KLEPN SW: P06219"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="enzyme; respiration"
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/gene="narJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="orf, hypothetical protein"
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/protein_id="AAC74312.1"
/db_xref="G1:1787481"
/translation="MVVGEGLLSAARFALRVVACGNALSLALKSNLGRSFSSFPAWAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="narl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAGAVAPQYLNITTGGQH"
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LQLNSRELPDHLPLYLEYLAQLPQSEAVEGLKDIAPILALLSARLQQRESRYAVLFDL
LLKLANTAIDSDKVAEKIADEARDDTPQALDAVWEEEQVKFFADKGCGDSAITAHQRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAC74310.1"
/db_xref="GI:1787479"
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oshima,T., Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A., Ikemoto,K., Inada,T., Itoh,T., Kajihara,M., Kanai,K., Kashimoto,K., Kimura,S., Kitagawa,M., Makino,K., Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K., Nakamura,Y., Nashimoto,H., Nishio,Y., Saito,N., Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C., Yamamoto,Y., Yano,M. and Horiuchi,T. A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map DNA Res. 3 (3), 137-155 (1996)
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Complete and shotgun sequencing; narK; narG;
corr narI: chlI; tpr; purU; ychJ; rrsA; ych
                                                                                                                                                                                                                                                                                                      The Japan E.coli genome DNA sequencing group Members: (1995.4 - 1996.3)
Alba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A.,
Horluchi,T., Ikemoto,K., Inada,T., Isono,K., Isono,S.,
Itoh,T., Kanai,K., Kasai,H., Kashinoto,K., Kim,S.,
Itoh,T., Kanai,K., Missai,H., Kashinoto,K., Moromura,K.,
Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K.,
Nakamura,Y., Nashinoto,H., Nishio,Y., Oshima,T., Saito,N.,
Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C.,
Yamamoto,Y. and Yano,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (29-JUL-1996) to the DDBJ/EMBL/GenBank databases.
Hirotada Mori, NARA Institute of Science and Technology, Res. &
Edu. Center for Genetic Info.; 8916-5 Takayama, Ikoma, Nara 630-01,
Japan (E-mail:hmori@tc.aist-nara.ac.jp, Tel:81-7437-2-5660,
Fax:81-7437-2-5660,
Collaboration Information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   narJ; narI; chl1; tpr; purU; ychJ; rrsA; ychK; rrsB; hrn; drdx; osmZ; bglV; hns.
Escherichia coll(strain:Kl2) DNA, clone:Kohara clone #249.
                           URL:
The Japan E. coli genome database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Group:
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3 (bases 1 to 13860)
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                                                                                                                                                                                          Information operator:
                                                                                                                  Address: NARA Institute of Science Ikoma, 630-01, Japan
                                                                                            E-mail: hmori@gtc.aist-nara.ac.jp
                                                                                                                                                                                                                   E-mail: kishori@nibb.ac.jp
                        http:bsw3.aist-nara.ac
                                                                                                                                                                      Name: Hirotada Mori
                                                                                                                                                                                                                                          Address: National Institute of
                                                                                                                                                                                                                                                                Name: Takashi Horiuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (sites)
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                                                                                                                                                                                                                                       Biology, Okazaki,
                                                                                                                                           Technology,
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translation="MKIRSQVGMVLNLDKCIGCHTCSVTCKNVWTSREGVEYAWFNNV/
                      /protein_id="BAA36095.1"
/db_xref="GI:1651621"
                                                                   'product="Respiratory nitrate reductase 1 beta chain
(.7.99.4)."
                                                                                                                                                                                                                                                              /gene-"narH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="bisD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="narK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Escherichia
                                                                                                                                                                                                                   'gene≖"narH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ⁄transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="bisD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="ORF_ID:0248#13
                                                                                                                       transl_table=11/
                                                                                                                                           codon_start=1
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                                                                                                                                                                                        note-"ORF_ID:o250#1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="narC; narG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "nark"
                                                                                                                                                                 Accession
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DWYCDLPPASPQTWGEQTDVPESADWYNSYIIAWGSNVPQTRTPDAHFFTEVRYKGT
KTVAVTPDYASIAKLCDLWLAPKQGTDAAMALAMGVMLEEFHLDNPSQYFTDYVRRY
TDMPMLYMLEERDGYYAAGRMLRAADLVDALGQENNPEWKTVAFNTIGEMVAPNGSIG
FRWGEKGKWNLEQRDCKTGEETELQLSLLGSQDEIAEVGFPYFGGGTEHENKVELEN
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EQITGVSRSQIIRIARAFDLYTTVYDLTLANGLIHWYHLDMNYRGYTPAWA
EQITGVSRSQIIRIARAFDANADKTHGRSMIIVGAELHWYHLDMNYRGYFYNHSSQWRYETV
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TAEELLSPMADKSRYTGHLIDFNVRAERMGWLPSAPQLGTNPLTIAGEAEKAGMNPVD
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GKDLGQQGGVKPEEVDWODNGLEGKLDLVVTLDFRLSSTCLYSDIILFTATWYEKDDM
NTSDMHPFIHPLSAAVDPAWEAKSDWEIYKAIAKKFSEVCVGHLGKETDIVTLPIQHD
SAAELAQPLDVKDWKKGECDLIPGKTAPHIMVVERDYATYERTTSIGPLMEKIGNGG
KGIAMNTQSEMDLLRKLNYTKAEGPAKQDMLNTAIDAEMILTLAPETNGQVAVKAW
AALSETGROHTHLALMKEDEKIRFDIQAQPRKIISSPTWSGLEDEHYSYNAGYINV
HELIPWRTLSGRQQLYQDHQWRDFGESLLVYRPPIDTRSVKEVIGOKSNGNQEKALN
FLTPHOKWGIHSTYSDNLLMLTLGRGGEVVMLSBADAKDLGIADNDWIEVFNSNGALT
FLTPHOKWGIHSTYSDNLLMLTLGRGGEVVMLSBADAKDLGIADNDWIEVFNSNGALT
FLTPHOKWGIHSTYSDNLLMLTLGRGGEVVMLSBADAKDLGIADNDWIEVFNSNGALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="ORF_ID:0249#1 similar to SwissProt Accession Number P09152"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="DLATSKASIKEQLPVLKRGHLWIMSLLYLATFGSFIGFSAGFAM
LSKTQFPDVQILQYAFFGPFIGALARSAGGALSDRLGGTRVTLVNFILMAIFSGLLFL
TLPTDGQGGSFMAFFAVFLALFLTAGLGSGSTFQMISVIFRKLIMDRVKAEGGSDERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similar to PIR Accession Number S05239"
                                                         ARAVVSQRVPAGMTMMYHAQERIVNLPGSEITQQRGGIHNSVTRITPKPTHMIGGYAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSWQEVNELIAASNVYTIKNYGPDRVAGFSPIPAMSMVSYASGARYLSLIGGTCLSFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Nitrate transport protein nark."
/protein_id="BAA36093.1"
/db_xref="GI:1651619"
AYGFNYYGTVGSNRDEFVVVRKMKNIDWLDGEGNDQVQESVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IVRSTHGVNCTGSCSWKIYVKNGLVTWETQQTDYPRTRPDLPNHEPRGCPRGASYSWY
LYSANRLKYPMMRKRLMKMWREAKALHSDPVEAWASIIEDADKAKSFKQARGRGGFVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAA36094.1"
/db_xref="GI:4062800"
/translation="MSKFLDRFRYFKQKGETFADGHGQLLNTNRDWEDGYRQRWQHDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Nucleotide position 1281562-1295421 from initiation site of ThrA (0 min.). This clone is Kohara lambda miniset library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="Kohara clone #249"
/map="27.6-27.9 min"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'product="Respiratory nitrate reductase 1 alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coli"
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Number P11349"

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Query Match
Best Local
ATTCGCGCATCATGCAGTATTCCAGGACTCATGGCACCTGTTGCACATAACGGCTACTGG
                                                   CTTCTCGGCAGCTGTGCAATTCCCCGGCATATTTGAACCCGTTGAGTATAAGAATTACTTG 459
                                                                                                                                                                 GCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCGGAAGGGAGTTTAATCCCCCGCA 399
                                                                                                                                                                                                                                 107;
                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MQFLNMFFFDIYPYIAGAVFLIGSWLRYDYGQYTWRAASSQMLD
RKGMNLASNLFHIGILGIFYGHFFGMLTPHWMYEAWLPIEVKQKMAMFAGGASGVLCL
IGGVLLLKRRLFSPRVRATTTGADILILSLLVIQCALGLLTIPFSAQHMDGSEMMKLV
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GWRMCITGCPYKKIYFNWKSGKSEKCIFCYPRIEAGQPTVCSETCVGRIRYLGVLLYD
ADAIERAASTENEKDLYQRQLDVFLDPNDPKVIEQAIKDGIPLSVIEAAQQSPVYKMA
                                                                                                                                                                                                                                                                                                                                                                                 similar to PIR Accession Number A90813"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MMVVGEGLLSAARFALRVVACGNALSLALESNLGRSFSSFPAWAEVLIADSLGSSGTFESDGGGGRIRTFEVDDGRFTVCSLWPLGNPTRGNSNFEVMLEMVVGEGLFVASLLTLRAVACGNVLSLSLESNLSRRFSPFPDECKLSQSHRSYHIAVVNYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MIELVIVSRLLEYPDAALMOHOQEMFEAIAASKNLPKEDAHALG
IFLRDLITMDPLDAQAQYSELFDRGRATSLLLFEHVHGESRDRGQAMVDLLAQYEQHG
LQLMSRELPDHLPIYLEYLAQLPQSEAVEGIKDIAPILALLSARLQQRESRYAVLFDL
LLKLANTAIDSDKVAEKIADEARDDTPQALDAVWEEEQVKFFADKGCGDSAITAHORR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="ORF_ID:o250#2
similar to PIR Accession Number B27737"
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6478. .7188
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PFDFDYQNLHTAPEGSKSQPIARPRSLITGERWAKIEKGPNWEDDLGGEFDKLAKDKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(8426. .8527)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(8426.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLVRARH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GWAQSVVTFHGGASQHLDGVAFIFRLHLVLGMTLFLLFPFSRLIHIWSVPVEYLTRKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similar to SwissProt Accession Number P11350"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAGAVAPQYLNITTGGQH"
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/protein_id="BAA36096.1"
/db_xref="GI:1651622"
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NYEDRFVVPSSHRELAREAF PEKNGCGFTFGDGCHGSDTKFNLFNSRR I DA I DVTSKT
                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="BAA36098.1"
/db_xref="GI:4062801"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="ORF_ID:0250#4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.7.99.4) (cytochrome B-I
/protein_id="BAA36097.1"
/db_xref="GI:1651623"
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                                                                                                                                                                                                                                                          6.4%;
                                                                                                                                                                                                                              Score 48.2; DB Pred. No. 0.005; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Group:
The Japan E.coli genome DNA sequencing group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Japan (E-mail:hmori@gtc.aist-nara.ac.jp, Tel:81-7437-2-5660, Fax:81-7437-2-5669)
On Dec 24, 1998 this sequence version replaced gi:1651628.
Collaboration Information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (29-JUL-1996) to the DDBJ/EMBL/GenBank databases. Hirotada Mori, NARA Institute of Science and Technology, Res. & Edu. Center for Genetic Info.; 8916-5 Takayama, Ikoma, Nara 630-01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The systematic sequencing of the Escherichia coli genome in Japan Unpublished (1996) 3 (bases 1 to 16397)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alba H., Baba,T., Fujita,K., Hayashi,K., Honjo,A., Horiuchi,T., Ikemoto,K., Inada,T., Isono,K., Isono,S., Itchi,T., Kanai,K., Kasai,H., Kashinoto,K., Kin,S., Kinura,S., Kitagawa,M., Mori,H., Kitakawa,M., Makino,K., Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K., Nakamura,Y., Nashimoto,H., Nishio,Y., Oshima,T., Saito,N., Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C., Yamamoto,Y. and Yano,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wada,C., Yamamoto,Y., Yano,M. and Horiuchi,T.
A 718-Kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map DNA Res. 3 (3), 137-155 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oshima,T., Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A., Ikemoto,K., Inada,T., Itoh,T., Kajihara,M., Kanai,K., Kashimoto,K., Kimayawa,M., Makino,K., Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K., Nakamura,Y., Nashimoto,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete and shotgun sequencing; narG; narG; bisD; narH; narG; chl; tpr; purU; ychJ; rrsA; ychK; rrsB; hrn; galU; osmZ; bglY; hns; tdk; ychG; adhE; ychE.
Escherichia coli(strain:K12) DNA, clone:Kohara clone #250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mori,H.
Direct Submission
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                           Information operator:
Name: Hirotada Mori
                                                                                                                                               Headed by:
Name: Takashi Horiuchi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Members: (1995
                                                                                                                                                                                                                              Aiba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Horiuchi, T., Ikemoto, K., Inada, T., Isono, K., Isono, S., Itoh, T., Kanai, K., Kasai, H., Kashimoto, K., Kim, S., Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K., Motomura, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Saito, N., Sampei, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C.,
                                                                                     E-mail: kishori@nibb.ac.jp
                                                                                                                Address: National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Japan E.coli genome
                                                                                                                                                                                                   Yamamoto, Y. and Yano, M.
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NARA Institute of Science and Technology,
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                                                                                                             Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequencing
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                                                                                                                Basic
                                                                                                             Biology,
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                                                                                                                Okazaki, 444, Japan
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FEATURES
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URL:
The Japan 1
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hmori@gtc.aist-nara.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                              2135. . 2845
/gene="narJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GWRMCITGCPYKKIYFNWKSGKSEKCIFCYPRIEAGQPTVCSETCVGRIRYLGVLLYD
ADAIERAASTENEKDLYQRQLDVFLDPNDPKVIEQAIKDGIPLSVIEAAQQSPVYKMA
MEWKLALPLHPEYRTLPMVWYVPPLSPIQSAADAGELGSNGILPDVESLRIPVQYLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            **C+TANS-1ation="MKIRSOVGMVLNLDKCIGCHTCSVTCKNVWTSREGVEXAWENNVETKPGGGFPTDWENQEKYKGGWIRKINGKLQPEWGNRAMLLGKIFANPHLPGIDDYKEPTKPGGGFPTDWENQEKYKGGWIRKINGKLQPEWGNRAMLIGKIFANPHLPGIDDXHKFPDYGNLHTAPEGGKXQPIARPSLITGEBEMKAKIEKGPNWEDDLGGEFDKLAKKN FDNIQKAMYSQFENTFMMYLPRLCEHCLNPACVATCPSGAIYKREEDGIVLIDQDKCR
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LLKLANTAIDSDKVAEKIADEARDDTPQALDAVWEEEQVKFFADKGCGDSAITAHQRR
                                                                                                                                                                                                                                                                                                            similar to PIR Accession Number B27737"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="ORF_ID:0249#1
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                                                                        FAGAVAPQYLNITTGGQH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLTAGDTKPVLRALKRMLAMRHYKRAETVDGKVDTRALEEVGLTEAQAQEMYRYLAIA
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1.7.99.4)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
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1.7.99.4)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="bisD"
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                                                                                                                                                                                                                                                                                             codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="narH"
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Best Local
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                                                                      Local 107;
                                                                                                                   Similarity
                                                                                            Conservative
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6577 GCCACCAATTTAAGTACGGGACGTGAATTATGGTTTACTGAAGGCGATCTCCATCTTGCT 6636
                                                  GCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCGGAAGGGAGTTTAATCCCCGCA 399
                                                                                                                                                                                                                                                                                                                    similar to PIR Accession Number 155006"
                                                                                                                                                                                                                                                                                                                                                                         complement(5670. .6128)
/gene="ychJ"
                                                                                                                                                                                                                                                                                                                                                                                                                           complement(5670./gene="ychJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Formyltetrahydrofolate deformylase (EC 3.5.1.10)
(formyl-fh(4) hydrolase)."
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/gene="tpr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(4083.
/gene="tpr"
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/codon_start=1
                                                                                                                                                                                                          /transl_table=11
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YVNDNLDEGPIIMQDVIHVDHTYTAEDMMRAGRDVEKNVLSRALYKVLAQRVFVYGNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(4778. .5620)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(4778. .5620)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similar to PIR Accession Number A90813"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGRIRTFEVDDGRFTVCSLWPLGNPTTG'
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IGGVLLLKRRLFSPRVRATTTGADILILSLLVIQCALGLLTIPFSAQHMDGSEMMKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="purU"
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/protein_id="BAA36109.
/db_xref="GI:1651632"
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1.7.99.4) (cytochrome B-NR)."
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/gene="chlI"
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                                                                                                                                                                                                                                                                                                                                                note="ORF_ID:0250#7
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                                                                                                                             Score 48.2; DB 2
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E.coli genomic D
D90852 AB001340
D90852.1 GI:180
                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-DEC-1996) to the DDBJ/EMBL/GenBank databases. Hirotada Mori, NARA Institute of Science and Technology, Res Edu. Center for Genetic Info.; 8916-5 Takayama, Ikoma, Nara Japan (E-mail:hmori@gtc.aist-nara.ac.jp, Tel:81-7437-2-5660, Fax:81-7437-2-5669)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto,Y. and Horiuchi,T.
A 570 kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage m DNA Res. 3 (6), 363-377 (1996)
97251357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Itoh, T., Kasai, H., Kashimoto, K., Kimura, S., Kitakawa, M., Kitagawa, M., Makino, K., Miki, T., Mizobuchi, K., Mori, H., Mori, Kitagawa, M., Makino, K., Miki, T., Mizobuchi, K., Nishio, Y., Motomura, K., Nakade, S., Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Saito, N., Sampel, G., Seki, Y., Sivasundaram, S., Tagami, H., Takeda, J., Takemoto, K., Takeuchi, Y., Wada, C., Yangami, H., Takeda, J., Takemoto, K., Takeuchi, Y., Wada, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete and shotgun sequencing; IS2; adhE; bglY; bisD; chlI; drdx; galU; hrn; narC; narG; narH; narI; narJ; oppA; osmZ; purU; tdk; tgs_; tpr; ychE; ychJ.
tgs_cherichia coll (strain:K12) DNA, clone_lib:Kohara lambda miniset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The systematic sequencing of the Escherichia coli genome in Japan Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                           Collaboration Information:
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                                                                                                                                                                                                                          The Japan E.coli genome DNA sequencing Members: (1995.4 - 1996.3)
                                                                                                                                                                                                                                                                                                                                   Project:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli
                  Kimura,S., Kitagawa,M., Kitakawa,M., Makino,K., Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K., Nakamura,Y., Nashimoto,H., Nishio,Y., Oshima,T., Saito, Sampel,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C., Yamamoto,Y. and Yano,M.
                                                                                                                                             Aiba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Horiuchi, T., Ikemoto, K., Inada, T., Isono, K., Isono Itoh, T., Kanai, K., Kasai, H., Kashimoto, K., Kim, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ibrary clone:Kohara clone #251.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 23203)
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by:
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                                                                                                                                                                                                                                                                                                        genome DNA sequencing
                                                                                                                                                                                                                                                     group
                                                                                                                                                                                                                                                                                                        project
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                                                                                                                                                                          Isono, S.,
                                                                        Saito, N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E-mail: kishori@nibb.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Address: NARA Institute of Science Ikoma, 630-01, Japan
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Address: National Institute of
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                                                                                                                                                                                                                  /gene="narJ"
2135. .2845
/gene="narJ"
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PFDFDYQNLHTAPEĞSKSQPIARPRSLITĞERMAKIEKGPNWEDDLGGEPÜKLAKDKN
FDNIOKAMYSQFENTFMMYLPRLCEHPLCLNPACYATCPSGAIYKREEDGIYLIDQDKCR
GWRMCITĞCPYKKIYFMWKSĞKSEKCIFCYPRLEAĞQPTVCSETCYĞRIRYLĞVLLYD
ADAIERAASTENEKDLYQRQLDYFLDDNDFKYIEQAIKDĞIPLSVIEAAQQSPYYKMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHQKWGIHSTYSDNLIMLTLGRGGPVVWLSEADAKDLGIADNDWIEVFNSNGALTARA
VVSQRVPAGMTWMYHAQERIVNLPGSEITQQRGGIHNSVTRITPKPTHMIGGYAHLAY
GENYYGTYGSNRDEFVVVRKMKNIDWLDGEGNDQVQESVK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="ORF_ID:0249#2 similar to [SwissProt Accession Number P11349]"
                                                                                                                                                                                                                                                                                                                                                                            MEWKLALPLHPEYRTLPMVWYVPPLSPIQSAADAGELGSNGILPDVESLRIPVQYLAN
LLTAGDTKPVLRALKRMLAMRHYKRAETVDGKVDTRALEEVGLTEAQAQEMYRYLAIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similar to [SwissProt Accession Number P09152]*
                         /product="narJ protein"
/protein_id="BAA16023.1"
/db_xref="GI:1805506"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAA16022.1"
/db_xref="GI:1805505"
/translation="MKIRSQVGMVLNLDKCIGCHTCSVTCKNVWTSREGVEYAWFNNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Nucleotide position 1285695-1308897 from
initiation site of ThrA (0 min.).-This clone is
Kohara lambda miniset library"
                                                                                                                                                                                                                                                                                                                                                        NYEDRFVVPSSHRELAREAFPEKNGCGFTFGDGCHGSDTKFNLFNSRRIDAIDVTSKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="RESPIRATORY NITRATE REDUCTASE 1 BETA CHAIN
1.7.99.4)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="narH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAA16021.1"
/db_xref="GI:1805504"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product="respiratory nitrate reductase 1 alpha Chain 1.7.99.4)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="narC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="Kohara clone #251"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:562"
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                                                                                                                                                          note="ORF_ID:0249#3
imilar to [PIR Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="narH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="DHQWMRDFGESLLVYRPPIDTRSVKEVIGQKSNGNQEKALNFLT"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Escherichia coli"
translation="MIELVIVSRLLEYPDAALWQHQQEMFEAIAASKNLPKEDAHALG
                                                                                                       transl_table=11
                                                                                                                                   codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            narG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Basic
                                                                                                                                                               Number B27737]"
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                            complement(5670. .6128)
/gene="ychJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MHSLQRKVLRTICPDQKGLIARITNICYKHELNIVQNNEFYDHR
TGRFFMRTELEGIFNDSTLLADDDSALPEGSVBELNPAGRRIVTULVTKBAHCLGDLL
MKANYGGLDVEIAAVIGHDFLRSLVERFDIPFELVSHEGLTRNEHDQKMADAIDAY
PDYVVLAKYMRVLTPEFVARFPNKIINIHHSFLPAFIGARPYHQAYERGVKIIGATAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"ORF_ID:0249#4 similar to [SwissProt Accession Number P11350]"
                                                                                                similar to [PIR Accession
                                                                                                                                                                                                /translation="mSQLCPCGSAVEYSLCCHPYVSGEKVAPDPEHLMRSRYCAFVMQ
DADYLIKTWHPSCGAAALRAELMAGFAHTEWLGLTVFEHCWQDADNIGFVSFVARFTE
                                                                                                                                                                                                                                                                                                                       /note="ORF_ID:0249#9
similar to [SwissProt Accession Number P37052]"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(5670.
/gene="ychJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"ORF_ID:0249#8 similar to [SwissProt Accession Number P37051]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(4778. .5620)
/gene="purU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MRGRMRSFDQGSTRAPARERCRRQRPEGRSAQR"
complement(4778. .5620)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="ORF_ID:0249#7
similar to [PIR Accession
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(4083. .4184)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="Mofinnefediypyiagavfligswlrydyggytwraassomld
RKGMNLASNLFHIGILGIFVGHFFGMLTPHWMYEAWLFIEVKOMAMFAGGASGYVLCL
IGGYVLLLKRRLFSPRVRATTTGADILILISLLVJQCALGLTIPFSAQHHDGSEMMYL
GWAQSVVTFHGGASQHLDGVAFIFRLHLVLGMTLFLLFPFSRLIHIWSVPVEYLTRKY
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/gene="chll"
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LQLNSRELPDHLPLYLEYLAQLPQSEAVEGLKDIAPILALLSARLQQRESRYAVLFDL
LLKLANTAIDSDKVAEKIADEARDDTPQALDAVWEEEQVKFFADKGCGDSAITAHQRR
                                                                                                                                                                         GGKTGAIIERSRFLKENGQWYYIDGTRPQFGRNDPCPCGSGKKFKKCCGQ"
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/protein_id="BAA16027.1"
/db_xref="GI:1805510"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YVNDNLDEGPIIMQDVIHVDHTYTAEDMMRAGRDVEKNVLSRALYKVLAQRVFVYGNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FORMYL-FH(4) HYDROLASE)."
/protein_id="BAA16026.1"
/db_xref="GI:1805509"
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/protein_id="BAA16025.1"
/db_xref="GI:1805508"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(4083.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="RESPIRATORY NITRATE REDUCTASE 1 GAMMA CHAIN 17.99.4) (CYTOCHROME B-NR)."
/protein_id="BaAi6024.1"
/db_xref="GI:1805507"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAGAVAPOYLNITTGGOH'
                                                                                                               /note="ORF_ID:0249#10
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/transl_table=11
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                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="FORMYLTETRAHYDROFOLATE DEFORMYLASE (EC 3.5.1.10)
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  Score 48.2; DB 2; Pred. No. 0.0054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .6128)
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                                                                                                  Number B36871]"
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                         Length 23203;
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                                                           6697
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GATATTGTGATAGCGGTTGACCTGC 6781
                           CCCACCGTTTGCGTTGATGTCCTTC 544
                                                                                                                                     CTTCTCGGCAGCTGTGCAATTCCCCGGCATATTTGAACCCGTTGAGTATAAGAATTACTTG
                                                         CTGGTTGATGGAGCAGTCGTTAACCCAATTCCTATTTCCCTCACGCGTGCATTGGGGGGCT
                                                                                       CTCGTTGACGGAGGTATAGTTAACAACCTTCCCGTTGAGCCCCTTTCAGGAAAGCGGTATT
                                                                                                                    ATTCGCGCATCATGCAGTATTCCAGGACTCATGGCACCTGTTGCACATAACGGCTACTGG
                                                                                                                                                                              GCCACCAATTTAAGTACGGGACGTGAATTATGGTTTACTGAAGGCGATCTCCATCTTGCT 6636
                                                                                                                                                                                                          GCGACGGATTTATACTCGGGAAGGGCTCTATACCTCTCGGAAGGGAGTTTAATCCCCGCA 399
                                                                                                                                                                                                                                         107;
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                         98;
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                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                       Gaps
                                                           6756
                                                                                       519
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                                                                                                                                                  459
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Search completed: June 2, 2001, 20:36:27 Job time: 24485 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 200000000
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789
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gb_est5:*
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1154.754 Million cell updates/sec
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em_estro7:*
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              gb_est44:
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Result
No.
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   U4484400000048000
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Match
               the number of results predicted by chance to have than or equal to the score of the result being pure by analysis of the total score distribution.
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em_gss_vrt2:
em_gss1:**13:
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em_gss_pln2:*
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1101
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741
820
855
855
854
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264
471
1088
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  BF047003
ARA669816
BF041063
CNS000D1
BF0347880
BE0347880
BE0373365
BR7588419
BG180158
BF981465
AR462708
CNS0006J
                                                                                                                                                                                                                                                             SUMMARIES
BF047003 EST1100 M
AW669846 113436 MA
BF041063 BP250009B
AL065414 Drosophi1
BF545880 UI-R-BT0-
BE03749 MP02C04 M
W31742 zb93c02.r1
AW773365 rp03h07.y
BG178365 rp03h07.y
BG178653 602329533
BF688419 602184812
BG180158 602329749
BF981465 602309286
H96434 yv92h09.r1
AW462708 BP230010A
AL052532 DU-Scophi1
A195365 7010SOphi1
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9b_est48:*
9b_est50:*
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9b_est55:*
9b_est58:*
9b_est58:*
9b_est68:*

em_gss_other:*

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ACCESSION
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AUTHORS
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36.8
36.8
36.4
                                                                                                                                                                                                             Unpublished (2000)
Contact: Robertson HM
Department of Entomology
University of Illinois at Urbana-Champaign
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea; Sphingidae; Sphinginae; Manduca.
                                                                                                                                                                                                                                                                                                                                                                                  BF047003 664 bp mRN
EST1100 Manduca sexta male
sexta cDNA clone pMsmalfF7
                                                                                                                                                                                                                                                                              1 (bases 1 to 664)
Robertson, H.M., Patch, H.M., Walden, K.K.O. and Nardi, J.B.
                                                                                                                                                                                                                                                                                                                                                                 BF047003
BF047003.1 GI:10764059
                                                                                                                                                           Email: hughrobe@uiuc.edu
Seq primer: T3
                                                                                                                                                                                                    505 S. Goodwin, Orbana, IL 61801,
                                                                                                                                                                                                                                                         male Manduca sexta moths
                                                                                                                                                                                                                                                                    Partially normalized expressed
                                                                                                                                                                                                                                                                                                                                   Manduca sexta
                                                                                                                                                                                                                                                                                                                                            tobacco hornworm.
                                                                                                                                                                                 217 333-0489
217 244 3499
                                                                                                                                      quality sequence stop: 600
Location/Qualifiers
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/dev_stage="newly eclosed adults and pharate adults"
/lab_host="XL1 Blue MRF and SOLR"
/note="Organ: Annehonae; Vector: Uni-ZAP XR; Site_1: Ec
Site_2: XhoI; The library was prepared by Stratagene v
oligo-T priming and unidirectional cloning with an
adaptor at the 5' end (GGCACGAG) following the EcoRI
                                                                                   /db_xref="taxon:7130"
/clone="pMsma16F7"
/clone_lib="Manduca sexta male antennae Uni-ZAP
                                                               /sex="male"
                                                                                                                  /organism="Manduca sexta"
                                                                                                                              . 664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                   NA EST 10-OCT-2000 antennae Uni-ZAP XR library Manduca 5' similar to hydrolases, mRNA sequence
                                                                                                                                                                                                                                                                   sequence tags from the antennae
                                Uni-ZAP XR; Site_1: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL106628 Drosophil
BF645033 NF031A05E
AA261636 mz87e09.r
BF650258 NF087A05E
BF644903 NF017B01E
BF644903 NF017B01E
BF6449558 NF079G10E
AL098379 Drosophil
AL052709 Drosophil
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BE204219 601867672
AW314925 11506 MAR
AL067645 Drosophil
AZ653873 1M0527E13
AW773701 EST332687
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AL073739 Drosophil
AV194762 AV194762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGGGTTCTTGCTCTAATCCTCATAGGTGGTGGGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTCGTCGGACATTCATTCGGAACAATGATCTCTATGAAGTACTGTTCGGAGTATCGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGAATTACTGGTTGAGGATGTACGCGATCTTATTCGACAATTGGGACGCGAGAAATGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTTGACTTAAGAGGGTATGGAGACTCAGAGAGGCCGGAAGGTGTATCCTCGTATAAAAT 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCTGTGATTGCTCCATTATGCTGGGCAGCACGTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAGAACTTCATTTCAGATTTAGATGCGGTTGTTAGGGAGACTGGAGTGGAGAAATTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTTTGGTATTCATGGCGACACCAAATAGTCGAGTTCAATAAAAATTATTGGTGCATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 517)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW669846 517 bp
113436 MARC 1BOV Bos
AW669846
                                                                                                                                        Single pass sequencing. Bases call v0.980904.e. Vector identified by
                                                                                                                                                                                                                                                                                      Unpublished (2000)
                              Plate: 108 row: P column: 15
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                           and -minmatch 12 options
                                                                                                                                                                                               Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                 USDA, ARS, US Meat Animal PO Box 166, Clay Center, N
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                      BACKWARD:
                                                                                       FORWARD: AGGAAACAGCTATGACCAT
                                                                                                        PCR PRimers
                                                                                                                                                                          Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                       Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                            Design and use of four pooled tissue normalized cDNA libraries
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               Location/Qualifiers
                                                                      GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:7526360
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47.58;
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                                                                                          Tel: 217 333 5998

Fax: 217 244 5617

Email: h-lewin@uiuc.edu

Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National

Funding for cattle EST sequencing was provided by the USDA National

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Funding for cattle EST sequencing was provided by the USDA National

Funding for cattle EST sequencing was provided by the USDA National

Funding for cattle EST sequencing was provided by the USDA National

From Washington University Genome Center PHRAP suite.

Crosss_match from Washington University Genome Center PHRAP suite.
                                                                                                                                                                                                                                                                                                                                                                                 Contact: Lewin, H. A.

W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF041063.1 GI:10758118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP250009B20D7 Soares normalized bovine placenta clone BP250009B20D7 5', mRNA sequence.
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BP250009B20D7 Soares
                             Insert Length: 572
                                               FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACCCTCACTAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovine ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lewin, H.A., Soares, M.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos.
1 (bases 1 to 572)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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/tissue_type="pooled"
/lab_host="PuHlOB"
/lab_host="PuHlOB"
/note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: xhoI;
/ibzary made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
164 c 133 g 96 t
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49.8%;
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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo. NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACTTCTTGGCTTCTGTACA
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACRO1J16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                     Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.f)
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scomorpha; Ephydroidea; Drosophilidae; Drosophila.
(bases 1 to 1101)
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/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRAGDGKDKKKGKDKDRTDDAKATDGKDTWRDTTDTAKRRRKRRRRAGRGRDRKGDKKK 1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKAGRKRKWTRKTWKRDTADWKAWAAWRWRWRRDRKDRRGRRDRWRRWRGADKKWKWDD
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                                                                                                                                                                                                                                                                                                     BF545880 467 bp mRNA EST 11
UI-R-BT0-qe-g-06-0-UI.rl UI-R-BT0 Rattus norvegicus
UI-R-BT0-qe-g-06-0-UI 5', mRNA sequence.
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                              Contact: Soares, MB Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                     Rattus norvegicus
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   University of Iowa
451 Eckstein Medic
                                                                    97044477
                                                                                                      discovery
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Bonaldo, M.F., Lenno
                                                                                                                                                                                                       Eukaryota;
                                                                                                                                                                                                                                                                         BF545880.1 GI:11636987
                                                                                   Genome Res. 6 (9),
                                                                                                                    Normalization and subtraction:
                                                                                                                                                                      Rattus
                                                                                                                                                                                     Mammalia; Eutheria;
                                                                                                                                                                                                                                         Norway rat.
Eckstein Medical Research Building Iowa City, IA 52242, USA
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/db_xref="taxon:7227"
/db_ref="RPCI-98"
/clone="BACR01J16"
/clone="BACR01J16"
/note="end: TET3"
104 c 123 g 211 t 383
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                                                                                                                                    Lennon, G. and Soares, M.B.
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                                                                                   791-806 (1996)
                                                                                                                                                                                  Chordata;
Rodentia;
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                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
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129; Conserv
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Fax: 319 335 9565
Email: mscaares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.
This clone is also available through the I.M.A.G.E. Consortium
LLNL (info@image.llnl.gov). IMAGE ID- 1788663
Seg primer: M13 Forward.
                                                   Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; core eudicots; Caryop
                                                                                                                                                           BE037499 1022 bp mRNA
MP02C04 MP Mesembryanthemum
BE037499
BE037499.1 GI:8332515
                 Caryophyllales; Aizoaceae; Mesembryanthemum.
1 (bases 1 to 1022)
                                                                                                                                            EST
                                                                                                                        common ice
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; This library
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/clone_lib="UI-R-BT0"
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Borchert, C.,
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Caryophyllidae;
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Brazille, S., Brooks, J.,

Eaton, M., Ferrea

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                                                                                                                                                                                                                                                                                                                                                                                                         W31742 445 bp mrvm
zb93c02.rl Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone
IMAGE:320354 5', mrNA sequence.
                       Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
This clone is available royalty-free through LINL; contact the
                                                                                                                      Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                         Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J. Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                           Contact: Wilson RK
                                                                                                                                                                             Unpublished (1995)
                                                                                                                                                                                          R., Williamson, A., The WashU-Merck EST
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Contact: Michalowski, C.B.
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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quality sequence stop: 407
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/db_xref="taxon:3544"
/clone_lib="MP"
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/dev_stage="6 weeks"
/note="3 d 500mM NaCl"
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                                                      Cephaloboidea; Cephalobidae; Zeldia.

1 (bases 1 to 741)

McCarter, J., Clifton, S., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

The Washington Univ. Nematode EST Project, 1999

Unpublished (1999)

Contact: McCart.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTCATAATCGACTTTTAGCTTCTGTGCA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTGATCATCCCAAACTCGGGGCATTGCGTAATGCTTGAGAGTCCAAGTGAGGTTAATAG
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The Washington Univ. Nematode EST Project, Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                          AW773365 741 bp mRNA rp03h07.y1 Kloek Brook Zeldia Similar to WP:K07C5.5 CE06115
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//note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
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1. .445
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/dev_stage="adult"
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   Louis, MO 63108, USA
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602328533F1 NIH_MGC_91 Homo sapiens cDNA
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                                               Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                              Unpublished (1999)
Contact: Robert Strausberg,
                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                                        Mammalia; Eutheria; Primates; Catarrhini; 1 (bases 1 to 820)
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                                                                                              (301) 496-1550
Library Preparation: Life Technologies, Inc. Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      were non-directionally cloned into pcrii-1000 (Invitrogen) following the Topo TA cloning protocol. The cDNA insert can be excised by digestion with EcoRI. This library was constructed by Merry Brook and Dr. Andrew Kloek at Divergence LLC. The strain PDL3 used in this work was provided by the Caenorhabilitis Genetics Center at the University of Minnesota. The Caenorhabilitis Genetics Center at the University of Minnesota.
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/dev_stage="Mixed"
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Pred. No. 0.076;
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clone IMAGE:4429737
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http://image.llnl.gov
Plate: LLCM1156 row: g column: 04
High quality sequence stop: 750.
                                                                                                                                                                           Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 855)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   602184812F1 NIH_MGC_43 Homo sapiens cDNA
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                                                                  found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                         CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.G.E. Consortium (LLN DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information
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Clone distribution: MGC clone distribution information can
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/lab_host="DHIOB (phage resistant)"
/note="Organ: prostate; Vector: pcMv-SpORT6; Site_1: Not Site_2: Sall; Cloned unidirectionally; oligo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
a 217 c 205 g 182 t 1 others
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/clone="IMAGE:4429737"
/clone_lib="NIH_MGC_91"
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Pred. No. 0.
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Best Local :
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                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10185 row: b column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
BG180158
BG180158.1 GI:12686861
                                                                                                                                                                                                                                                                             Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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602329749F1 NIH_MGC_91 Homo sapiens
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1 (bases 1 to 855)
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                                                                                    quality sequence start: 6 quality sequence stop: 717.
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/tissue_type="normal pigmented retinal epithelium"
/tissue_type="normal pigmented retinal epithelium"
/lab_nost="DulOB (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
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/db_xref="taxon:9606"
/clone="IMAGE:4299291"
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                              Location/Qualifiers
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Pred. No. 0.079
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/tissue_type="duodenal adenocarcinoma, cell line"

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SOURCE
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BF981465
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Best Local
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                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM10105 row: 1 column: 21
                                                                                                                                                                                                                                                                                                            Email: Robert_Strausberg@nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
BF981465
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                                                                                                          High quality sequence stop: 752.
Location/Qualifiers
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1 (bases 1 to 934)
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/clone_lib="NIH_MGC_91"
/tissue_type="ademocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pcMV-SpoRT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

a 240 c 202 g 185 t
/clone="IMAGE:4400420"
/clone_lib="NIH_MGC_88"
                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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48.4%;
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                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
High quality sequence stops: 219
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 562 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons, Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterst,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H96434 264 bp mRNA EST 25-NOV-19
yv92h09.rl Soares melanocyte 2NbHM Homo sapiens cDNA clone
IMAGE:250241 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rhe WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1995)
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314 286 1810
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/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
a 263 c 223 g 216 t
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a modified
                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:3867947"
/db_xref="taxon:9606"
/clone="IMAGE:250241"
                                                             /sex="Male"
                                                                                       /clone_lib="Soares melanocyte 2NbHM"
                                                                                                                                                                                                                  Location/Qualifiers
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Primates;
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Pred. No. 0.081
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                                                                                       Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g: Cross_match from Washington University Genome Center PHRAP suite.
                                                                                                                                                                                                                                                                     61801,
                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Lewin, H. A.
Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Ur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP230010A10G12 Soares normalized bovine clone BP230010A10G12 5', mRNA sequence.
FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACCCTCACTAAAG
                                                                                                                                                                                                                     Tel: 217 333 5998 Fax: 217 244 5617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COW
                                                                 Sequences submitted are vector
                                                                                                                                                                                                                                                                                                                                                                                                             Bovine ESTs
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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Pred. No. 0.074;
D; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu, L. and Larson
                                                                                                                                                                                                                                                                                              Dr., Urbana,
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Insert Length: 471 Std Error: 0.00 Plate: BP230010A10 row: G column: Seq primer: AGCGGATAACAATTTCACACAGGA

quality sequence stop:

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RESULT 15
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                                                                                                                                                                                 AL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)

Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster genome using these BACs. For further the Department of ABTON Mammoser in Pleater de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library and how to crafe individual BAC clanes the antire library or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 CCCACGCAGATCATCTGGGGGAAACAAGACCAGGTGCTCGATGTGTCCGGGGCAGACATG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGATGGAGAGGCCCAGGAAGACAGCCAAGCTCCTTGTCGACTTCTTGGCTTCTGTACA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1088)
                                                                                                                                    and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
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                                                                                                          found at http://bacpac.med.buffalo.edu/drosophila_bac.htm
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/organism="Drosophila
/db_xref="taxon:7227"
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/lab_host="DH10B"
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/db_xref="taxon:9913"
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Pred. No. 0.29;
0; Mismatches 86;
                          melanogaster"
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                                                                                                                              954 MTTWTAMAHTWTANAVTATANAKAHRGWWKTRVARAAYARTNNNTVTAAMKGGAAKWKGK 895
                                                                                                                                                           142 ATGATGTTGTTGTCGATAACAGAGGTCATGGCAGGTCCGATAAGCCACTTGGATACGAT 201
                             262 GAGAAATTTGTTCTCGTCGGACATTCATT 290
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                                                                                            TTCTACAGATTTGAGAACTTCATTTCAGATTTAGATGCGGTTGTTAGGGAGACTGGAGTG 261
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Pred. No. 0.55;
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2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

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5: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

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	atch cal Si 106; TCTTG tctcc	JLT 1 99-801-333-6557 SUBERAL INFORMATION: REPELCANT: GLUCKSMANN, M. Ale FITLE OF INVENTION: HUMAN BR FILE REFERENCE: 1600.1037-005 URRENT FILING DATE: 2001-03 PRIOR REPLICATION NUMBER: 01 ORIOR FILING DATE: 1999-08-10 PRIOR FILING DATE: 1998-08-10 PRIOR PPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR PILING DATE: 1998-08-10 PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR APPLICATION N	300 300 300 300 300 300 300 300 300 300 300
GCACTATTGCCCGTTA	imilarity ; Conserva GAAAATATCTT 	33-6557 Applicat NFORMATION: TI GLUCKSMANN, INVENTION: NU INVENTION: H FERENCE: 1600. II APPLICATION NU FILING DATE: PELICATION NUMB LING DATE: 199 PLICATION NUMB LING DATE: 199 FEGO ID NOS: FESTESEQ FOR 33-6557	
CGTTAGC tgtgtct AAACTCC aaactgt ATTCATT	5.5%; Sc milarity 50.5%; Pr Conservative 0; AAAATATCTTGGAGAAAATAG 	33-6557 Application US/0980 NFORMATION: T' GLUCKSMANN, M. Alexand INVENTION: NUCLEIC ACID INVENTION: HUMAN BRAIN TERENCE: 1600,1037-005 APPLICATION NUMBER: US/09 FILING DATE: 2001-03-13 FPLICATION NUMBER: 09/371, LING DATE: 1999-08-10 PLICATION NUMBER: 60/095, LING DATE: 1998-08-10 PLICATION NUMBER: 60/103, FING DATE: 1998-10-05 PLICATION NUMBER: 60/103, FING DATE: 1998-10-05 PLICATION NUMBER: 60/103, FREQ ID NOS: 8285 F SEQ ID NOS: 8285 F SEQ FOR WINDOWS VER 06557 MM: Homo sapiens 33-6557	101880 177276 343 628 1360 15223 45865 745443 13269 13769 13769 13769 13769 13769 13769 13769 13769 13769
DAAATC 19999c 3GGCA 1111 1111 1111 1111 1111	.5%; 5%; 2AAA	ion US/0980 M. Alexand CLEIC ACID UMAN BRAIN 037-005 MBER: US/09 2001-03-13 2201-03-13 9-08-10 9-08-10 ER: 60/095, 8-10-05 8-10-05 8-10-05 8-10-05 8-10-05 8-10-05 8-10-05 8-10-05 8-10-05	. ¿
AGTTGAGCT	ore 43.6; DB 5 ed. No. 0.0063; Mismatches 10 ACTGTCCAACACTGA 	1833 ra MOLECULES DERIVED LIBRARY /801,833 168 907 145 145	80 6 US-60-248-505-650 76 6 US-60-248-505-22 43 5 US-09-833-23-795 85 US-09-811-380-150 85 US-09-820-001-1 85 US-09-724-866A-4895 85 US-09-724-865A-1221 85 US-09-335-032-1221 85 US-09-335-032-1221 86 US-60-248-505-348 87 US-08-276-163D-6537 88 US-60-248-505-385 89 US-60-248-505-385 89 US-60-248-505-385 89 US-60-248-505-385 89 US-60-248-505-385 89 US-60-248-505-417 89 US-60-248-505-417 89 US-60-248-505-417 89 US-60-248-505-417 89 US-60-248-505-415 89 US-60-248-505-415 89 US-60-248-505-415 89 US-60-248-505-415 89 US-60-248-505-415 89 US-60-248-505-415 89 US-60-248-505-415 89 US-60-248-505-415 89 US-60-248-505-415 89 US-60-248-505-415 89 US-60-248-505-415
GAGCAGGAGGATAGAAAACTCAAAGCT 692	.; Length 2207; 4; Indels 0; Gaps 0; TTATCGTTGGAGAAGAGA 632	FROM A	Sequence 22, Appl Sequence 22, Appl Sequence 150, App Sequence 150, App Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1213, Appli Sequence 12213, A Sequence 344, Appl Sequence 345, App Sequence 6537, Ap Sequence 417, App Sequence 113, App

RESULT 2
US-60-248-505-354/c
; Sequence 354, Application
; GENERAL INFORMATION:

US/60248505

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                                                                                                                                                                                                                                                              ; FEATURE:
, NAME/KEY: misc_feature
; LOCATION: (1)...(150471)
; OTHER INFORMATION: n = A,T,C or G
US-60-248-505-148
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Db 120654 ATTGAATTATTTGCTTCATACACATCACTGAAAAATATATCTAGACAACCAAGATGTTTT 120595
                                                                           Db 120714 TCTTTTAGATATTGCAGTATGAAAATCTGTAATTAAATCTGTATTAGAACTGAATAATAA 120655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
ITITLE OF INVENTION: ISOLATE
ITITLE OF INVENTION: RECEPT
ITITLE OF INVENTION: PROTEINERINGE: C1000918
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; LCCATION: (1)...(55248)
; OTHER INFORMATION: n = A,T,C
US-60-248-505-354
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LENGTH: 55248
TYPE: DNA
ORGANISM: human
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TITLE OF INVENTION: ISOLATI
TITLE OF INVENTION: RECEF
TITLE OF INVENTION: PROTE
FILE REFERENCE: cl000918
                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 148
LENGTH: 150471
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.4%;
Best Local Similarity 53.2%;
Matches 74; Conservative
                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51943 TCCAATGAAAAGAAAGTTA 51925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52063 TCTTTTAGATATTGCAGTATGAAAATCTGTAATTAAAATCTGTATTAGAACTGAATAATAA 52004
                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127
                           67 ATTGTCTTTCACGGATGGACAGCAAATATGAATTTTTTGGAAAGAGCAAAGACGTTAT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 ATTGTCTTTGTTCACGGATGGACAGCAAATATGAATTTTTGGAAAGAGCAAAGACGTTAT 126
                                                                                                  TTTGCAGGCAGGAATATGA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTGAATTATTTGCTTCATACACATCACTGAAAAATATATCTAGACAACCAAGATGTTTT 51944
                                                                                                                                                             74;
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOLATED HUMAN G-PROTEIN COUPLED
RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
PROTEINS, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISOLATED HUMAN G-PROTEIN COUPLED RECEPTORS, NUCLEIC ACID MOLECULES PROTEINS, AND USES THEREOF
                                                                                                                                                                                4.4%;
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                                                                                                                                                         Score 35; DB 6; Pred. No. 6.5; 0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65; Indels
                                                                                                                                                         65; Indels
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                                                                                                                                                                                                 Length 150471;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-956-171C-227
; Sequence 227, Applicat
; GENERAL INFORMATION:
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Best Local Similarity
Matches 116; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ
                                                              4609 TTTCATTTGTCGTTGGAGAATCAGATGATCCAATGAAACAAAAAGTATGTGACGTAGCAA 4668
                                                                                                                                                                                                                              4489 GTATTAGTGTCAATGAAGAGGTGGCACATGGGATTCCAAGTAAGCGTGTCATTCGTGAAG 4548
                                                                                                      143 TGATGTTGTCGATAACAGAGGTCATGGCAGGTCCGATAAGCCACTTGGATACGATT 202
203 TCTACAGATTTGAGAACTTCATTTCAGATTTAGATGCGGTTGTTAGGGAGACTGGAGTGG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 TTTGCAGGCAGGAATATGA 145
                                                                                                                                                                                      23 GTGTAAATATCTATTATGAACTGGTGGATGGACCTGAGCCACCAATTGTCTTTGTTCACG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/956,171C
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Charles Kunsch
                                                                                                                                               GAGATTTAGTAAATATTGATGTATCGGCTTTGAAGAATGGCTATTATGCAGATACAGGCA 4608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: HOOVET, KENLEY K. REGISTRATION NUMBER: 40,302 REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 6373 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (301)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: HP Vectra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08956171C
                                                                                                                                                                                                                                                                                                                  Conservative
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Patrick S. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steven C. Barash
                                                                                                                                                                                                                                                                                                                                   46.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309-8439
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Pred. No. 3.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          227:
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; FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(421)

OTHER INFORMATION: n =

US-09-737-223-36120
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TITLE OF INVENTION: KOOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT FILING DATE: 2000-12-13
CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 09/332,782
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTESQ for Windows Version 3.0
SEQ ID NO 36120
                                                                                                                                           NUMBER OF SEQ ID NOS: 67551
SOFTWARE: PERL Program .
SEQ ID NO 35143
NAME/KEY: misc_feature --
OTHER INFORMATION: Incyte ID No: hu00411539
-09-540-212A-35143
                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 35143, Application US/09540212A
                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/540,212A CURRENT FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                  TITLE OF INVENTION: POLYNUCLEOTIDES OF AIRWAY AND LUNG SYSTEM TISSUE FILE REFERENCE: PD-1034 CIP
                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Seilhamer, Jeffrey J. APPLICANT: Delegeane, Angelo M.
                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                  LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                              ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4729 GTAAAGCGGTGC 4740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    607 ACACTGATTATCGTTGGAGAAGAGGATGCACTATTGCCCCGTTAGCAAATCAGTTGAGCTG 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 atggaaagacccaggaagacagccaagctcataatcgactttttagcttctgtgca 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  727 CTTGAGAGTCCAAGTGAGGTTAATAGAGCAATGGACGAATTCATTTCTTCAGCACA 782
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Local Similarity 49.4%;
les 87; Conserva+1...
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                                                                                                                                                                                                                                                                                       Naughton,
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                                                                                                                                                                                                                                                                                                                                Stuve, Laura L
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                                                                                                                                                                                                                                                                                         Rebecca E.
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Pred. No. 2.8;
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                                                                                                                                                                                                                                                            US-09-820-001-3
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US-09-783-514-1810/c
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Best Local S
Matches 57
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Best Local S
Matches 57
                                                                                                                                                        Sequence 3, Application US/09820001
GENERAL INFORMATION:
APPLICANT: MERKULOV, Gennady et al
TITLE OF INVENTION: ISOLATED HUMAN LIPASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN LIPASE PROTEINS,
                CURRENT APPLICATION NUMBER: US/09/820,001
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1810
LENGTH: 2339
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APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Dougla
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                                                                                                                TITLE OF INVENTION: ISOLITITLE OF INVENTION: ACII
TITLE OF INVENTION: THE
TITLE REFERENCE: CL001186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 2346
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/783,514
CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 09/315,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/132,067 PRIOR FILING DATE: 1999-04-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (1)...(2339)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                               2152
                                                                                                                                                                                                                                                                                                                                                                                                                        2212 TAATGGGTGGGGAGCTGAGCAATGATGTCATCCAGAGGCCGTTCTACTGCCACGAGTG 2153
                                                                                                                                                                                                                                                                                                                                                                                 413 TTCTTGCATCCATTGCATACAAGAAGTCTTCAAGATT 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                353 TCATAGGTGGTGGGAGCAGAATAAAGCTTCTACACAGAATTGGATATCCTTTAGCAAAGA 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 TTCTTTCATCCAAAAGATCCATGAAGAGTAGAGGCTT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413 TTCTTGCATCCATTGCATACAAGAAGTCTTCAAGATT 449
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mes 57; Conserv
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22067
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57; Conserv
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Pred. No.
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Pred. No. 7;
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د.
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-849B-132899
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                                                                                                                                                                                                                                                                                               US-09-668-337-427/c
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LENGTH: 659
TYPE: DNA
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Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 195450
SOFTWARE: PACENTIN Ver. 2.0
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                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Insect genome survey devices
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Swimmer et al.
                                                            APPLICANT
                                                                                                           APPLICANT
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                                                                                           PPLICANT
                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                            247 CGTCCTTCACTCGGCCGTAATTGTGGAGAGACTATCGAG
                                                                                                                                                                                                                                                                                                                                                                                        457 GATCTTTCCTTTGGCAAAAATGCTGGTGAACTTAAAGAG 495
                                                                                                                                                                                                                                                                                                                                                                                                                          307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
mes 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                        TATGGCTCCTCAACTGGTGTTGCATACATGAAATTGATGATGTCAGGAAGATTTGACACA 248
                                                                                                                                      Banville, Steve C.
Bratcher, Shawn R.
Dufour, Gerard E.
Cohen, Howard J.
                                                                                                                                                                                                                                                 Hodgson, David M.
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                                                                         Hillman,
                                                                                                      Rosen, Bruce H.
Shah, Purvi
                                                                                                                                                                                                    Lincoln, Stephen E. Russo, Frank D. Spiro, Peter A.
                           Yu, Jimmy Y.
Greenawalt, Lila B.
              Panzer, Scott R.
                                                                                      Chalup, Michael S.
Roseberry,
                                                            Jones,
                                                                                                                                                                                                                                                                                 Application US/09668337
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                                                          Anissa L.
                                                                         Jennifer L.
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57.6%;
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 Mismatches

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Pred. No. 11
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Pred. No. 20;
0; Mismatches 31;
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                                      Query Match
Best Local S
Matches 73
                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5874
LENGTH: 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5874, Application US/09737223 GENERAL INFORMATION:
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SEQ ID NO 427
LENGTH: 404
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Best Local
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CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 09/332,782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT FILE REFERENCE: PT-0086 US CURRENT FILING DATE: 2000-09-22 PRIOR APPLICATION NUMBER: US/09/668,337 PRIOR APPLICATION NUMBER: 60/156,565 PRIOR APPLICATION NUMBER: 60/156,565 PRIOR APPLICATION NUMBER: 60/156,565 PRIOR PILING DATE: 1999-09-28 PRIOR PILING DATE: 1999-11-30 PRIOR FILING DATE: 1999-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
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                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
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                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (1)...(437)
OTHER INFORMATION: n = A,T,C
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NAME/KBY: misc_feature
OTHER INFORMATION: Incyte ID No: 958381.1.dec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 GATACCGCTCACCAGAGCACTGTGCCTTAGAAGG 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 AAATAGCTTGGTAGACATGAGCCGTGCAGCATTGAACACTGCAGGAGAAGAGCCACCAGT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    579 AAATATCTTGGAGAAAATAGACTGTCCAACACTGATTATCGTTGGAGAAGAGGATGCACT 638
76
                                      Local Similarity
les 73; Conserv
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les 55; Conserv
GTTCACGGATGGACAGCAAATATGAATTTTTGGAAAGAGCAAAGACGTTATTTTGCAGGC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hyseq, Inc
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                                        Conservative
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Pred. No. 11;
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Pred. No. 10;
0; Mismatches
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RESULT 13
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Stephens, J. Claiborne
TITLE OF INVENTION: Haplotypes of the MMP3 Gene
FILE REFERENCE: MWH-0525PCT MMP3
CURRENT APPLICATION NUMBER: PCT/US01/12452
CURRENT FILING DATE: 2001-04-17
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NUMBER OF SEQ ID NOS: 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (5693)..(5695)
OTHER INFORMATION: Nucleotide identity unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Nucleotide identity unknown NAME/KEY: allele LOCATION: (5688)
OTHER INFORMATION: Nucleotide identity unknown
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LOCATION: (5693).
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LOCATION: (5677)
OTHER INFORMATION:
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                                                                                                                                                                                                                                            4987
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LOCATION: (5682)
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                                                                                5107 ttgagaaagctctgaaagtctg 5128
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Choi, Julie Y.
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                                                                                                                                                                                                                                                                                                                      Conservative
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51.4%;
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Pred. No. 31;
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 114
LENGTH: 15506
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TITLE OF INVENTION: Haplotypes of the MMP3 Gene
FILE REFERENCE: MWH-0525PCT MMP3
CURRENT APPLICATION NUMBER: PCT/US01/12452
CURRENT FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 60/197,911
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LOCATION: (5680)
OTHER INFORMATION:
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LOCATION: (4692)
OTHER INFORMATION:
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LOCATION: (4590)
OTHER INFORMATION:
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LOCATION: (3693)
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: (5682)
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OTHER INFORMATION:
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LOCATION: (4173)
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LOCATION: (3738)
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LOCATION: (4920)
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LOCATION: (4902)
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LOCATION: (4747)
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LOCATION: (3650)
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LOCATION: (4863
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                                                                                       Nucleotide identity unknown
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OTHER INFORMATION:

PS11: Polymorphic base G

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                                                                                                                    APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF AIRWAY AND
FILE REFERENCE: PD-1034 CIP
                                                                                                                                                                                       APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Sture, Laura L.
                                                NUMBER OF SEQ ID NOS: 67551
SOFTWARE: PERL Program
                                                                                   CURRENT APPLICATION NUMBER: US/09/540,212A
                                                                                                                                                                        APPLICANT:
TYPE: DNA
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LOCATION: (10449
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OTHER INFORMATION:
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LOCATION: (8622)
OTHER INFORMATION:
                2 ID NO 64789
CENGTH: 261
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LOCATION: (10203)
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LOCATION: (7599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 51.4 les 73; Conservative
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Pred. No. 3:
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US-08-956-171C-709/c
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; LOCATION: 112, 178, 183-184
; OTHER INFORMATION: a, t, c,
US-09-540-212A-64789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 709, Application US/08956171C GENERAL INFORMATION:
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                                                        INFORMATION FOR SEQ ID NO: 709
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 TGGAAAAGTATGAAACCCTCAACCTCCGTGAACACGCAAAACTGTTCACACCTTTCNGTC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                667 AGCAGGAGGATAGAAAACTCAAAGCTTGTGATCATCCCAAACTCGGGGCATTGCGTAATG 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 AGACAAAATATGGCTGCTGTAGAAAGTGTACATTTCCCCTTCCCNNTACANAATAATCTG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                607 ACACTGATTATCGTTGGAGAAGAGGATGCACTATTGCCCGTTAGCAAATCAGTTGAGCTG 666
                                                                                                                                                                            APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: HOOVET, Kenley K.
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     727 CTTGAGAGTCCAAGTG 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 50.7 los 69; Conservative
                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171C
FILING DATE: 20-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
                                                                                                                                    REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Michael R. Fannon TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5255
                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Maryland
STRANDEDNESS: double
                                                                                                  TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                   ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craig A. Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patrick S. Dillon
                                                                                                (301)
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                                                                                                                     (301) 610-5790
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Pred. No. 12;
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Search Job ti	Qу	Оy	ф	; US-08. Quer Best
Search completed: June 3, 2001, 01:00:27 Job time: 17046 sec	536 TGGCAATGGACACGTACAGAACTCTAACGAAAGTGAATCTTGAAAATATCTTGGAGAAAA 595 	476 ATGCTGGTGAACTTAAAGAGTGGGGATGGAAACAGGCAATGGATTATACACCCTCCTACG 535	416 TTGCATCCATTGCATACAAGAAGTCTTCAAGATTGGTCGCAGATCTTTCCTTTGGCAAAA 475 	; SEQUENCE DESCRIPTION: SEQ ID NO: 709: US-08-956-171C-709 Query Match Query Match 4.0%; Score 31.2; DB 4; Length 1448; Best Local Similarity 48.3%; Pred. No. 20; Matches 87; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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US-09-489-039A-2616	US-09-565-309A-39169	US-08-466-194-14	-09-382-242-	US-09-515-694-9776	-09-332-782-977	-09-465-877-	-09-340-623-	US-09-205-070-5677	09-699-997-	-09-698-013-	-09-652-911	-09-644-873	-09-644-870-	52	-164	US-09-644-873-8602	US-09-644-870-8818	-09-371-168	US-09-354-899-7328	US-09-770-155-82	US-09-419-553-82	US-60-233-468-1454	-176-	-60-185-213-1	S	-09-434-6	09-800-729-73	US-09-488-725A-1276	-09-488-725A-469	-09-471-275-1062	US-09-488-725A-4848	-09-471-275-	-09-461-325-9	-US99-13418-9	-09-644-870-57	S-09-528-409	-00-608-013	115-60-137-490-350	V - 906 - 553 - 00 -	US-60-166-560-3775	E-60-160-403-771	-09-684-016-133	S-09-654-617-13335	IIS-09-382-242-25	ID
Sequence 2616, Ap	e 391	14,				12347,	5677,	5677,	9186,	Sequence 6781, Ap	equence	10937,	10302,	8749,	8371,	8602,	8818,	6557, A	7328, A		82, A	1454,	1454,	1453, A	1123	N	73,	1276,	4695,	1062, A	4848, A	1531	e 91	Sequence 91, Appl	5756	Sequence 43340. A	7007	35007	14607				0 (Sequence 25, Appl	ription

US-09-382-242-25
; Sequence 25, Application US/09382242
; GENERAL INFORMATION:

ROBERTSON, Daniel E.

Dennis

APPLICANT: APPLICANT: RESULT

ALIGNMENTS

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                                                                                                                                                                                                                                                 Query Match 100.0%; Score 789; DB 17; Best Local Similarity 100.0%; Pred. No. 2e-219; Matches 789; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 619-678-507
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/602,3
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 789 NUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS-DOS
SOTTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/382,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 EXECUTIVE SQUARE, STE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WARREN, Patrick V. APPLICANT: KOSMOTKA, Anna TITLE OF INVENTION: ESTERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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              181 GATAAGCCACTTGGATACGATTTCTACAGATTTGAGAACTTCATTTCAGATTTAGATGCG 240
                                                             121
                                                                                          121
181 GATAAGCCACTTGGATACGATTTCTACAGATTTGAGAACTTCATTTCAGATTTAGATGCG
                                                                                                                           61
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TOPOLOGY: LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: LA JOLLA
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                     CGTTATTTTGCAGGCAGGAATATGATGTTGTTGTTGTCGATAACAGAGGTCATGGCAGGTCC 180
                                                                                                                    CCACCAATIGTCTTTGTTCACGGATGGACAGCAAATAIGAATTTTTGGAAAGAGCAAAGA 120
                                                                                                                                                                                    NUCLEIC ACID
DEDNESS: SINGLE
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REID, John
MAFFIA, Ant
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                                                                                                                                                                                                                                                                              Length 789;
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240
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623 GAGAAGAGGATGCACTATTGCCCGTTAGCAAATCAGTTGAGCTGAGCAGGAGGATAGAAA 682

GAGCCGAAGACGCACTTGTTCCCCTCAAGTCCTCCCAAGTCATGGCTTCAAAACTCGAAA

502

683 ACTCAAAGCTTGTGATCATCCCAAACTCGGGGCATTGCGTAATGCTTGAGAGTCCAAGTG 742

	622 562	CGAAAGTGAATCTTGAAAATATCTTGGAGAAAATAGACTGTCCAACACTGATTATCGTTG 	AACACT	ACTGTCCA	GAAAGTGAATCTTGAAAATATCTTGGAGAAAATAGACTG 	ATATCTT !TTCTCAA	TTGAAA GTCACC	GAATC:	CGAAAGT	563 621	Дy
0	sdt	rth 706; ls 0; Ga	Length Indels	DB 25; 038; % 102;	Score 44.8; I Pred. No. 0.03); Mismatches	5.7%; S 51.0%; P tive 0;	vai	larit; Conse	itch sal Similarity 106; Conser	ery Match st Local tches 10	Que Bes Mat
				ns	l n locatio	chaliana ure at all	is t	bidop: TION: 353	TYPE: DNA ORGANISM: Arabidops ORGANISM: Arabidops OTHER INFORMATION: 19-654-617-133353	TYPE: ORGANI OTHER 9-654-	S-C
					73	10-09-05 4631	: 200 S:	DATE ID NO.	CURRENT FILING DATE: 05/09/05/ CURRENT FILING DATE: 2000-09-05/ NUMBER OF SEQ ID NOS: 463173 SEQ ID NO 133353	CORRENT FOURBER OF EQ ID NO CORRENT FOURBER OF EQ ID NO CORRENT FOURBER OF EACH OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE OF THE EXAMPLE O	S Z C C
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						David	valic,	TION:	INFORMA'	NERAL PPLICA	 B & &
		·			9654617	on us/0	licati	353/c	617-133 133353	LT 2 9-654- quence	RESULT US-09- ; Sequ
							v	AA 789	CAGTTCTAA	781	B
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	780	GTAATGCTTGAGAGTCCAAGTGAGGTTAATAGAGCAATGGACGAATTCATTTCTTCAGCA	AATTCA	ATGGACG	TTAATAGAGCA	AGTGAGG	AGTCCA	TTGAG	GTAATGC	721	B 2
										2 2	} {
	720	GAGCTGAGCAGGAGGATAGAAAACTCAAAGCTTGTGATCATCCCAAACTCGGGGCATTGC	CAAACT	ATCATCO	CAAAGCTTGTG	GAAAACT	AGGATA	GCAGG!	GAGCTGA	61	\$ 5
	660	TGTCCAACACTGATTATCGTTGGAGAAGAGGATGCACTATTGCCCGTTAGCAAATCAGTT 	CCGTTA	CTATTGC	AAGAGGATGCA AAGAGGATGCA	GTTGGAG	ATTATC	CACTG	TGTCCAA	601	PP QV
	600	ATGGACACGTACAGAACTCTAACGAAAGTGAATCTTGAAAATATCTTGGAGAAAATAGAC 	rcttee 	GAAAATA GAAAATA	AAGTGAATCTT AAGTGAATCTT	CTAACGA CTAACGA	AGAACT AGAACT	CGTACA	ATGGACA	541 541	Дy
	540 540	GGTGAACTTAAAGAGTGGGGATGGAAACAGGCAATGGATTATACACCCTCCTACGTGGCA 	CACCCT	GATTATA GATTATA	GGTGAACTTAAAGAGTGGGGATGGAAACAGGCAATGGATTATACACCCTCCTACGTGGC 	GGATGGA GGATGGA	SAGTGG SAGTGG	TTAAAC HILLI TTAAAC	GGTGAAC: GGTGAAC:	481 481	Db VQ
	480	TCATTGCATACAAGAAGTCTTCAAGATTGGTCGCAGATCTTTCCTTTGGCAAAAATGCT	CTTTG	GATCTTT	GATTGGTCGCA	TCTTCAA	\AGAAG	CATACA	TCCATTG		Db
	480	GCAAAAATGCT	CTTTG	GATCTTT	GATTGGTCGCA	TCTTCAA	AGAAG	CATAC	TCCATTG	421	Qy
	420 420	GGTGGGAGCAGAATAAAGCTTCTACACAGAATTGGATATCCTTTAGCAAAGATTCTTGCA 	TAGCAA TAGCAA	TATCCTT	ACAGAATTGGA ACAGAATTGGA	CTTCTAC	YTAAAG YTAAAG	GCAGA	GGTGGGA	361 361	Qy Qy
	360 360	ATCTCTATGAAGTACTGTTCGGAGTATCGGGAATCGGGTTCTTGCTCTAATCCTCATAGGT	TCTAA	GTTCTTG	ATCGGAATCGG ATCGGAATCGG	TCGGAGT.	PACTGT	rgaags rgaags	ATCTCTA: ATCTCTA:	301	Фу Ф
	300	GTTGTTAGGGAGACTGGAGTGGAGAAATTTGTTCTCGGTCGG	ATTCAT	GTCGGAC GTCGGAC	AATTTGTTCTC AATTTGTTCTC	GTGGAGA.	ACTGGA ACTGGA	GGAGA GGAGA	GTTGTTA(241	Дy

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441 CACTTCTTGCAGCCATGTGCCCCATTCAT 414

AGGTTAATAGAGCAATGGACGAATTCAT 770

ACTCTAGGCTAGTAGCAATCTCAGGATGCGGACATCTGCCACATGAGGAGTGTCCCAAGG 442

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CURRENT APPLICATION NUMBER: US/09/684,016
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US/09/654,61
PRIOR APPLICATION NUMBER: 2000-09-05
NUMBER OF SEQ ID NOS: 463173
SEQ ID NO 13353
LENGTH: 706
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, NAME/KEY: unsure
; LOCATION: (1)..(706)
; OTHER INFORMATION: unsure at all n locations
US-09-684-016-133353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-684-016-133353/c
; Sequence 133353, Application US/09684016
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                                                                                                    CURRENT APPLICATION NUMBER: US/60/169,403
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 3,249
SOFTWARE: PERL Program
SEQ ID NO 771
LENGTH: 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.7%;
Best Local Similarity 51.0%;
                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     Sequence 771, Application US/60169403
FEATURE: -
OTHER INFORMATION: 702212773H1
-60-169-403-771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kovalic, APPLICANT: Liu, Jingdong TITLE OF INVENTION:
                                                                                                                                                                                                                                 APPLICANT: Kleefeld, Yael
APPLICANT: Mullahy, Sara J.
APPLICANT: Goralski, Thomas J.
TITLE OF INVENTION: Polynucleotides and Polypeptides Derived from Rat Lung
FILE REFERENCE: PZ-0152 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                     TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    561 GAGCCGAAGACGCACTTGTTCCCCTCAAGTCCTCCCAAGTCATGGCTTCAAAACTCGAAA 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           621 CARARATGCATTGTCACCTTCTCAAGGCGGTGGAAAACTTACCAGTATTAGTCGTTGCTG 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 563 CGAAAGTGAATCTTGAAAATATCTTGGAGAAAATAGACTGTCCAACACTGATTATCGTTG 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            623 GAGAAGAGGATGCACTATTGCCCGTTAGCAAATCAGTTGAGCTGAGCAGGAGGATAGAAA 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 441 CACTTCTTGCAGCCATGTGCCCATTCAT 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTCTAGGCTAGTAGCAATCTCAGGATGCGGACATCTGCCACATGAGGAGTGTCCCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTCAAAGCTTGTGATCATCCCAAACTCGGGGCATTGCGTAATGCTTGAGAGTCCAAGTG 742
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US-09-166-560-3775
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EARLIER FILING DATE: 98-04-06
NUMBER OF SEQ ID NOS: 3904
SOFTWARE: PERL Program
SEQ ID NO 3775
LENGTH: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      Matches 119;
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3775, Application US/09166560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GATROW, BONDIE L.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM RAT
TITLE OF INVENTION: HYPOTHALAMUS
FILE REFERENCE: PZ-0033 US
CURRENT APPLICATION NUMBER: US/09/166,560
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: 60/061,478
EARLIER FILING DATE: 97-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Stuve, Laura L. APPLICANT: Mullahy, Sara J. APPLICANT: Garrow, Bonnie L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: -
197 atgttttggactccttggggtataacaaatgtgtcctgattggccatgactggggaggca
                                                239
                                                                                                                                                                                                   119 GACGTTATTTTGCAGGCAGGAATATGATGTTTGTTGTCGATAACAGAGGTCATGGCAGGT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 cctgattggccatgactggggaggcatgat 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 ggactgtctaattgcagacataaaggatgttttggactccttggggtataacaaatgtgt 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 TGAGAACTTCATTTCAGATTTAGATGCGGTTGTTAGGGAGACTGGAGTGGAGAATTTGT 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 actggatttgaggggttacggagagtccgatgcacctattcatcaagagagttacaagct 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 TGTCGATAACAGAGGTCATGGCAGGTCCGATAAGCCACTTGGATACGATTTCTACAGATT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 attctggtattcttggcgtcaccaactgagagaatttaaaagtgaatacagagtcgttgc 183
                                                                                                                                                                             77
                                                                                                                                                                                                                                                             17 aacccctcatgctgcttcatggatttccagaattctggtattcttggcgtcaccaac 76
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 ctatgttgctgctggagagaggggcaaacccctcatgctgctgcttcatggatttccaga 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 CTATTATGAACTGGTGGATGGACCTGAGCCACCAATTGTCTTTGTTCACGGATGGACAGC 92
                                                                                                                                                                                                                                                                                                        59 AGCCACCAATTGTCTTTGTTCACGGATGGACAGCAAATATGAATTTTTGGAAAGAGCAAA 118
                               CCGATAAGCCACTTGGATACGATTTCTACAGATTTGAGAACTTCATTTCAGATTTAGATG 238
                                                                                    ccgatgcacctattcatcaagagagttacaagctggactgtctaattgcagacataaagg 196
                                                                                                                                                                         tgagagaatttaaaagtgaatacagagtcgttgcactggatttgaggggttacggagagt 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                    5.6%;
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                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 15; Length 271; Pred. No. 0.045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44.4; DB 48;
Pred. No. 0.047;
0; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                    Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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Sequence 359, Application US/60137499

Sequence 359, Application US/60137499

GENERAL INFORMATION:
APPLICANT: Mullaby, Sara, J.
APPLICANT: Mullaby, Sara, J.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM RAT LIVER FILE REFERENCE: PZ-0123 P.
CURRENT APPLICATION NUMBER: US/60/137,499

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 1430

SOFTWARE: PERL Program

SEQ ID NO 359

LENGTH: 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: rat00061254
US-09-535-896-14607
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SEQ ID NO 14607
LENGTH: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/535,896
CURRENT FILING DATE: 2000-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNICLEOTIDES ENCODING OR REGULATING HYDROLASES
FILE REFERENCE: PD-1003 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 46268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 GACGTTATTTTGCAGGCAGGAATATGATGTTGTTGTTGTCGATAACAGAGGTCATGGCAGGT 178
                                                                                                                                                                                                                                                                                                                             257
                                                                                                                                                                                                                                                                                                                                                                                                 197 atgttttggactccttggggtataacaaatgtgtcctgattggccatgactggggaggca
                                                                                                                                                                                                                                                                                                                                                                                                                                       257
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DNA
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                                                                                                                                                                                                                                                                                                                                                               TGAT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ccgatgcacctattcatcaagagagttacaagctggactgtctaattgcagacataaagg 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGATAAGCCACTTGGATACGATTTCTACAGATTTGAGAACTTCATTTCAGATTTAGATG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tgagagaatttaaaagtgaatacagagtcgttgcactggatttgaggggttacggagagt 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aacccctcatgctgcttcatggatttccagaattctggtattcttggcgtcaccaac 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stuart, Susan G.
Stuve, Laura L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Delegeane, Angelo M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seilhamer, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No. 0.045;
0; Mismatches 125;
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).045;
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SOFTWARE: FASTSEQ for W. SEQ ID NO 5084
LENGTH: 458
TYPE: DNA
ORGANISM: Homo sapiens
US-09-698-013-5084
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                                                                                                                                                                                                                                                  Query Match 5.5%;
Best Local Similarity 50.5%;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5084, Application US/09698013
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
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Best Local Similarity 48.5
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 1600.2013-001
CURRENT APPLICATION NUMBER: US/09/698,013
CURRENT FILING DATE: 2000-10-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gearing, David P.
APPLICANT: Comrack, Christopher
APPLICANT: Kingsbury, Gillian A.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/:
PRIOR FILING DATE: 1999-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
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LOCATION: 29, 33, 277
OTHER INFORMATION: a or g or c or t, unknown, or other
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Rattus norvegicus
693 TGTGATCATCCCAAACTCGGGGCATTGCGTAATGCTTGAGAGTCCAAGTGAGGTTAATAG
                                                                                                                                                                                                      573 TCTTGAAAATATCTTGGAGAAAATAGACTGTCCAACACTGATTATCGTTGGAGAAGAGGA 632
                                                                 104 ccaggtgctggatgtgtctggggcagacatgttggccaagtcaattgccaactgccaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 a 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          662 AGCTGAGCAGGAGGATAGAAAACTCAAAGCTTGTGATCATCCCAAACTCGGGGCATTGCG 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   602 GTCCAACACTGATTATCGTTGGAGAAGAGGATGCACTATTGCCCCGTTAGCAAATCAGTTG 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            542 TGGACACGTACAGAACTCTAACGAAAGTGAATCTTGAAAATATCTTGGAGAAAATAGACT 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 tattagccaagtccatcactaactcccaggtagaggttctggaaaactgtggccattcag 194
                                                                                                                                                            44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 tcccaacacagatcatttggggaaaacaagaccaggtgcttgatgtgtcgggggcagaca 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 tggaaatcgtcagtnaganatccagatactctctgcatgagaacatggacaagatcaagg 74
                                                                                                             TGCACTATTGCCCGTTAGCAAATCAGTTGAGCTGAGCAGGAGGATAGAAAACTCAAAGCT 692
                                                                                                                                                       tctccatcagaacatggacaagatcaaggttccgacgcagatcatctgggggaaacaaga 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tggtgatggagagaccgaggaagacagccaagctcatcgtcgactttttagcttctgtgc 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.68;
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                                                                                                                                                                                                                                                                     Score 43.6; DB 27;
Pred. No. 0.072;
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Pred. No. 0.052;
0; Mismatches 124;
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                                                                                                                                                                                                                                                                                          Length 458;
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TYPE: DNA
ORGANISM: Homo sapiens
US-09-528-409-43340
                                                                                                                                                                                                                                                                                                     US-09-644-870-5756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-528-409-43340
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                                                                                                                                                                                                                                                        Sequence 5756, Application US/09644870 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                   APPLICANT: Holtzman, Douglas A.
APPLICANT: Curtis, Rory A.J.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: THEREFOR FILE REFERENCE: 1600.1172-001
CURRENT APPLICATION NUMBER: US/09/644,870
CURRENT APPLICATION NUMBER: 05/150,752
PRIOR APPLICATION NUMBER: 60/150,752
PRIOR FILING DATE: 1999-08-26
PRIOR FILING DATE: 1999-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1:
NUMBER OF SEQ ID NOS:
SOFTWARE: Hy-patent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/528,409
CURRENT FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/125,453
PRIOR FILING DATE: 1999-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Novel Nucleic Acid Sequences
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APPLICANT:
                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
NUMBER OF SEQ ID NOS: 10434
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 actggatttgagaggttatggagaaacagatgctcccattcatcgacagaattataaatt 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 attctggtattcttggcgttaccaactgagagaatttaaaagtgaatatcgagttgtagc 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 ggattgtctaattacagatataaaggatattttagattctttagggtatagcaaatgtgt 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 TGTCGATAACAGAGGTCATGGCAGGTCCGATAAGCCACTTGGATACGATTTCTACAGATT 212
                                                                                                                                                                                                                                                                                                                                                                                      293 tcttattggccatgactgggggggcatgattgct 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 5.5%;
Local Similarity 47.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCAATGGACGAATTCATTTCTTCAGCACA 782
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                                                                                                                                                                                                                                                                                                                                                                                                                                TCTCGTCGGACATTCATTCGGAACAATGATCTCT 306
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Jones, Lee W.
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Stache-Crain, Birgit
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                                                                                                                                                                                                                                  DiStefano, Peter
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-644-870-5756
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EARLIER FILING DATE: 1998-06-16
EARLIER FILING DATE: 1998-06-16
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/090,112
EARLIER APPLICATION NUMBER: 60/090,112
EARLIER FILING DATE: 1998-06-22
EARLIER FILING DATE: 1998-06-22
EARLIER FILING DATE: 1998-06-22
RUMBER OF SEQ ID NOS: 502
RUMBER:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US99-13418-91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US99-13418-91
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LENGTH: 517
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Best Local Similarity 50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 130; Conserv
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EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/089,507
EARLIER FILING DATE: 1998-06-16
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CURRENT FILING DATE: 1999-06-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Human Genome Sciences, Inc
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448 actggatttgagaggttatggagaaacagatgctcccattcatcgacagaattataaatt 507
                                                                            153
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                                                                                                                                                388 attctggtattcttggcgttaccaactgagagaatttaaaaagtgaatatcgagttgtagc 447
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                                        TGTCGATAACAGAGGTCATGGCAGGTCCGATAAGCCACTTGGATACGATTTCTACAGATT 212
                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.5%;
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Pred. No. 0.11;
0; Mismatches 144; Indels 0
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RESULT 13
US-09-471-275-1531
Sequence 1531, Application US/09471275
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-461-325-91
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EARLIER APPLICATION NUMBER: 60/089,507
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EARLIER APPLICATION NUMBER: 60/089,508
EARLIER APPLICATION NUMBER: 60/089,508
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/089,509
EARLIER FILING DATE: 1998-06-16
EARLIER FILING DATE: 1998-06-16
EARLIER APPLICATION NUMBER: 60/090,112
EARLIER APPLICATION NUMBER: 60/090,112
EARLIER APPLICATION NUMBER: 60/090,112
EARLIER APPLICATION NUMBER: 60/090,113
EARLIER APPLICATION NUMBER: 60/090,113
EARLIER APPLICATION NUMBER: 60/090,113
EARLIER FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: 60/090,113
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Best Local :
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LENGTH: 1316
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APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Contigs Obtained
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: P2029P1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     93
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les 130; Conserv
                                                                                                                                                                                                                                                                                                                                                   TGTCGATAACAGAGGTCATGGCAGGTCCGATAAGCCACTTGGATACGATTTCTACAGATT 212
                                                                                                                                                                                    TCTCGTCGGACATTCATTCGGAACAATGATCTCT
                                                                                                                                                                                                                                            ggattgtctaattacagatataaaggatattttagattctttagggtatagcaaatgtgt
                                                                                                                                                                                                                                                                   TGAGAACTTCATTTCAGATTTTAGATGCGGTTGTTAGGGAAGACTGGAGTGGAGAAATTTGT 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tcttattggccatgactgggggggcatgattgct 601
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Pred. No. 0.11;
0; Mismatches 144;
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Best Local Similarity
Matches 130; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: pt_CT_genes Version 1.0
SEQ ID NO 1531
LENGTH: 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: US 09/404,284 EARLIER FILING DATE: 1999-09-21 EARLIER APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/471,275
CURRENT FILING DATE: 1999-12-23
EARLIER APPLICATION NUMBER: US 09/235,076
EARLIER FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (134)...(1129)
OTHER INFORMATION: similar to gi3878325 in the genepept database
OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: US 09/234,611 EARLIER FILING DATE: 1999-01-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: HOMO FEATURE:
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      540
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                                         273 TCTCGTCGGACATTCATTCGGAACAATGATCTCT 306
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                                                                                                                                                                                                                                              360 attctggtattcttggcgttaccaactgagagaatttaaaaagtgaatatcgagttgtagc 419
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                                                                                                                                                                                        TGTCGATAACAGAGGTCATGGCAGGTCCGATAAGGCCACTTGGATACGATTTTCTACAGATT
tcttattggccatgactgggggggcatgattgct 573
                                                                                  ggattgtctaattacagatataaaggatattttagattctttagggtatagcaaatgtgt
                                                                                                                        TGAGAACTTCATTTCAGATTTAGATGCGGTTGTTAGGGAGACTGGAGTGGAGAAATTTGT
                                                                                                                                                             actggatttgagaggttatggagaaacagatgctcccattcatcgacagaattataaatt
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 09/306,350
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1999-09-21
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47.4%;
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RESULT 14
US-09-488-725A-4848
; Sequence 4848, Application
; GENERAL INFORMATION:

US/09488725A

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; SOFTWARE: pt_FL_genes_b (SEQ ID NO 4848); LENGTH: 1467; LENGTH: DNA; TYPE: DNA; ORGANISM: Homo sapiens US-09-488-725A-4848
                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-471-275-1062
; Sequence 1062, Applic
; GENERAL INFORMATION:
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EARLIER APPLICATION NUMBER: US 09/235,076
EARLIER FILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: US 09/234,611
EARLIER FILING DATE: 1999-01-22
EARLIER APPLICATION NUMBER: US 09/240,371
EARLIER FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: US 09/277,227
EARLIER FILING DATE: 1999-03-25
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Best Local Similarity
Matches 130; Conserv
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TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 782
                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/471,275
CURRENT FILING DATE: 1999-12-23
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PRIOR APPLICATION NUMBER: US09/552,317
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CURRENT FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US09/620,312 FILING DATE: 2000-07-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTCGATAACAGAGGTCATGGCAGGTCCGATAAGCCACTTGGATACGATTTCTACAGATT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggattgtctaattacagatataaaggatattttagattctttagggtatagcaaatgtgt 539
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0; Mismatches
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Pred. No. 0.11;
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; NAME/KEY: misc_feature; LOCATION: (293)...(1072); COTHER INFORMATION: similar to gi747876 in the genepept database release 114, corner information: Run with FASTXY 3.3t00, default parameters US-09-471-275-1062
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SEQ ID NO 1062
LENGTH: 1499
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              Matches 106;
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EARLIER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                        1012
                                                                                                                                                                           952
                                                                                                                               693 TGTGATCATCCCAAACTCGGGGCATTGCGTAATGCTTGAGAGTCCAAGTGAGGTTAATAG 752
                                                                                                                                                                                                                 633 TGCACTATTGCCCGTTAGCAAATCAGTTGAGCTGAGCAGGAGGATAGAAAACTCAAAGCT 692
                                                                                                                                                                                                                                                        892 totocatcagaacatggacaagatcaaggttccgacgcagatcatctgggggaaacaaga 951
                                                                                                                                                                                                                                                                                                  573 TCTTGAAAATATCTTGGAGAAAATAGACTGTCCAACACTGATTATCGTTGGAGAAGAGGA 632
                                            753 AGCAATGGACGAATTCATTCTTCAGCACA 782
gctcataatcgactttttagcttctgtgca 1101
                                                                                     ggagcttctggaaaactgtgggcactcagtagtgatggaaagacccaggaagacagccaa
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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                         MURPHY, L.
THID, John
Ant
LINK, Steven SWANSON, Ronald
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                     MAFFIA,
                                                        ROBERTSON, Daniel
                                                                                                                                                    789
                      Anthony
                                             Dennis
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100.0%; Pred. No. 8e-245;
tive 0; Mismatches 0;
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US-08-232-463-14/c
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Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 619-678-5099 INFORMATION FOR SEQ ID NO:
SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,46
                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                                   APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER,
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 53 NUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
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NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
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TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
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APPLICANT: KOSMOTKA, Anna
                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1800 Diag
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SOFTWARE: WORD PERFECT 6.0
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STATE: CALIFORI
                                                                                                            ZIP:
                                                                                                                                           STATE:
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les 42; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                       COUNTRY:
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22313-0299
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97.7%;
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 US/08/232,463
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Pred. No. 0.00019;
0; Mismatches 1
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FILING DATE: CLASSIFICATION:

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                            quence 7, Applic
tent No. 5942430
                                                                                                                                     APPLICANT:
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IMMEDIATE SOURCE:
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                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION:
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                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                               APPLICANT:
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APPLICATION NUMBER: US/07/935,313
                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                  706 AACTCGGGGCATTGCGTAATGCTTGAGAGTCCAAGTGAGGTTAATAGAGCAATGGACGAA 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                              646 GTTAGCAAATCAGTTGAGCTGAGCAGGAGGATAGAAAACTCAAAGCTTGTGATCATCCCA 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    526 CCCTCCTACGTGGCAATGGACACGTACAGAACTCTAACGAAAGTGAAATCTTGAAAAATATC 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 466 TTTGGCAAAAATGCTGGTGAACTTAAAGAGTGGGGATGGAAACAGGCAATGGATTATACA 525
                         CITY: LA JOLLA
STATE: CALIFORNIA
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nes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                         ADDRESSEE:
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92037
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                                                                                                      WAKNELL
KOSMOTKA, Anna
KOSMOTKA, Anna
KOSMOTKA, Anna
                                                           4225 EXECUTIVE SQUARE, STE 1400
                                                                                                                                                                                                       MURPHY, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (703)683-4109
                                                                                                                                                   SWANSON, Ronald V. WARREN, Patrick V.
                                                                                                                                                                                                  MAFFIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conservative
                                                                                                                                                                                                                                               ROBERTSON, Daniel E
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                                                                        FISH & RICHARDSON P.C
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                                                                                                                                                                                   Steven
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                                                                                                                                                                                               Anthony
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RESULT 5
US-08-605-150A-11
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Best Local
                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,150,
FILING DATE: 01-MAR-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                              FILING DATE: 02-SEP-PRIOR APPLICATION NUMBER: 1
                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT\
FILING DATE: 02-SEP-1994
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 49 NUCLEOTIDES
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
              FILING DATE: 03-SEP-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Klein & Szekeres
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MOLECULE TYPE:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: 3.5 INCH DISKETTE
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NAME: HAILE, LISA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 92715
                                                                                                                                                                                                                                                                                                                            CITY: Irvine
STATE: CA
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les 38; Conserv
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SOFTWARE: WORD PERFECT 6.0
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Szekeres,
                                                                                                                                                                                                                                                                                                                                                             4199 Campus Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hausmann, Ludger
Schell, Jozef
                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                        Floppy disk
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N: 435
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97.48;
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                                                DE P4329827.3
                                                                                                 PCT\EP94\02936
                                                                                                                                                                                                      Release #1.0, Version
                                                                                                                                                                       US/08/605,150A
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Pred. No. 0
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Gaps

REGISTRATION NUMBER: 28
REFERENCE/DOCKET NUMBER:

28,675

542-04-PA

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                                                                                                                                                   NAME/KEY: CDS
LOCATION: (233)..(3391)
PUBLICATION INFORMATION:
JOURNAL: DNA
VOLUME: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 714-854-4897
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 2955 base pairs
TYPE: nucleic acid
Query Match
                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 3791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09377310B Patent No. 6133031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                 DATABASE ACCESSION NUMBER: L13616/Genbank DATABASE ENTRY DATE: 1995-01-02
-09-377-310-1
                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase TITLE OF INVENTION: Expression FILE REFERENCE: ISPH-0389
                                                                                                   ISSUE: 9
PAGES: 823-830
DATE: 1993-11
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-854-5502
TELEFAX: 714-854-4897
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LIBRARY: Genom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        433 GATGCAGATTGCAGATGATAGAACTATTGTCAGATTCATTATGCATATAGGATAGGCCTT 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 GATGTTGTTGTCGATAACAGAGGTCATGGCAGGTCCGATAAGCCACTTGGATACGATTT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
LOCATION:
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TOPOLOGY: lir
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join(1182..1326, 1837..1913, 2010..2082, 2180

...2397, 2480..2587, 2668..2731, 2848..2885, 2947
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Score 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
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DB 4;

Length 3791;

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; MOLECULE TYPE:
US-08-501-572-6
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                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 71; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 59.8 Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202)408-440
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 35,391
REFERENCE/DOCKET NUMBER: 02481.1453-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Toohey, Kimberlin M
REGISTRATION NUMBER: 35,39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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979 TATTACTGGTGCATACCT
                      408 AAAGATTCTTGCATCCAT 425
                                                                      919 CTTCCTCACTGGAGGTGGTTGCAGTTCACAGTTGCTCTGCCCCAACTTCTTCTTCTTGCTC
                                                                                                     348 AATCCTCATAGGTGGTGGGAGCAGAATAAAGCTTCTACACAGAATTGGATATCCTTTAGC 407
                                                                                                                                         859 ATTTTTTACCAAGTTGCCTATACAGTTGGGCTCCTGGTGCTAGCTGGGGTGGCTTACGCA 918
                                                                                                                                                                            288 ATTCGGAACAATGATCTCTATGAAGTACTGTTCGGAGTATCGGAATCGGGTTCTTGCTCT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            825 aaaaagatgttggtttaaagcgatttt 851
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                                                                                                                                                                                                                                                                                                                                  TYPE.
STRANDEDNESS: SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (202)408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                3.9%;
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n, Dirk
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Pred. No. 3;
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0; Mismatches
                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                DB 3;
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                                                                                                                                                                                                                                                Length 1896;
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RESULT 9
PCT-US93-07261-10
; Sequence 10, Application PC/TUS9307261
; GENERAL INFORMATION:
; TITLE OF INVENTION: PfEMP3 MALARIA ANTIGEN, ANALOGS, ANTIBODIES AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; NUMBER OF SEQUENCES: 23
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US-09-040-444-6
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ZIP: 2005-331.
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COMPUTER: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: O'CONDOY, Steven P
REGISTRATION NUMBER: 41,225
REFERENCE/DOCKET NUMBER: 2481
TELECOMMUNICATION INFORMATION:
TELECHONE: (202)408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202)408-440 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1896 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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APPLICANT: Gorboulev, Valentin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                           348 AATCCTCATAGGTGGGGGGGGAGCAGAATAAAGCTTCTACACAGAATTGGATATCCTTTAGC 407
                                                                                                                                                                                                                                                                                408 AAAGATTCTTGCATCCAT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                    288 ATTCGGAACAATGATCTCTATGAAGTACTGTTCGGAGTATCGGAATCGGGTTCTTGCTCT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 3.9%;
Local Similarity 51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: March
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                         TATTACTGGTGCATACCT 996
                                                                                                                                                                                                                                                                                                                    CTTCCTCACTGGAGGTGGTTGCAGTTCACAGTTGCTCTGCCCCAACTTCTTCTTCTTGCTC 978
                                                                                                                                                                                                                                                                                                                                                                                                 ATTTTTTACCAAGTTGCCTATACAGTTGGGCTCCTGGTGCTAGCTGGGTGGCTTACGCA 918
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1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (202)408-4400
TD NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Grundeman, Dirk
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March 18, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30.8;
Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2481.1453-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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APPLICANT: Fu, Yiny
APPLICANT: Yu, Chang-En
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Milligan, John T.
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TTTLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
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US-08-781-891-205/c
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APPLICATION NUMBER: 1930805
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/927,
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Blasdale, John H. C.
NAME: Blasdale, John H. C.
NAME: Blasdale, John H. C.
NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: N
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Best Local :
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TELEFAX: 201-822-7039
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ORIGINAL SOURCE:
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SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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COUNTRY:
STREET:
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Pred. No. 5.5;
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     701 Fifth Avenue
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FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/ACENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELEPHONE: (266) 622-4900
TELEPHONE: (266) 622-4900
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                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: FITZPATRICK,
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LENGTH: 4792 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: NOVEL DNA, NOVEL POLYPEPTIDE
TITLE OF INVENTION: AND NOVEL ANTIBODY
NUMBER OF SEQUENCES: 17
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                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                               COUNTRY: U.S.A. ZIP: 10172-0194
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Local Similarity 55.8%;
FILING DATE:
                     APPLICATION NUMBER:
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August 12, 1997
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                 US/08/909,965C
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                                                                                                                                                                                                                                                                 CELLA, HARPER AND SCINTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 30.4; DB 3; Pred. No. 6.4;
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Patent No. 5866412
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                              COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                            SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 APPLICANT: Chen, Hong
APPLICANT: Friemer, Nelson, B.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF NEUROPSYCHIATRIC
TITLE OF INVENTION: DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 212-758-2400
                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE: F2232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309 GAAGTACTGTTCGGAGTATCGGAATCGGGTTCTTGCTCTAATCCTCA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 GGATAATGGAGCTGTAATGGAATTTCACGTTTCTGAAGATTTTAATAAAATGAACTTTAT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 27-MAR-1997
                                                                                                                                                                                                                   CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 26 to 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 212-758-2982
                                                                                                               OPERATING SYSTEM:
                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & STREET: 1155 Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 12-No. 5936 FILING DATE: 12-Dec-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
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DEDNESS: double
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                                                                                                                                IBM Compatible
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55.1%;
                                                                US/08/828,007
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Pred. No. 4
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US-08-828-007-1
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TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE 3216 base pairs
FRIGHT: 3216 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08514975B Patent No. 5789229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: AGIER Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5899
                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE: 30-SEP-
                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                                                  TELEPHONE: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                                     STREET: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 TGAGAACTTCATTTCAGATTTAGATGCGGTTGTTA 247
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                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                COMPUTER: Apple
OPERATING SYSTEM: Macintosh 7.5.3
                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 77071
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Local Similarity 49.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 30,742
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                                                                                                                                                                                                                                                                                                                                                                                                                      E: Dr. Benjamin A. Adler
8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dr. Gail W. Wertz et al
                                                                                                                                                                                                                                                                   Macintosh Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                  UMBER: US/08/514,975B
September 29, 1995
                                                                                                                                                       30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene Therapy Vectors and Vaccines
Based on No. 5789229-Segmented Negative Stranded RNA Viruses
                                                                                                                                                                   US 08/316,438
                                                                                     D5899CIP2
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                   PCT-US95-12507-1
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Best Local Similarity
                                                                                                                                                                                 TELEFAX: (617)227-594 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 30-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                  FEATURE:
                                                                                   MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 02109-1875
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STRANDEDNESS: sing
TOPOLOGY: linear
                                    NAME/KEY:
LOCATION:
                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                             NAME: Arnold, Beth E. (BEA)
REGISTRATION NUMBER: 35,430
                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US95/12507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                       : 6578 base pairs
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                                                                                                                                                                                                  (617)227-5941
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4139 ACCATACTTTTCTGTTAATATGCGATTAATAGGGCTAGTGTCAAAGTGATAATT 4086
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                                                                                                                                                                                                                                                                                                                                                               GATAACAGAGGTCATGGCAGGTCCGATAAGCCACTTGGATACGATTTCTACAGATTTGAG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                              60 State Street, Suite 510
                                                                                                  Dr. Gail W. Wertz et al
                    LAHIVE & COCKFIELD
                                                                             Prevention and Treatment of Respiratory Tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30; DB Pred. No. 10; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 6578; 10;
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Query Match
Best Local Similarity
Matches 84; Conserve
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US-08-801-898A-23/c
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                                                                                     US-08-801-898A-23
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Best Local
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                                                                                                                                                                                                                               TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4139 ACCATACTTTTCTGTTAATATGCGATTAATAGGGCTAGTGTCAAAGTGATAATT 4086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:

NAME/KEY: RSV-A2
LOCATION: 1...15222
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/801,898A FILING DATE: 18-FEB-1997 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 AACTTCATTTCAGATTTAGATGCGGTTGTTAGGGAGACTGGAGTGGAGAAATTT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 GATAACAGAGGTCATGGCAGGTCCGATAAGCCACTTGGATACGATTTCTACAGATTTGAG 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT: Xiao, Wei
ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                     NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: NY
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TOPOLOGY: 11r
                                                                                                                                                                                                    TYPE: nucleic acid
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              Conservative
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OLIGONUCLEOTIDES EFFECTIVE TO TREAT RSV INFECTIONS
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           Score 30; DB 2; Length 15222;
Pred. No. 16;
0; Mismatches 90; Indels
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Pred. No.
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Search completed: June 2, 2001, 20:12:20 Job time: 23038 sec

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Maximum DB seq length: 2000000000
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3: /SIDSZ/gcgdata/geneseq/geneseqn/NA1983.DAT:*
4: /SIDSZ/gcgdata/geneseq/geneseqn/NA1983.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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	T13635 C47577	21	1297	. w	30.2	3 4 2
	X24302	20	6476		.0	41
	V35114	19	5058			40
	X83004	18	4792		30.4	39
	V35115	19	4206	•	0	38
	T13655	17	2631	3.9	30.4	37
	V35129		1404	٠	30.4	36
	X84336	N	846	3.9	30.4	35
	X13323	N	8145	3.9	30.6	34
	A70095		7326	3.9	0	ω ω
	N70824		5274	3.9	0.	32
	Q70102	ш.	4766	3.9	0.	31
	A54210		1425	3.9	0	30
	V52324	_	10357	3.9	0	29
	Z96384		1167	٠		28
	T98694		1087	3.9	0	27
	F22305		1082138		31	26
	V74347		7620	3.9	31	25
	C65534	22	3791	3.9	31	24
	V75020	18	1448		31.2	23
	X20580	20	19142	4.0	31.4	22
	Z15805	20	789	4.0		21
	C49196	21	1221	4.0	•	20
	X12945	20	8377	4.2	32.8	19
	X84332	20	5059	4.2	2	18
		21		4.2	32.8	17
		21		4.2		16
	Þ	21		4.2	ω	15
	V21209	19	76	4.4	34.4	14
	V74538	18		4.4	34.4	13
	Z51224	21	9	4.4	34.4	12

ALIGNMENTS

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Callen W,
Reid J, R
                                                                                                                                                                                                                                                                                                                                                                                                                                       Esterase; thermostable enzyme; ester; chiral compound; cheese; pulp; paper; lignin removal; sugar; lignocellulose; disease resistance; feedstuff; ss.
                                                               (RECO-) RECOMBINANT BIOCATALYSIS INC.
                                                                                                 16-FEB-1996; 96US-0602359
                                                                                                                                                     11-FEB-1997;
                                                                                                                                                                                                21-AUG-1997.
                                                                                                                                                                                                                                           WO9730160-A1.
                                                                                                                                                                                                                                                                                                                                                                                              Archaeoglobus venificus strain SNP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding Archaeoglobus venificus esterase SNP6-24LC
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, Kosmotka A,
Robertson DE,
                                                                                                                                                     97WO-US02039
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Link S, Maffia AM, M
Swanson RV, Warren PV;
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                    Murphy D;
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Best Local S
Matches 789
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                                      481
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DB; W23070.
   ATGGACACGTACAGAACTCTAACGAAAGTGAATCTTGAAAATATCTTGGAGAAAATAGAC
                                                                                                                 TCCATTGCATACAAGAAGTCTTCAAGATTGGTCGCAGATCTTTCCTTTGGCAAAAATGCT
                                                                                                                                                                                     GGTGGGAGCAGAATAAAGCTTCTACACAGAATTGGATATCCTTTAGCAAAGATTCTTGCA 420
                                                                                                                                                                                                                                                       ATCTCTATGAAGTACTGTTCGGAGTATCGGGAATCGGGTTCTTGCTCTAATCCTCATAGGT
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                                                                                               tccattgcatacaagaagtcttcaagattggtcgcagatctttcctttggcaaaaatgct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 789; DB 18; ilarity 100.0%; Pred. No. 1.5e-234; Conservative 0; Mismatches 0;
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16-JUN-1998;
16-JUN-1998;
16-JUN-1998;
22-JUN-1998;
22-JUN-1998;
                                                                                                                                                                                                                                                                                                                                          Soppet D
Lafleur
                                                                                                                                                                                                                                                                                                                                                                 Ruben SM,
Soppet DR,
z97019 to z97137 represent 94 isolated human secreted protein genes Y86215 to Y86333 are the secreted proteins encoded by the 94 human This sequence represents a fragment of one of the human secreted proteins. The genes and their corresponding secreted polypeptides a useful for preventing, treating or ameliorating medical conditions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
                                                                                                                                                                              New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         digestive disorder; endocrine disorder; infection; AIDS;
                                                                                                                                                                                                                                                                           P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-1999;
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DB; Y86295.
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                                                                                                                                                                                                                                                                                                                                            W,
                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
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Olsen
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98US-0089508.
98US-0089509.
98US-0089510.
98US-0090112.
98US-0090113.
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                                                                                                                                                                                                                                                                                                                                            HS,
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                                                                                                                                      586pp; English.
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Shi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 cDNA clone HL2AG87,
                                                                                                                                                                                                                                                                                                                                                                    GA,
                                                                                                                                                                                                                                                                                                                                            Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumour; developmental abnormality;
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Carter KC,
                                                                                                                                                                                                                                                                                                                                            PA,
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soulis G;
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RESULT 3
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TD T79304 standard; cDNA;
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Best Local Similarity 47.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g., by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 94 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney disorders, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. The sequences shown in Y86334 to Y86585 represent fragments of the
            Callen W,
Reid J, F
                                                                                                                                                                                                                                                                          Esterase; thermostable enzyme; ester; chiral compound; cheese; pulp; paper; lignin removal; sugar; lignocellulose; disease resistance; feedstuff; primer; PCR; ss.
                                                                                                                              11-FEB-1997;
                                                                                                                                                               21-AUG-1997.
                                                                                                                                                                                                WO9730160-A1
                                                                                                                                                                                                                             Archaeoglobus
                                                                                                                                                                                                                                                                                                                                            Archaeoglobus venificus esterase SNP6-24LC gene 3' PCR primer
                                                                                                                                                                                                                                                                                                                                                                                17-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1316 BP; 360 A; 294 C; 284 G; 378 T; 0 other;
                                                            (RECO-) RECOMBINANT BIOCATALYSIS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctatgttgctgctggagaaagaggcaaaccacttatgctgcttccatggatttccaga 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTATTATGAACTGGTGGATGGACCTGAGCCACCAATTGTCTTTGTTCACGGATGGACAGC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggattgtctaattacagatataaaggatattttagattctttagggtatagcaaatgtgt 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAGAACTTCATTTCAGATTTAGATGCGGTTGTTAGGGAGACTGGAGAGATTTGT 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTCGATAACAGAGGTCATGGCAGGTCCGATAAGCCACTTGGATACGATTTCTACAGATT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                attctggtattcttggcgttaccaactgagagaatttaaaagtgaatatcgagttgtagc
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            Robertson
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            Kosmotka A,
obertson DE,
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                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                               venificus strain SNP6
                                                                                             96US-0602359
                                                                                                                            97WO-US02039
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             Swanson
                         Link S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43.6; DB 21; Pred. No. 0.0015;
             RV,
                           Maffia AM,
               P۷
                           Murphy D;
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Best Local S
Matches 42
            23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
08-APR-1999;
16-APR-1999;
16-APR-1999;
21-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Either of two 3' PCR primers (T79304 and T79305) can be used with a 5' PCR primer (T79303) to amplify the esterase SNP6-24LC gene (see T79323) of Archaeoglobus venificus SNP6 from a pBluescript vector containing the DNA. The amplified sequence can then be inserted into a pQET vector, and the esterase (see W23070) expressed in bacterial host cells. Novel esterases (see W23070) are provided that are stable at high temperature and in organic solvents, making them superior for use in production of pure chiral compounds used in the pharmaceutical, agricultural and other chemical industries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in cheese paper manufacture, and to study plant resistance to disease
                                                                                                                                                                                                                                05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                      metabolic pathway; promoter; termination sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                Hybridisation assay; genetic mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana DNA fragment SEQ ID NO: 13372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C36323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C36323 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                          25-FEB-1999;
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                                                                                                                                                                                                                                                                                                            06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                    protein identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 28; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                747 TAATAGAGCAATGGACGAATTCATTTCTTCAGCACAGTTCTAA 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 TAATAGAGCAATGGACGAATTTATTTCTTCAGCACAGTTCTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                  2000EP-0301439
990S-0130449.
990S-0130510.
990S-0130891.
990S-0131449.
990S-0132484.
990S-0132484.
990S-0132484.
990S-0132486.
                                                                                                                                                                 99US-0126264.
99US-0126785.
99US-0127462.
99US-0128234.
                                                                                                                                         99US-0128714.
99US-0129845.
                                                                                                                                                                                                                                99US-0123180
99US-0123548
                                                                                                                              990S-0130077
                                                                                                                                                                                                                      99US-0125788
                                                                                                                                                                                                                                                          99US-0121825
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97.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41.4; Depred. No. 0.00
O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    transduction pathway;
                                                                                                                                                                                                                                                                                                                                                                                                              gene expression control;
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	99US-0160	US-O	us-o	0S-0	us-0	US-0	05-0	us-c	us-c	08-0	O-Su	US-C	2-2	us-c	os-c	us-C	US-C	US-C	S-C	us-c	US-C	0S-0	S-C	us-c	ŪS-C	0-S0	us-c	ūs-c	25-0	US-C	0S-0	US-C	08-0	us-c	US-C	us-c	0S-C	US-C	US-C	0S-C	us-c	08-0	S-C	os-c	os-c	US-C	0S-0	08-0	US-C	os-c	
	1608	160	1607	1595)1596	1593	159	159	159	159)158	158	157	157	156	155)155,	155	154)154	153	153	151)151)151	151	151	150	1150	149	149)149	149	149	148	148)148)148	1479	147	147)147	147:	147	146	146	145	1145	145	145)145	
į	0814.	768.	741.	84.	537.	331.	330.	295.	294.	369.	232.)29.	χ. Συ	117.	596.	559.	186.	ωv	779.	018.	758.)70.	930.	138.	303.	080	Š	884.	7.0	902.	929.	722.	126.	368.	584.	341.	171. 319.	335.	116.	303.	192.	302.	338.	389.	386.	951.	918.	313.	224.	L45.	
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RESULT 5
T79305/c
ID T79305 standard; cDNA; 52
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28-OCT-1999;
29-OCT-1999;
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22-OCT-1999;
22-OCT-1999;
25-OCT-1999;
25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
Either of two 3' PCR primers (T79304 and T79305) can be used with a 5' PCR primer (T79303) to amplify the esterase SNP6-24LC gene (see T79323) of Archaeoglobus venificus SNP6 from a pBluescript vector containing the DNA. The amplified sequence can then be inserted
                                                                                                                                                       Callen |
Reid J,
                                                                                                                                                                                                                                                                                                                                            Esterase; thermostable enzyme; ester; chiral compound; pulp; paper; lignin removal; sugar; lignocellulose; disease resistance; feedstuff; primer; PCR; ss.
                                                                               Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in ch paper manufacture, and to study plant resistance to disease
                                                                                                                                                                                          (RECO-) RECOMBINANT BIOCATALYSIS
                                                                                                                                                                                                                 16-FEB-1996;
                                                                                                                                                                                                                                        11-FEB-1997;
                                                                                                                                                                                                                                                                21-AUG-1997
                                                                                                                                                                                                                                                                                      WO9730160-A1
                                                                                                                                                                                                                                                                                                             Archaeoglobus venificus strain SNP6
                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                           Archaeoglobus venificus esterase SNP6-24LC
                                                                                                                                                                                                                                                                                                                                                                                                                   17-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                          T79305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 597 AGACTGTCCAACACTGATTATCGTTGGAGAAGAGGATGCACTATTGCCCGTTAGCAAATC 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              657
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                                                                                                                                 1997-425035/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGCGTAATGCTTGAGAGTCCAAGTGAGGTTAATAGAGCAATGGACGAATTCAT 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTTGAGCTGAGCAGGAGGATAGAAAACTCAAAGCTTGTGATCATCCCAAACTCGGGGCA 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aaacttaccagtattagtcgttgctggagccgaagacgcacttgttcccctcaagtcctc 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tctgccacatgaggagtgtcccaaggcacttcttgcagccatgtgcccattcat 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ccaagtcatggcttcaaaactcgaaaactctaggctagtagcaatctcaggatgcggaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                     Kosmotka A,
Robertson DE,
                                                             Page 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
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99US-0161405.
99US-0161406.
99US-0161359.
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99US-0160981.
99US-0160989.
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                                                                                                                                                                                                                 96US-0602359
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                                                            113pp;
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51.7%;
                                                                                                                                                     Swanson RV,
                                                                                                                                                                   Link S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39.6; DB 21;
Pred. No. 0.025;
0; Mismatches 84;
                                                                                                                                                                                         INC.
                                                                                                                                                      Maffia AM, M
/, Warren PV;
                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                   Murphy
                                                                                                                                                                                                                                                                                                                                                                                             3' PCR
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                                                                                                                                                                                                                                                                                                                                                                    cheese;
                                                                                                                                                                                                                                                                                                                                                                                           primer
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                                                                                             cheese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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RESULT
X91103
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PA XXX PT PT XXX PT PT XXX
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Matches
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                                                                                             Boyer M,
Rioux C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  into a pQET vector, and the esterase (see W23070) expressed in bacterial host cells. Novel esterases (see W23069-88) are provided that are stable at high temperature and in organic solvents, making them superior for use in production of pure chiral compounds used in the pharmaceutical, agricultural and other chemical industries.
                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                           Group B Streptococcus; GBS; antigen; vaccine; Streptococcus infection; sepsis; meningitis; pneumonia; immunocompromise; diabetes; liver disea cancer; vetinary; mastitis; ss.
                   Claim
                                   Novel group B Streptococcus antigens - useful as vaccine compositions for prophylaxis or therapy of Streptococcus
                                                                WPI; 1999-540309/45.
P-PSDB; Y27336, Y27337, Y27338, Y27339, Y27340
                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Group B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                          (BIOC-) BIOCHEM VACCINS
                                                                                                                                                                17-FEB-1999;
                                                                                                                                                                                                       WO9942588-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X91103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X91103 standard;
                                                                                                                                              20-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 4.8%;
Local Similarity 95.1%;
hes 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                  10; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52
                                                                                                       Brodeur BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                1A; 154pp; English
                                                                                                                                              98US-0075425
                                                                                                                                                                99WO-CA00114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15
                                                                                                                                                                                                                                            2735..4291
                                                                                                                                                                                                                                                                                                                                   534..890
                                                                                                                                                                                                                                                                                                                                         /*tag= a
/note= "see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                                                                                                               /*tag= b
/note= "see Y27337"
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/note= "see
                                                                                                                                                                                                                                                                       /note= "see Y27338"
1841..4291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GBS)
                                                                                                      Charlebois I,
                                                                                                                                                                                                                          "see Y27340"
                                                                                                                          INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                       Y27339"
                                                                                                                                                                                                                                                                                                                                             Y27336"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigens encoding DNA (clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 G; 16 T; 0 other;
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Pred. No. 0.02
0; Mismatches
                                                                                                      Hamel J,
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                                                                                                      Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                      Ö
                                    infections
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The invention provides Group B Streptococcus (GBS) antigens (Y27336-370)

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                                                                                                                                                      19-MAR-1999;
11-JUN-1999;
03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      can be recombinantly expressed using standard recombinant methodology. The GBS antigens of the invention can be used as vaccine components for the treatment or prophylaxis of diseases and symptoms mediated by Streptococcus infection, especially group A Streptococcus (S. pyogenes), GBS or S. agalactiae, S. dysgalactiae, S. uberis, S. nocardia, as well as Staphylococcus aureus. The vaccines are administered to those individuals at risk of GBS infection, particularly pregnant women and infants for sepsis, meningitis, and pneumonia, as well as immunocompromised individuals, such as those with diabetes, liver disease or cancer. The vaccines also have vetinary applications, such as for the treatment of mastitis in cattle. The present sequence represents a DNA encoding 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1065
Isolated nucleic acid molecule encoding a human secreted protein
                                WPI; 2000-579482/54.
P-PSDB; B34581.
                                                                                     Rosen
                                                                                                                                                                                                                           09-MAR-2000;
                                                                                                                                                                                                                                                            28-SEP-2000
                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                  ocular disorder;
                                                                                                                                                                                                                                                                                                                                                                                           fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; cancer; cardiovascular disorder; infection; cerebrovascular disorder; anglogenesis; nervous system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein gene 5 SEQ ID NO:15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C59742 standard; cDNA; 1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1185 ggatagtagagggcatggca 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4514 BP; 1317 A; 650 C; 869
                                                                                                                      (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                            WO200056751-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 CGATAACAGAGGTCATGGCA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 TTATGAACTGGTGGATGGACCTGAGCCACCAATTGTCTTTGTTCACGGATGGACAGCAAA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antigens of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acids (X91103-X91111) encoding the antigens. The GBS antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tagtcgctattttgataagcaaatagcatatttttctaagtattaccaagttattgttat 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                     Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                           2000WO-US06013.
                                                                                                                                                      99US-0125360.
99US-0138626.
99US-0168662.
                                                                                                                                                                                                                                                                                                                                                                              wound healing; skin aging; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.8%;
54.3%;
                                                                                                                      SCI INC
                                                                                     Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37.6; D
Pred. No. 0.19
0; Mismatches
                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G; 1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4514;
                                                                                                                                                                                                                                                                                                                                                                              preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  angiogenesis, nervous system disorders, infections caused by bacteria, viruses and fungi and ocular disorders. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent ski aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The proteins can also be used as a food additive or preservative to increase or decrease storage capabilities. C59729 to C59737 and B34576 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressive; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; notropic; neuroprotective; antibacterial; virucide; fungicide; and ophthalmological. The polynucleotides and proteins can be are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases, hyperpoliferative disorders e.g. neoplasms and cancers of the breast or liver, cardiovascular disorders, cerebrovascular disorders,
                                                                                                                                                                                                          17-SEP-1990
                                                                                                                                                                                                                                                                                N80747 standard; DNA; 4656 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               secreted proteins have activities based on the tissues and cells the genes are expressed in. Example of activities include: antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human secreted polypeptide sequences and proteins homologous to twhich are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
intron
                                     exon
                                                                                            Lycopersicon
                                                                                                                             2All transcription initiation region;
                                                                                                                                                                  Sequence of 2All genomic DNA cloned into pCGN1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   573
                                                                                                                                                                                                                                                                                                                                                                                724
                                                                                                                                                                                                                                                                                                                                                                                                                    752
                                                                                                                                                                                                                                                                                                                                                                                                                                                           664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotide sequences given in C59738 to C59787 encode reted proteins given in B34577 to B34626. B34627 to B34686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present
                                                                                                                                                                                                                                                                                                                                                                              agctcataatcgactttttagcttctgtgca
                                                                                                                                                                                                                                                                                                                                                                                                                  GAGCAATGGACGAATTCATTTCTTCAGCACA 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cgcaggtgctggatgtctggggcagacatgttggccaagtcaattgccaactgccagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCA-CTATTGCCCGTTAGCAAATCAGTTGAGCTGAGCAGGAGGAGGATAGAAAACTCAAAGC 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                       tggagcttctggaaaactgtgggcactcagtagtgatggaaagacccaggaagacagcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGTGATCATCCCAAACTCGGGGCATTGCGTAATGCTTGAGAGTCCAAGTGAGGTTAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tctccatcagaacatggacaagatcaaggttccgacgcagatcatctgggggaaacaaga 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTTGAAAATATCTTGGAGAAAATAGACTGTCCAACACTGATTATCGTTGGAGAAGAGGA 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 344-345; 419pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
                                                                                                                                                                                                          (first entry)
                                                                                              esculentum cv UC82B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP;
                                   Location/Qualifiers 1379..1444
/*tag=
..2158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               539 A; 432 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37.4;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409 G;
                                                                                                                                                                                                                                                                                                                                                                                754
                                                                                                                               clone pCGN1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
.15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1811;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           723
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                     3870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 It provides for abundant messanger, being activated at or shortly after anthesis, and remaining active until the red fruit stage. The construct pCON1273 allows modification of the plant phenotype during fruit maturation and ripening.
                                                                                                                  Transgenic plant; promoter; tissue-specific gene expression; fruit-specific expression; tomato; 2All; ss.
                                                                                                                                                                                                                                                                                       3930
                                                                                                                                                                                                                                                                                                                                                                                     3810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fruit specific DNA constructs to modify fruit phenotype comprising transcription initiation and termination regidesired DNA sequence, eg poly galacturonase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
                                                          CDS
                                                                                                                                                     Tomato fruit-specific clone
                                                                                                                                                                                                      V36972;
                                                                                                                                                                                                                             V36972 standard;
                       intron
                                                                                             Lycopersicon
                                                                                                                                                                              26-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4656 BP; 1709 A; 710 C; 652 G; 1580 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2All is a tomato fruit-specific transcription initiation region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; ; pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1988-353919/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Houck CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CALG-) CALGENE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-1987;
15-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO8809334-A
                                                                                                                                                                                                                                                                                                                                                                                                           577
                                                                                                                                                                                                                                                                                                               695
                                                                                                                                                                                                                                                                                                                                                             637
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                    φ
                                                                                                                                                                                                                                                                                                                                               CTATTGCCCGTTAGCAAATCAGTTGAGCTGAGCAGGAGGATAGAAAACTCAAAGCTT--G 694
                                                                                                                                                                                                                                                                                      tattcaacgcaaatatggcactctactcaatgaagtacaaattaactcaggatactcga
                                                                                                                                                                                                                                                                                                            TGATCATCCCAAACTCGGGGCATTGCGTAATGCTTGAGAGTCCAAGTGAGGTTAATAGA 753
                                                                                                                                                                                                                                                                                                                                   tacttacctcttttcaactcaactcaaattaagaataagatactcaactcaaagattagg
                                                                                                                                                                                                                                                                                                                                                                                 gagtatgtaagggaaattctaaagtataacataagcttgatacttgaataaaaggaaaca 3869
                                                                                                                                                                                                                                                                                                                                                                                                          GAAAATATCTTGGAGAAAATAGACTGTCCAACACTGATTATCGTTGGAGAAGAGGATGCA 636
                                                                                                                                                                                                                                                                                                                                                                                                                                   96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pear JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                            esculentum cv. UC82B
                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87US-0054369
88US-0168190
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/*tag= c
                /*tag= a
/note= "contains an intron"
1446..2199
                                                        1379..2393
                                                                     Location/Qualifiers
                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             4.5%;
                                                                                                                                                                                                                             4656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              poly galacturonase gene
                                                                                                                                                                                                                             B₽.
                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                    2All genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35:4;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches . 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                              .93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4656;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regions and
                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
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                                                                                                                                                                                                                                                                                                                                    3929
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This nucleotide sequence comprises tomato cv. UC62B 2All genomic DNA cloned into pCGN1273 from the XhoI site (position 1 at the 5' end) to the EcoRI site (position 4654). 2All genomic DNA was obtained by hybridisation using 2All cDNA (see V36971) as probe. 2All has been characterised as a fruit-specific gene. The 2All gene promoter can be incorporated into an expression cassette and used in a novel method for producing a plant with a regulatable phenotype. In this method, regulatory regions from plant genes expressed during a particular developmental stage or in a specific tissue are identified by cDNA screening. The regulatory regions (a T-DNA and Ti or Ri plasmids) are manipulated for use with foreign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-1986;
26-MAY-1987;
28-JUL-1987;
25-JAN-1988;
                         sequences for introduction into plant cells to provide transformed plants having a phenotypic property that can be modulated. The invention is exemplified with light, seed and fruit-specific promoters. Also claimed are methods for altering the phenotype of fruit tissue as distinct from other plant tissue, modifying the genotype of a plant to impart a desired characteristic to fruit, modifying transcription in fruit tissue, and expressing a heterologous DNA sequence of interest specifically in fruit tissue. The method provides transformation without gall formation in plants which have historically not been Agrobacterium hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transformation of plants - with regulatory sequence containing constructs for tissue specific expression of genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; W59610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-311403/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-AUG-1991;
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21-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAR-1988
29-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5753475-A
                                                                                                                                                                                                                                                                                                                                                                                                                   Example 10; Fig 7A-F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Houck CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-SEP-1990;
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88US-0168190.
88US-0188361.
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90US-0526123
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86US-0891529
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Sequence 4656 BP; 1710 A; 723 C; 643 G; 1580 T; 0 other;

(and

Š 밁 Š 밁 Q Query Match Best Local Matches 3810 577 Local Similarity les 96; Conserv GAAAATATCTTGGAGAAAATAGACTGTCCAACACTGATTATCGTTGGAGAAGAGGATGCA 636 CTATTGCCCGTTAGCAAATCAGTTGAGCTGAGCAGGAGGATAGAAAACTCAAAGCTT--G gagtatgtaagggaaattctaaagtataacataagcttgatacttgaataaaaggaaaca 3869 TGATCATCCCAAACTCGGGGCATTGCGTAATGCTTGAGAGTCCAAGTGAGGTTAATAGA 753 tacttacctcttttcaactcaactcaaattaagaataagatactcaaactcaaagattagg Conservative 4.5%; 0 Score 35.4; D Pred. No. 0.93 0; Mismatches DB 19; .93; 81; Indels Length 4656; 2; • Gaps 3929 694

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tattcaacgcaaatatggcactctactcaatgaagtacaaattaactcaggatactcga 3988

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RESULT 10
V27949
                                                           This nucleotide sequence comprises tomato cv. UC82B 2A11 genomic CDNA cloned into pCGN1273 from the XhoI site (position 1 at the 5'CDNA cloned into pCGN1273 from the XhoI site (position 1 at the 5'CDNA cloned into pCGN1273 from the XhoI site (position 1 at the 5'CDNA cloned by hybridisation using 2A11 cDNA (see V27948) as probe.

CONTROL 2A11 has been characterised as a fruit-specific gene. The promoter region of the 2A11 gene can be incorporated into an expression cassette and used in a novel method for producing a plant with an altered phenotype. In this method, regulatory regions from genes caspette and used in a novel method, regulatory regions from genes expressed during a particular developmental stage or in a specific cissue are identified by cDNA screening. The regulatory regions are manipulated for use with foreign sequences for introduction into plant cells to provide transformed plants having a phenotypic property that can be modulated. The invention is exemplified with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-1987;
25-JAN-1988;
15-MAR-1988;
15-APR-1988;
29-APR-1988;
07-NOV-1988;
21-MAY-1990;
                                   light, seed and fruit-specific promoters. Transformation gall formation of cells which are not Agrobacterium hosts,
                                                                                                                                                                                                                                                                                     Producing transgenic plant of modified expression of heterologous genes which
                                                                                                                                                                                                                                                                                                                              P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                      Facciotti D,
                                                                                                                                                                                                                                                                                                                                                                                                                         08-AUG-1991;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5750385-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V27949
                                                                                                                                                                                                                                                          Example 10; Fig 7A-E; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              (CALJ ) CALGENE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JAN-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lycopersicon esculentum cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transgenic plant; tissue-specific fruit-specific expression; tomato;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V27949 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAY-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L7-JAN-1
                                                                                                                                                                                                                                                                                                                              1998-296772/26
DB; W30673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fruit-specific genomic DNA clone 2All.
                          cereals and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                      Shewmaker
                                                                                                                                                                                                                                                                                                                                                                                                                       8705-0078538

8805-0168190

8805-0168190

8805-018361

8805-0267865

9005-0526123

9005-0550804

9005-0580241

9105-058241

9105-058244
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85US-0692605.
86US-0891529.
87US-0054369.
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/note= "contains an
1446..2199
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1379..2393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4656
                        legumes,
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                          is
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; 2All; ss.
                          achieved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron"
                                                                                                                                                                                                                                                                                    phenotype - is useful
are light-inducible
                                                    Transformation without
                                                                                                                                                                                                                                                                                                    for
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Sequence

4656

1711

A; 724 C;

644 G; 1577 T; 0 other;

heterologous genes in plants. They

n gene, a DNA n be used for y can be used

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RESULT 11
235695
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Best Local S
Matches 96
                                                                                                                                                                                                                                                                      10-AUG-1993;
07-JUN-1995;
31-JUL-1986;
26-MAY-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3810
            The present invention describes genetic constructs (I) for transforming plants with a DNA sequence of interest, comprising a promoter from a napin, EA9 or acyl carrier protein gene, a DNA sequence of interest and flanking T-DNA. The constructs can be used for the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        light promoter; seed promoter; fruit promoter; regulatory region; napin; soybean; rapeseed; cotton; safflower; sunflower; expression; phenotype; modification; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3930
                                                                                                  New genetic constructs useful for transforming plants with sequence of interest {\mbox{-}}
                                                                                                                                     WPI; 2000-012275/01.
                                                                                                                                                              Kridl
                                                                                                                                                                                                                        21-MAY-1990;
14-SEP-1990;
                                                                                                                                                                                                                                               28-JUL-1987
15-MAR-1988
                                                                                                                                                                                                                                                                                                                       09-JUL-1990
                                                                                                                                                                                                                                                                                                                                  02-NOV-1988;
                                                                                                                                                                                                                                                                                                                                            25-JAN-1988
29-APR-1988
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                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                           US5981839-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phenotype;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brassica; regulation; development; identification; screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z35695
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                                                                                                                                                                                    (CALJ ) CALGENE LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2All genomic DNA cloned into pCGN1273 nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGATCATCCCAAACTCGGGGCATTGCGTAATGCTTGAGAGTCCAAGTGAGGTTAATAGA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTATTGCCCGTTAGCAAATCAGTTGAGCTGAGCAGGAGGATAGAAAACTCAAAGCTT--G 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gagtatgtaagggaaattctaaagtataacataagcttgatacttgaataaaaggaaaca 3869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAAATATCTTGGAGAAAATAGACTGTCCAACACTGATTATCGTTGGAGAAGAGGATGCA 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; DNA; 4656 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 4.5%;
Similarity 53.6%;
96; Conservative
                                                                                                                                                              Knauf VC;
                                                                         Fig 7; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                      95US-0484941.
86US-0891529.
87US-0054369.
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91US-0742834
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88US-0168190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35.4;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .93;
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"NA sequence of interest and or the expression of d for modific."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4656;
                                                                                                              a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSSSSXX
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                     Staphylococcus aureus polypeptide useful for preventing or attenuating a Staphylococcal infection comprises one of 32 sequences of 100-1277 amino acids or their fragments -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccine; antibacterial; prevention; attenuation; detection; Staphylococcal infection; neonatal conjunctivitis; skin infection; toxic shock syndrome; osteomyelitis; MapM; methionine aminopeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plants such as soybean, rapeseed, cotton, safflower or sunflower. The present sequence represents the 2All genomic DNA cloned into pCGN1273 nuclearide secures.
  prevention or S.aureus infec
                                         The present sequence is a gene encoding methion from Staphylococcus aureus genomic DNA library. The present sequence is useful in preparation of the present sequence is useful in preparation of the present sequence is useful in preparation of the present sequence is useful in preparation of the present sequence is useful in preparation of the present sequence is a gene encoding methion of the present sequence is a gene encoding methion of the present sequence is a gene encoding methion of the present sequence is a gene encoding methion of the present sequence is a gene encoding methion of the present sequence is a gene encoding methion of the present sequence is a gene encoding methion of the present sequence is a gene encoding methion of the present sequence is useful in preparation of the preparation of the present sequence is useful in preparation of the present sequence is useful in preparation of the present sequence is useful in preparation of the preparation of the present sequence is useful in preparation of the preparation of the present sequence is useful in preparation of the present sequence is useful in preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation of the preparation 
                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                            Bailey CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200012678-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus methionine aminopeptidase gene mapM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251224 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4656 BP; 1710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phenotype of plants. The DNA sequence of interest may or may comprise an antisense sequence. The constructs
                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          577 GAAAATATCTTGGAGAAAATAGACTGTCCAACACTGATTATCGTTGGAGAAGAGGATGCA 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTATTGCCCGTTAGCAAATCAGTTGAGCTGAGCAGGAGGATAGAAAACTCAAAAGCTT--G
                                                                                                                                                                                                                                                                                         2000-237864/20
)B; Y70139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gagtatgtaagggaaattctaaagtataacataagcttgatacttgaataaaaggaaaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGATCATCCCAAACTCGGGGCATTGCGTAATGCTTGAGAGTCCAAGTGAGGTTAATAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tacttacctcttttcaactcaactcaaattaagaataagatactcaactcaaagattagg 3929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tattcaacgcaaatatggcactctactcaatgaagtacaaattaactcaggatactcga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96;
                                                                                                                                              Page 15;
    infections) which may
                                                                                                                                                                                                                                                                                                                                                              Choi GH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             GENOME SCI INC
                          attenuation of Staphylococcal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0098964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US19726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                           144pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             723 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "MapM protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             643
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No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G;
                                                                                             methionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelld infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 992-996; 3271pp; English.
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                                                                                                                                                                                                                                                                                        143
                                                                                                                                                                            203
                                                                                                                                                                                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                                                                                                                                                                                                                         GTGTAAATATCTATTATGAACTGGTGGATGGACCTGAGCCACCAATTGTCTTTGTTCACG 82
                                                             AGAAATTTGTTC 274
                                                                                                            cgatggcatttgagaatgcaattgcaaaagtaaaaccgggtactaagttaagtaacattg
                                                                                                                                               TCTACAGATTTGAGAACTTCATTTCAGATTTAGATGCGGTTGTTAGGGAGAGACTGGAGTGG
                                                                                                                                                                                                                           tttcatttgtcgttggagaatcagatgatccaatgaaacaaaagtatgtgacgtagcaa 4668
                                                                                                                                                                                                                                                                                   TGATGTTGTTGTCGATAACAGAGGTCATGGCAGGTCCGATAAGCCACTTGGATACGATT 202
                                                                                                                                                                                                                                                                                                                                    gagatttagtaaatattgatgtatcggctttgaagaatggctattatgcagatacaggca
                                                                                                                                                                                                                                                                                                                                                                                                                                                      gtattagtgtcaatgaagaggtggcacatgggattccaagtaagcgtgtcattcgtgaag 4548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         on computer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Choi GH, Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        read-only memory (ROM) or CD-ROM. Homology searches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0009861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and proteins derived readable medium and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34.4;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fannon MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from
used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus in the production of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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RESULT 14 V21209/c ID V21209 standard; DNA; 1664976 BP

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                                                                                                                                                                                                                                                                                                                                                                                                                                             genome sequence. The invention also describes a computer based system of for identifying fragments of the M. jannaschii genome that are chomologous to target nucleotide sequences, comprising: (a) data storage means comprising the nucleotide sequence of the 164976, 58407 or 16550 by sequence (see V21209, V21210 and V21211), or a nucleotide sequence of the sequence at cleast 99.9% identical to it; (b) search means for comparing a target cleast 99.9% identical to it; (b) search means for comparing a target cleast 99.9% identical to it; (b) search means for obtaining a target cleant of the nucleotide sequence of the data storage means to comparing a target comparing a target comparing a target condition of the nucleotide sequence of the data storage means to comparing a target condition of which consists of an autotrophic archaeon M. jannaschii, the genome converted to the sequence given in v21209), and a sequence given in v21210), and a sequence given in v21210), and a sequence given in v21210), can be used in the identification of M. jannaschii genome
1396227 GATGAGATAGTCAAAATATTGGGGCATAGAAACCCTGGAGAAAGTTATAAGACGGTTCAT 1396168
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1664976 BP; 568133 A; 264649 C; 258701 G; 573392 T; 101 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention describes M. jannaschii open reading frames from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents the complete 1.66-megabase pair genome sequence of the Methanococcus jannaschil circular chromosome. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Page 152-585; 614pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bult CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanococcus jannaschii; methanogenic archaeon; circular chromosome; genome; autotrophic; extrachromosomal element; identification; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome; autotrophic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete genome sequence of methano-genic archaeon, Methanoccoccus jannaschii - useful in identification of M. jannaschii genome
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(UNII ) UNIV ILLINOIS FOUND
(UYJO ) UNIV JOHNS HOPKINS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V21209
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                                        691 CTTGTGATCATCCCAAACTCGGGGCATTGCGTAATGCTTGAGAGTCCAAGTGAGGTTAAT 750
                                                                                                                                  631 GATGCACTATTGCCCCGTTAGCAAATCAGTTGAGCTGAGCAGGAGGATAGAAAACTCAAAG 690
                                                                                                                                                                                                                          571 AATCTTGAAAATATCTTGGAGAAAATAGACTGTCCAACACTGATTATCGTTGGAGAAGAG 630
                                                                                                                                                                                                                                                                            Local Similarity nes 101; Conserv
                                                                                       AATAGAAGAAAGCACATGAATCCAGAGGTTGAGTTAAAAAAGCTGAGAGACATTCCAGAT 1396228
                                                                                                                                                                               AATGGTGATTGGATGGCATACAAACCACAATTTTATCCTGGAAATACTTTAATTGCTGAG 1396288
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                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                               4.48;
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                                                                                                                                                                                                                                                                                               Score 34.4;
Pred. No. 27;
                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                    DB 19;
                                                                                                                                                                                                                                                                            111;
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RESULT 15
A02289
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 Query Match 4.2%;
Best Local Similarity 47.4%;
Matches 99; Conservative
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                                                                                                                                                                    A00010 to A02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used in diagnosis and prognosis of diseases and disorders (e.g. identification of concerner and the content of concerner correctants of concerner correctants.
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21-OCT-1998;
27-OCT-1998;
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Reinhard C, Giese K,
Lamson G, Drmanac R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                               Sequence
                                                                                                                          pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 897; 1097pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human colon cancer cell line polynucleotide sequence SEQ ID NO:2280.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-мат-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-126369/11.
                                                                                 734
                                                                                                               breast cancer, lung cancer,
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98US-0085696.
98US-0105234.
98US-0105877.
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                                                                               216 A; 142
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Randazzo F, Kennew,
Crkvenjakov R, Dickson
Crroia V, Jones LW,
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Score 33; DB 21; Length 734; Pred. No. 2.2; 0; Mismatches 110; Indels
                                                                               142 G;
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                                                                                                               and colon cancer.
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                                                                               11
                                                                               other;
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                                                                              ACTICAITICAGATITAGAIGCGGTIGITAGGGAGAGCTGGAGIGGAGAAAITTGTICTCG 277
ttggccatgactgggggggcatgattgct 354
                                                              gtctaattacagatataaaggatattttagattctttagggtatagcaaatgtgttctta
                                                                                                                                                                                                                         TCGGACATTCATTCGGAACAATGATCTCT 306
                                                                                                                          atttgagaggttatggagaaacagatgctcccattcatcgacagaattataaattggatt
                                                                                                                                                         ATAACAGAGGTCATGGCAGGTCCGATAAGCCACTTGGATACGATTTCTACAGATTTGAGA 217
                                                                                                                                                                                       tgtattcttggcgttaccaactgagagaatttaaaagtgaatatcgagttgtagcactgg
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Search completed: June Job time: 30026 sec 2, 2001, 22:08:48

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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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789
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                      em_htg_hum6:*
em_htg_hum7:*
em_htg_hum8:*
em_htg_inv1:*
em_htg_inv2:*
em_htg_other:*
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9b_ph: *
9b_pl1: *
9b_pl2: *
9b_pl3: *
9b_pl3: *
9b_pl4: *
em_bal: *
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em_in:*
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em_hum6:*
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em_fun:*
em_or:
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44 em_op: *

45 em_pai: *

46 em_pi: *

48 em_ro: *

49 em_sts: *

50 em_sts: *

51 em_un: *

52 em_vi: *

53 gb_sts3: *

56 gb_sts3: *

57 gb_sts4: *

58 gb_vi1: *

59 gb_vv2: *

60 gb_htg1: *

61 gb_htg3: *

62 gb_htg3: *

63 gb_htg4: *

64 gb_htg4: *

65 gb_htg4: *

66 gb_htg1: *

70 gb_htg1: *

71 gb_htg6: *

69 gb_htg1: *

71 gb_htg1: *

72 gb_htg1: *

73 gb_htg1: *

74 gb_htg1: *

75 gb_htg1: *

76 gb_htg1: *

77 gb_htg1: *

78 gb_htg1: *

79 gb_htg1: *

79 gb_htg1: *

79 gb_htg1: *

79 gb_htg2: *

80 gb_pb3: *

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81 gb_pb3: *

82 gb_pb3: *

83 gb_pb3: *

84 gb_pb3: *

85 gb_pb4: *

86 gb_pb5: *

86 gb_pb6: *

87 gb_pb6: *

88 gb_pb6: *

89 gb_pb7: *

80 gb_pb7: *

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80 gb_pb7: *

81 gb_pb7: *

82 gb_pb7: *

83 gb_pb8: *

94 gb_pb7: *

95 gb_pb7: *

95 gb_pb7: *

95 gb_pb7: *

95 gb_pb7: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 11	c 10	9	8	7	6	Մ	c 4	c 3	c 2	c 1	Result
38.8	39	39	39.4	40.4	40.6	40.6	40.8	41	48.8	310.6	Score
4.9	4.9	4.9	5.0	5.1	5.1	5.1	5.2	5.2	6.2	39.4	Query Match
172413	204302	184346	908	197196	210440	53533	7218	10391	12421	13675	Query Match Length DB
82	67	74	54	73	N	N	10	μ	ட	1	BB
AP001449	AC021439	AC069138	CNS078EM	AC068272	BSUB0006	BSY09476	166494	AE000996	AE000943	AE001044	ID
AP001449 Homo sapi	ACO21439 Homo sapi	AC069138 Homo sapi	AL433892 T3 end of	AC068272 Homo sapi	Z99109 Bacillus su	Y09476 B.subtilis	I66494 Sequence 14	AE000996 Archaeogl	AE000943 Archaeogl	AE001044 Archaeogl	Description

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REFERENCE
AUTHORS
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ORGANISM
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KEYWORDS
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MEDLINE
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                                                                                                                                                                                                                                                                Fleischmann,R.D., Quackenbush,J., Lee,N.H., Sutton,G.G., Gill, Kirkness,E.F., Dougherty,B.A., McKenney,K., Adams,M.D., Loftus Feterson,S., Reich,C.I., McNeil,L.K., Badger,J.H., Glodek,A., Zhou,L., Overbeek,R., Gocayne,J.D., Weidman,J.F., McDonald,L., Utterback,T., Cotton,M.D., Spriggs,T., Artiach,P., Kaine,B.P., Sykes,S.M., Sadow,P.W., D'Andrea,K.P., Bowman,C., Fujii,C., Garland,S.A., Mason,T.M., Olsen,G.J., Fraser,C.M., Smith,H.O.,
                                                                                                                                                                         The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus Nature 390 (6658), 384-370 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                Klenk, H.P., Clayton, R.A., Tomb, J., White, O., Nelson, K.E., Ketchum, K.A., Dodson, R.J., Gwinn, M., Hickey, E.K., Peterson, J.D., Ketchum, C.L., Kerlavage, A.R., Graham, D.E., Kyrpides, N.C., Richardson, D.L., Kerlavage, A.R., Graham, D.E., Kyrpides, N.C., Richardson, D.E., Richardson, 
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AE001044 AE000782
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enk, H.P., Clayton, R.A., Tomb, J.,
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AE003474 Drosophil
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In order to show the genes in ascending order on the genome, the
origin of this version has been moved by TIGR to position 2093570
of the original version and the opposite strand is shown from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhou, L., Overbeek, R., Gocayne, J.D., Weidman, J.F., McDonald, L., Utterback, T., Cotton, M.D., Spriggs, T., Artiach, P., Kaine, B.P., Sykes, S.M., Sadow, P.W., D'Andrea, K.P., Bowman, C., Fujii, C., Garland, S.A., Mason, T.M., Olsen, G.J., Fraser, C.M., Smith, H.O., Woese, C.R., and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (15-DEC-1997) The Institute for Genomic Research, 9712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dec 16, 1997 this sequence
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'product="conserved hypothetical protein"

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protein_id="AAB90372'."

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RLESSILNVEDUKPLIKKLIDELFVAVPSGVGSEGRIRVSDRELDEIFVEGARMAVEN

RYGYERDLKHCEEEGALEGAPFVVSKKARDRGRPQLGTLGSGKHFLEVQYVDKVFDE

GYGYERDLKHCEEEGALEGAPFVVSKKARDRGRPQLGTLGSGKHFLEVQYVDXHUAFA

GYGYERDLKHCEEGALEGAPFVVSKKARDRGRPQLGTLGSGKHFLEVQTVDAHUAFA

KVAAKFGIEEGAVTVMJHCGSRGLGHOVCTDFLEVLDGAVKKTGPSYILVGT

SKAMEGIFFGSTCHGSGRVMSRAAKRKLRGNVVKQNLERKGIYVRATHGALLAEEAPE

RKAMEGIFFGSTCHGSGRVMSRAAKRKLRGNVVKQNLERKGIYVRATHGALLAEEAPE
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/gene="AF0863"
                            complement(2778.
/gene="AF0865"
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complement(2778. .3578)
/gene="AF0865"
                                                                                                                                                                                                                                                                                                                                complement(2391.
/gene="AF0864"
                                                                                                                                                                                                                                                                                                                                                                          complement(2391.
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KAWWIKLGYDALEGKAILSTAFHHAKSLFVPLFKFELLILLGUTFFVFYAIVIDLKGTLSGIRRGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1505. .2398)
/gene="AF0863"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AYKLSDDVVDVVHRAGISKLVARLRPLGVAKG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(60. .1508)
/gene="AF0862"
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identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .13675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="hypothetical protein; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:2234"
           'note="similar to GB:D14529 PID:402521 percent identity:
                                                                                                                                                                                                                                                                      'codon_start=1
                                                                                                                                                                                                                                                                                                            'note="hypothetical protein; identified
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                                                                                                                                                                                                                                                                                                                                                      .2771)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     predicted coding region AF0863"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     version replaced g1:2649727
                                                                                                                                                                                                                          coding
                                                                                                                                                                                                                       region AF0864"
                                                                                                                                                                                                                                                                                                              by GeneMark;
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gene

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/product="glycerol kinase (glpk)"
protein_id="AAB90370.1"
/protein_id="AAB90370.1"
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/translation="MIGVIDAGTTTIKLAVYDEDKLVAIKKEPVVKHNPKPGWVEIDA
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LRELGEKKEKYDLKAGTVDSWLYYRLTGEHLTDYSNAAATGLYDSYYLRWSEPILKIV
GADEEMLPKTLESDRIFGEYRNVPVTGVIADQSASLYALGCWEEGDIKATNGTGTFVD
                                                                                                                                                                                                                                                              /product="alkyldihydroxyacetonephosphate synthase"
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FSAMEDAVVEPKSTEEVSVILKVANTYGIPVYVFGGGSGVIDAATPYEGGIALSTLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYRGGERAMKA I ERFEKSMRKVEVEPRDGK I LYFPGCSTFESGLFDVTVEVLEKLGVD
FAVKNLECCGMPYYELGLVDKFRGK I SSLKDAAAKYEGV I SNCPHCVHVMRENG I KAA
HLLAVLKPVK I GGDVSYHDPC I LARKLD I VEEPRRLLAEMGFVVHEPVFNGKDTHCCG
                                                    complement(7428.
                                                                                                                                                                                                                      DQIEIDEENMVVRAGAGVVGGRLEKILNHRGFTLRHSPQSLYCSTVGGWVATAASGQF
STGYGNIENLLVSLTAVLPDGEVVTERATPRRAGPDLKKIFVGSEGLLGVVTEAVMKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(6088. .7431)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(6088. .7431)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(5105. .6091)
/gene="AF0867"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNVGEEPQASPGGLLPLIAWKLKSEMRYMMEGMLFYSGSAVEKLKEIGIYDDVSKTSE
MAFRSKNDDMLLIPSFTGLATPHYVSVPGLLYGISNAMTREDIVKALLESIAFRIAEI
VEIMRKEFFYETDRIRCDGEMSSNDFFLQRIADVTGLKVERGAVLSGTSFGAHLVAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="AF0866"
                                                                                                  complement(7428.
                                                                                                                   DAERVYSEVLKAIRSVEGTVTASAHASHFYESGLCFYFTFAGLPADIESYYFEVWRRA
IEASLKNGGNLTHHHGVGRLRKRWLSAEIGGYYPLLRDLKSVLDRRNILNRGVML"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLHVCPVFDAERRLTVSPSVKSRLAYLGETEEAIYHCLPCDACKNACPMDISVNDNLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (5105. .6091)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3630. .5108)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KHRMLF I DNRGHGK SDK PFNRSFYEFDNFVSDLHAAVKDASFDRFVLVGHSFGTMISM
RYCVEH PGRVEALVLIGGGAR I QSLHRYGYPIGRLFATLAYGISAR IIANMAFGRKAG
ELRDWGLKEALENTPKHAALNTLWTLTTVDLRDIAREIEKPTLIVVGKEDALLPVSKS
                                                                         /gene="AF0869"
                                                                                                                                                                      EGRAASAKLKEARNLVRGRLVEGRAEKWLEKRFDVSDISRIVPLGFIFDTIEVACFWK
                                                                                                                                                                                                 FPLPEEFLTLSVEYDGIGEAVRDAKALMQLRPALMRIFDDEESLRYFDSESFTLIAVF
                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="AF0868"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="AF0868"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YGGVYRFVVPEMAEKVAERRMEHFEHQIVTLCPSCRMALKAKDIVEIIAEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="reductase, putative"
/protein_id="AAB90375.1"
/db_xref="GI:2649738"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GP:1890198 percent identity:
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="AF0867"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALGKWKKDFCMPFDKVFEPSLDLSEKYRRWKRLLEISKKLKV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to GB:M34393 SP:P18157 PID:142992
PID:2226137 GB:AL009126 percent identity: 33.83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EELSRLIKNSKMVIVPDAGHCVMLEQPEIVNRVLEEFIHTFSAMLIRA"
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/protein_id="AAB90371.1"
  /note="similar to GP:1402531 percent identity: 48.31;
                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                    identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to GP:1808596 percent identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MINPKVITRILANTDLKTKMRLAKVVPKLGKSDDVTKCMLCPNM/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="AF0866"
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3080 CTGAAGGAGGCACTGGAAAACACTCCCAAACATGCAGCCCTTAACACTCTCTGGACTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 GGTGTAAATATCTATTATGAACTGGTGGATGGACCTGAGCCACCAATTGTCTTTGTTCAC
AACTCAAAGCTTGTGATCATCCCAAACTCGGGGCATTGCGTAATGCTTGAGAGTCCAAGT 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGTATCGGAATCGGGTTCTTGCTCTAATCCTCATAGGTGGGAGCAGGAGCAGAATAAAGCTT
                                                                                                                                                                                                                                                                                                                                    GAGAAATTTGTTCTCGTCGGACATTCATTCGGAACAATGATCTCTATGAAGTACTGTTCG
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                                               GGAAAGGAGGACGCACTGCTCCCCGTAAGCAAGTCGGAGGAGCTTTCGAGGCTGATAAAG
                                                                                            GGAGAAGAGGATGCACTATTGCCCGTTAGCAAATCAGTTGAGCTGAGCAGGAGGATAGAA 681
                                                                                                                                                                                            ACGAAAGTGAATCTTGAAAATATCTTGGAGAAAATAGACTGTCCAACACTGATTATCGTT
                                                                                                                                                                                                                                                                                      TGGAAACAGGCAATGGATTATACACCCTCCTACGTGGCAATGGACACGTACAGAACTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCACCGCTACGGCTACCCAATTGGAAGGCTTTTCGCTACATTGGCTTACGGAATCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTACACAGAATTGGATATCCTTTAGCAAAGATTCTTGCATCCATTGCATACAAGAAGTCT
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                                                                                                                                            ACTACAGTGGATTTAAGGGACATTGCGAGAGAAATAGAGAAAACCGACGCTGATAGTTGTC
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/gene="AF0870"
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/protein_id="AAB90368.1"
/protein_id="AAB90368.1"
/db_xrefi="GI:2649731"
/tzanslation="MEKEIIITTETVPQREVAEILGVVFGNTVRAKHVGKDILAGLK
/TIGNSLESTEMLRDARMEALNRMIKEAKKLGADAVVNVRFTTSQTMAGAAELLAYG
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/product="A. fulgidus predicted
/protein_id="AAB90378.1"
/db_xref="GI:2649742"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="hypothetical protein;
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Pred. No. 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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gene .		gene	source	COMMENT	REMARK	JOURNAL					REFERENCE AUTHORS	JOURNAL MEDLINE	TITLE					AUTHORS		ORGANISM	VERSION KEYWORDS	DEFINITION ACCESSION	RESULT 2 AE000943/c	Db 2840 As	Qy 742 GI	pb 2900 A
/codon_start=1 /transl_table=11 /product="Glu-tRNA amidotransferase, subunit C (gatC)" /protein_id="AAB88922.1" /db_xref="G1:2648183" /db_xref="G1:2648183" /translation="MVSIEDVYHTAELAKIETTEEQAEKFRKEFETILDYFNILDEVE EDVEPTFHYLPLTNVFREDEPGECLKQEEALSNAKHKEEGYFKGPRVVE" 3651738 /gene="AF2329"	<pre>/gene="AF2328" /note="similar to PID:1001350 percent identity: 35.11; identified by sequence similarity; putative"</pre>	87368 /gene="AF2328" 87368	 112421 /organism="Archaeoglobus fulgidus" /db_xref="taxon:2234" 	original version. On Dec 16, 1997 this sequence version replaced gi:2648175. Location/Qualifiers	In order to show the genes in ascending order on the genome, the origin of this version has been moved by TIGR to position 2093570 of the original version and the opposite strand is shown from the	Direct Submission Submitted (15-DEC-1997) The Institute for Genomic Research, 9712 Medical Conter Dr. Bookwille, Mp. 20850 HGA	Syres, J.M., Sadow, F.M., D. Hilled, K.F., Bowlled, C., rujii, C., Garland, S.A., Mason, T.M., Olsen, G.J., Fraser, C.M., Smith, H.O., Woese, C.R. and Venter, J.C.	Zhou, L., Overbeek, R., Gocayne, J.D., Weidman, J.F., McDonald, L., Zhou, L., Cotton, M.D., Spriggs, T., Artiach, P., Kaine, B.P., Cyton, R. D. W., Cotton, M.D., Spriggs, T., Artiach, P., Kaine, B.P., Cyton, R. W., Cotton, M.D., Spriggs, T., Artiach, P., Kaine, B.P., Cyton, R. W., Caller, C. FigerChmann, K.D., Quackenbush, J., Lee, N.H., Sutton, G.G., Gili, S., Kirkness, E.F., Dougherty, B.A., McKenney, K., Adams, M.D., Loftus, B., Peterson. S., Reich, C.I., McNeil, L.K., Badger, J.H., Glodek, A.,	Ketchum, K.A., Dodson, R.J., Gwinn, M., Hickey, E.K., Peterson, J.D., Richardson, D.L., Kerlavage, A.R., Graham, D.E., Kyrpides, N.C.,	2 (bases 1 to 12421) Klenk, H.P., Clayton, R.A., Tomb, J., White, O., Nelson, K.E.,	Nature 390 (6658), 364-370 (1997) 98049343	The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus	<pre>Sykes, s.m., sadow, r.w., D. Hildred, K.r., Bowman, C., rujii, C., Garland, S.A., Mason, T.M., Olsen, G.J., Fraser, C.M., Smith, H.O., Woese, C.R. and Venter, J.C.</pre>	Zhou,L., Overbeek,K., Gocayne,J.U., Weldman,J.E., McDonald,L., Utterback,T., Cotton,M.D., Spriggs,T., Artiach,P., Kaine,B.P., Sykes S.M. Sadow, D.W. D'Andrea K.D. Bowman C. Fuill	Rirkness, E.F., Dougherty, B.A., McKenney, K., Adams, M.D., Loitus, B., Peterson, S., Reich, C.I., McNeil, L.K., Badger, J.H., Glodek, A.,	Richardson, D.L., Kerlavage, A.R., Graham, D.E., Kyrpides, N.C., Fleischmann, R.D., Quackenbush, J., Lee, N.H., Sutton, G.G., Gill, S.,	<pre>Ktenk,H.P., Clayton,R.A., Tomb,J., White,O., Neison,K.E., Ketchum,K.A., Dodson,R.J., Gwinn,M., Hickey,E.K., Peterson,J.D.,</pre>	Archaeoglobus. 1 (bases 1 to 12421)	Archaeoglobus fulgidus Archaeoglobus fulgidus Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;	AE000943.1 GI:2689266	AEU00943 12421 DP DNA BCT 15-DEC-1997 Archaeoglobus fulgidus section 164 of 172 of the complete genome. AE000943 AE000782		2840 ATCGTTAACAGGGTTTTGGAGGAGTTCAT 2812	SAGCAATGGACG	2900 AATTCAAAGATGGTGATCGTTCCCGATGCCGGACACTGCGTGATGCTTGAGCAGCCTGAA 2841	
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	CDS	gene				CDS	gene				CDS	gene						CDS	gene						-	CDS
/note 45.50 /codor /trans /produt /prote /db_xx /trans	/gene	FVPCMI RYAEFY COMDLE	/prote /db_xi /trans	/codon /trans /produ	/yene /note- PID:12 identi	/gene- 2663.	/ Lrans EKEYCI 2663.	/prote	/codoi /trans	/note	comple /gene	comple /qene	GCIIVI	/proce /db_xi	/produ	/codor	/gene-	/gene- comple	ERFGE(comple	MPSFKI RRIMLO ADPLTI	DTGGS: GKDTRI	/trans MAEKYI AIIIGI	/produ /prote /db_xi	/codor/trans	/gene	365.

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365.
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nsl_table=11

duct="Glu-trNA amidotransferase, subunit A (gatA-2)"

tein_id="AAB89921.1"

xref="GI:2648182"

xref=
duct="conserved hypothetical protein"
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KSAHISGVSYDNIGEAGLEWLESLDAKLKVPATLNPAGMDVERWREMGIDEEFH
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mavkidvopptgkeiilcfpkwfrncppytafikkfakgreirmiicyggfder
fyksfalkcgakkabyllykrrelrenpekvrdnikkwikis"
lement(3102. 4244)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        duct="flavodoxin; putative"
tein_id="AAB88920.1"
xref="GI:2648181"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on_start=1
nsl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e="AF2332"
e="AF2332"
to GB:L42023 SP:P44562 PID:1003282
1222108 PID:1204448 percent identity: 30.30;
tified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e-"AF2332"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            duct="conserved hypothetical protein"
tein_id="AAB88923.1"
xref="GI:2668184"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e="similar to PID:849180 percent identity: 32.39;
tified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nslation-"mrwqefegevrriceahdfstkfrfvfkdeegraeidyvaeryg
fdaklysasryrasqlrreaekhrrrcerfsaltgkraipyvysliddslrfhs
vpyhslnefltnlhfylaefgfl"
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duct="A, fulgidus predicted coding region AF2330"
tein_id="AAB8927.1"
tein_id="GI:2648189"
xref="GI:2648189"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lement(1760. .2149)
= "AF2330"
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KYALAAYYIIAMSEASSNLARYDGVRYGFALEKLDSWRRYFSKVRAEGFGDEVK
LGSYALSAGYYGKYYLKAQKVRTLVIRDFKKAFEEYDVLISPTMPALPFKIGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e="similar to PID:1652678 percent identity: 53.55;
tified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                    on_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lement(3102. .4244)
e="AF2333"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nslation="mpayvfskesflkfleghleddvvvvvssdvtdfckklsesmvg
Sfaefaffadifdadedeidemmkyaivfvekeklseagrnair"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lement(2146.
e="AF2331"
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                                                                                                                                                                                                                                                    sl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "AF2333"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "hypothetical protein; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -"AF2330"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               !MYKADVNTVPVNLAGLPALSVPVGMVKGLPVGLQVIGNYFSENTLLNFGKWVG
                                                                                                                                                                                                                                                                                                                                                               ;="similar to GB:L77117 PID:1591952 percent identity:
); identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ement(2146. .2424)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ement(1760.
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EKQMRVLRVFERLGVRMTLTCTPYYLLRPEFGDHLAWAESSAIVYANSIIGARTERES

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Query Match
Best Local
                                                  5758
                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                              gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trna
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652 AAATCAGTTGAGCTGAGCAGGAGGATAGAAAACTCAAAGCTTGTGATCATCCCAAACTCG 711
                                                                                            592 AAAATAGACTGTCCAACACTGATTATCGTTGGAGAAGAGGATGCACTATTGCCCGTTAGC 651
                                               AAGGTGGATATCCCAACGCTTCTCATCGTTGGGGAGAAAGACGCTTTAACACCCCGTGAAG 5699
                                                                                                                                                                            Similarity
                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                            /gene="AF2337"
complement(7115. .8026)
/gene="AF2337"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="AF2336"
complement(5567. .6310)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPSAIAAAIIGKIPYYGVHIKENRAPTIFVRIKGDIAAAGYKAGRELRDQIPYFVFDR
SVTEEELKLIGAALAATGNTVNFHAENYTPENKDFEKPAEKIFVDDRLEBACEPDLIT
IGCPHASVRELETILKLINGGRKAKKEEWVFTAADVARKAEKIYQKLEELGVKVFSDTC
MVVSPATSKFRCIMVNSGKALYYLPNKRDVDVAFGDLRKCVETAVS"
                                                                                                                                                                                                                                                                                                                                                 complement(7115. .8026)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MERITLEIDALKISVLKGKEKDVMYIHGSGCDATLWERQLEDVG
GYAIDLPNHGRSCAAEIRDIGDYAYFVAKTVKKLMGKAVIVGHSLGGAVAQKIYLEYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="carboxylesterase (est-3)"
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/db_xref="GI:2648185"
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IDRNVIDLSRKflkIDHGafederveiaimbgkeflrceifpyiivbSTDpvvyySDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(4211. .5020)
/gene="AF2334"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVIPEAGHMVMLEKPDEFNRALKNFIEKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVLHLDLSLCDRFDLLEDYRSGKVKVDIPTLLIVGEKDALTPVKYSEFFKKHIPSAEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVVKALVLVGTGARLRVMPEILTMLKEKPAEAAELVSKYAFSNQELAKEFSKVFAERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to 28.84; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(5567. .6310)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="malvyydvQEKLAPHIEGIEEMLKRTVKLVKAIVALKQPVIFTE
QIKLGKTVDELAEYAEEPIVKSTFSCYKDENFRRKIEELKPEKVILAGIEAHICVLQT
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/db_xref="GI:2648178"
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identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WSFIIGGEYDFSNLEERFERIKGKTVHYNPDVHRAAFALPEWLKKEVEACI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="spermidine synthase
/protein_id="AAB88918.1"
/db_xref="GI:2648179"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to GB:L77117 SP:Q57761 PID:1591033 percent
identity: 37.09; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="AF2334"
                                                                                                                                                                                                                                                    /note="similar to SP:Q04477 PID:817877 percent identity:
                                                                                                                                                                                                                                                                                                                                                                                      /gene="tRNA-Val-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Val GAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="AF2336"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \IDMKRAGYDVYVVADCTGSRKAEDKEIALMRLAGEGIKLTTWESIVYELLESAEHPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="AF2335"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="AF2335"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFDREFFELARQKCDVISLQSQSPLIQKEYFRTLLVNSAPFERRDVYLSCVPTYPLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="tRNA-Val-3"
                                                                                                                                                                            6.2%;
                                                                                                                                                    0
                                                                                                                                                                            Score 48.8; DB Pred. No. 0.019;
                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB:D14529 PID:402521 percent identity:
by sequence similarity; putative"
                                                                                                                                                                                                    DB 1;
                                                                                                                                                    82;
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                                                                                                                                                                                                 Length 12421;
                                                                                                                                                    Indels
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                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POCUS.
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AE000996/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5638 GGCCACATGGTTATGCTTGAAAAGCCCCGATGAGTTTAACAGAGCCCCTAAAAAATTTTATT 5579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5698 TACTCCGAGTTCTTCAAAAAGCACATTCCGTCAGCGGAAATGGTTGTTATCCCGGAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGCATTGCGTAATGCTTGAGAGTCCAAGTGAGGTTAATAGAGCAATGGACGAATTCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (15-DEC-1997) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA. In order to show the genes in ascending order on the genome, the origin of this version has been moved by TIGR to position 2093570 of the original version and the opposite strand is shown from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 10391)

Klenk, H.P., Clayton, R.A., Tomb, J., White, O., Nelson, K.E.,

Klenk, H.P., Clayton, R.A., Gwinn, M., Hickey, E.K., Peterson, J.D.,

Ketchum, K.A., Dodson, R.J., Gwinn, M., Hickey, E.K., Peterson, J.D.,

Richardson, D.L., Kerlavage, A.R., Graham, D.E., Kyrpides, N.C.,

Fleischmann, R.D., Quackenbush, J., Lee, N.H., Sutton, G.G., Gill, S.,

Kirkness, E.F., Dougherty, B.A., McKenney, K., Sdams, M.D., Loftus, B.,

Peterson, S., Reich, C.I., McNeil, L.K., Badger, J.H., Glodek, A.,

Zhou, L., Overbeek, R., Gocayne, J.D., Weidman, J.F., McDonald, L.,

Utterback, T., Cotton, M.D., Spriggs, T., Arilach, P., Kaine, B.P.,

Sykes, S.M., Sadow, P.W., D'Andrea, K.P., Bowman, C., Fujii, C.,

Garland, S.A., Mason, T.M., Olsen, G.J., Fraser, C.M., Smith, H.O.,

Noese, C.R. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus Nature 390 (6658), 364-370 (1997) 98049343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Dec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fleischmann,R.D., Quackenbush,J., Lee,N.H., Sutton,G.G., Gill,S., Kirkness,E.F., Dougherty,B.A., McKenney,K., Adams,M.D., Loftus,B., Peterson,S., Reich,C.I., McNeil,L.K., Badger,J.H., Glodek,A., Zhou,L., Overbeek,R., Gocayne,J.D., Reidman,J.F., McDonald,L., Utterback,T., Cotton,M.D., Spriggs,T., Artlach,P., Kaine,B.P., Sykes,S.M., Sadow,P.W., D'Andrea,K.P., Bowman,C., Fujil,C., Garland,S.A., Mason,T.M., Olsen,G.J., Fraser,C.M., Smith,H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaeoglobus fulgidus
Archaeoglobus fulgidus
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Archaeoglobus fulgidus
AE000996 AE000782
AE000996.1 GI:2689319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klenk, H.P., Clayton, R.A., Tomb, J., White, O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArchaeogLobus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               version.
                                                                                                                                                                                                                                                                                   /gene="AF1534"
142. .492
YKSDGTCEFKEGVHSSPTFTVVAPPDFWLAVLKGQEDPVSGFMMGKYRIEGNIMEAQR
                                                    /transl_table=11
/transl_table=11
/product="A. fulgidus predicted coding
/protein_id="AnaB9715.1"
/db_xref="GI:2649030"
                                                                                                                                                                                                 /note="hypothetical putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       , 1997 this sequence Location/Qualifiers
                          translation="MSEAKELIKKMCDLQNSNEEIQKEMAGWSGVVQYKLDGEEFYVE/
                                                                                                                                                                                                                                                                                                                                                               /organism="Archaeoglobus
/db_xref="taxon:2234"
                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                      /gene="AF1534"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          section
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                                                                                                                                                                                                                         protein; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  version replaced gi:2649016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nelson, K.E.,
                                                                                                         region
                                                                                                                                                                                                                         by GeneMark;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete
                                                                                                         AF1534
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gene
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                                                                                                                                                             CDS
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                                                    identity:
putative*
                                                                                                                                                                                                                                                                                                                                         /product="conserved hypothetical protein"
/protein_id="AAB99708.1"
/protein_id="AAB99708.1"
/db_xref="G1:2649023"
/translation="MEDGRYSALERMGARLCASVEKMMPDPLIFALLITIVTYLLVIV
/translation="MEDGRYSALERMGARLCASVEKMMPDPLIFALLITIVTYLLVIV
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IATLPSDTKSAAALTALIAMIAAWINWGLGLIVGAILATICHETKTKPLHYPYTLINL
AAGYAGLGLTWHWGLSASAPLLINTPNHFLKDVFVELFGRETVFLNETIFHPYTLINL
ALIISFGVLAYYALAPNRGELKGIDKVAPHIIELVKKEKEEELKEKSKERVTIADKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MLERVFIDVDGVKVSLLKGRERKVFYIHSSGSDATQWVNQLTAI
GGYALDLNHHGQSDTVEVNSVDEYAYYASESLKKTVGKAVVVGHSLGGAVAQKLYLRN
PEICLALVLYGTGARLRVLPEILEGLKKEPEKAVDLMLSMAFASKGEEYEKKRREFID
RVDVLHLDLSLCDRFDLLEDYRNGKLKIGVPTLVIVGEEDKLTFLKYHEFFHKHIPNS
ELVVIPGASHHYMLEKHVEFREALEKFLKKVGV"
                                                                                                                                                        complement(3614. .4489)
                                                                                                                                                                                                          complement(3614. .4489)
                                                                                                                                                                                                                                      IAGLINIFIPSGGEWAAVGEILARTSAALGVPIGKTVIAYGVGDAWTNLFQPFWAIP
LLGLTGTRARDVFGYTISVMILATIPLSLGLVLVPY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to GB:L42023 SP:P44051 PID:1005750 PID:120865 PID:1205020 percent identity: 37.20; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(1997. .3457)
/gene="AF1538"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="WAEVLMYGLSTCPHCKRTLEFLKREGVDFEVIWIDKLEGEERKK VIEKVHSISGSYSVPVVKGDKHVLGYNEEKLKELIRG" complement (1208. .1963)
/gene="AF1537"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="maekrgwrvnpdrellldfakalionkeoygiatcpcrlvtgkk
evdrliicpcvyaeddireygrcycglylsrekepadsvpdrhakyylev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="ferredoxin-thioredoxin reductase,
subunit (ftrB)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="AF1535"
/transl_table=11
                                                                                                                                                                                    /gene="AF1539"
                                                                                                                                                                                                                                                                                          RAAGAVAGILVQFPFYAGIMGMMRYSAVVAGGPNLATVIANSIASVATPFTWPAICLY
                                                                                                                                                                                                                                                                                                                         NSKVLALLISILGIITMGYWFYEKGFFGGLNLNSLNFTFIMVGLLLYMNPIAYMRAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (1997. .3457)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="carboxylesterase (est-2)"
/protein_1d="AAB89709.1"
/db_xref="GI:2649024"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1208. .1963)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="glutaredoxin (grx-1)"
/protein_id="AAB89710.1"
/db_xref="GI:2649025"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to PID:1652611 percent identity:
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (839.
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                                                                             /note="similar to GB:L77117
Identity: 56.94; identified
                                                                                                                                  /gene="AF1539"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="AF1538"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="AF1537"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="AF1536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="AF1536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to SP:P51386 percent identity:
identified by sequence similarity; putative"
                           codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to
29.02; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d-"AAB89711.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1087)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB:D14529 PID:402521 percent identity: by sequence similarity; putative"
                                                                        SP:Q58643 PID:1591879 percent
by sequence similarity;
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                             591 GAAAATAGACTGTCCAACACTGATTATCGTTGGAGAAGAGGATGCACTATTGCCCGTTAG 650
GAAAATAGGTGTCCCAACTCTCGTAATTGTCGGCGAGGAGGACAAGCTAACGCCGCTGAA 1347
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92; Conserv
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/protein_id-"AAB89706.1"
/db_xref-="G1:2649021"
/translation-"MMRLHEHQAKQIFAKHGIRVPRGEVATSPEEAEKIAEKLGGRVV
/translation-"MMRLHEHQAKQIFAKHGIRVPRGEVATSPEEAEKIAEKLGGRVV
/KAQILVGGROKAGGVKKANSPEEAKEKAKKILGMTIKGHRVEKVLVEEQLMMRKEYY
VGAVUDKSSKLALTVIFAKMGGMDVEEIAAKHDAIHRITDDHJMGLKDYEVRKALFEYY
VGYVVDKSSKLALTVIFAKMGGMDVEEIAAKHGIRVTDDFJFAKGLKDVEVRKALFEYY
VGYVVDKSSKLALTVIFAKMGGMDVEEIAAKHGIRVTDDFJFAKTATDHJMALYRH
GEGGEEFKOMEDIIKKLVDIAFAYEAELTEINPLAVTDEGFIAADARLNTDDMALYRH
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GKGGSEVHGIPVYNTVEEAVAETNADTSIIYVEAFFATDAILPDREFDAGLRLVVCYTEG
IPLVDEMLIHRKLREVKSMLLGPUFGVISPGRSVGLLDAIFEAFDAGLRLVVSNSGTL
TYQICENLTKAGIGQSTVVGIGGDPMPGLTFVDVLKMFEEDDETKAVLLVGEIGGTAE
                                                                                                                                                                                                                         7341. .8156
/gene="AF1543"
/note="hypothetical protein; identified by GeneMark;
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SFPLLSYHLAGYVDLKLIPLLYALAMGIDAISALISGRCYDRIGLKTLMLVPLLTPLI
LLALHPSIIGVLVGVAAWGAVMGMHEAITRAAVADLTGVKKRSTAYGVFNTVFGVAML
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/protein_id="AABB9705.1"
/db_xref="GI:2649920"
/ta_nslation="MNRAMKFILLMGLVSLFGDITYEGARSIVGPYLATFGLTAAAIG
LITGEGEFAGYGLRLLSGYIADRTGNYWLLTFLGYSLILAIFLLAFANYWWIAALLIV
AERLGKAIRTPARDAMLSFATKQVGRGTGFGIHEAMDQVGAYIGPLIYFSALAGYTFK
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/product="conserved hypothetical protein"
/protein_id="AAB89704.1"
/db_xref="GI:2649019"
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LYPILHEMEREGLLRSRKVVVDGRVRKMYRITEKGWKLLDDAREKVKELFEEIMEER"
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/db_xref="GI:2649022"
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/protein_id="AAB89707.1"
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Dorner,F., Scheiflinger,F. and Falkner,F
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis Bacillus/Clostridium group; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (14-NOV-1996) Seror
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seror, S.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seror, S.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                degrees position encoding Microbiology 143 (Pt 10),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (bases 17288 to 43091)
Roche, B., Autret, S., Levi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Med
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 43091 to 53533)
Medina, N., Vannier, F., Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seror,S.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subtilis chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      edina, N., Levine, A., Roche, B., Vannier, F. and Seror, S.J. 17 kb nucleotide sequence downstream of addAB of the Bacillus
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                                                                                                                                                                                                                                                                                                                            /translation="WTYPHQEVTQIFTKQSVSEIKRREYEDEYSGRAPVKPADGSIL
YRRPAFMMKKGLTAAEKGTAMHTVMQHIPLSHVPSIEEAEQYTHRLYEKELLTGEGKD
AIDLEEIVQFHTEIGGGLIGAKWKDREIPFSIALFAKEITPDAHEADEPLLVQGIIC
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QAFEHMTSRFRTDAVKIAASHIYVAGGNQTDSERPIEVGGAYTVAAESLPADAALRCA
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                                                                                                                                                                                                                                                                          described: one
                                                                                                                                                                                                                                                                                                                  GCALYFFDGGHILTL"
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                                                                                                                                                                                                         /protein_id="CAA70669.1"
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                         'db_xref="SPTREMBL:006712"
                                                                                                     'note≐"putative"
                                                                                                                                                                                /db_xref="SPTREMBL:006711"
/translation="MRILHTADWHLGKTLEGRSRLSEQADVLDELNTIVKDEQIDAIV
                                                                                                                                                                                                                                    /product="SbcD"
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                                                                                                                                                                                                                                                                      /note="difference with the nucleotide sequence
lescribed: one more G at position 1332"
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                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAA70668.1"
/db_xref="GI:2145362"
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NTGDFLLLNNAVNATNYIDDDVNDQDMVGNG"
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MDSSLNMFKEAFQNQSVDEAEKWQQAIEEKDRAAEECEKRIEKSIAFLAEHEAQKEKL
RESGHRLEREKLELHYAAERIKSVIADYEHELGDYAKGDSIPIQLRSVQQDLKLLKEK
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RGONROTELKOOLKSLOVTSDERKSCOQAAEWALRIROTEEQIKEKEKRSEELMLVLO
KMMEEKNTILVOKTEASENNIIQAYEAVOTVYHLVCETERSLTEMTEEARKSOETHLD
REKARVALLTKELAOKLTAGKPCPVCGSTDHDPSASVHETYEADSHLEEDIKRTDVLL
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KGAERRHMLQRLFNLEQYGDRLVKKLRRQAQEANARKNEMLAEQSGLGEASSEAVEQA
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                                                                                                                                                               complement(6343.
                                                                                                                                                                                                                                                                         /protein_id="CAA70675.1".
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'db_xref="GI:2145370"
                                                                                                                 codon_start=]
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IPADELEKMKTGIDQFMDKLNKMLQT"
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DEFINITION
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                         634 GCACTATTGCCCGTTAGCAAATCAGTTGAGCTGAGCAGGAGGATAGAAAACTCAAAGCTT 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               514 ATGGATTATACACCCTCCTACGTGGCAATGGACACGTACAGAACTCTAACGAAAGTGAAT 573
                                                                                                                                                                                                                                                                                                                                     694 GTGATCATCCCAAACTCGGGGCATTGCGTAATGCTTGAGAGTCCAAGTGAGGTTAATAGA 753
                                                                                                                                                                                                                                                  GCAATGGACGAATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCAGAAAGGAACTTGCTGCAATCAAGGTGCCGACGCTGATCCTGCACGGGAGAAAGGAT
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299109.1 GI:26
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/note="putative"
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/note="putative"
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/note="putative"
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ESLIIGPFAPLAPE"
           GI:2633260
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/db_xref="GI:2145373"
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47.5%;
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6 of 21): from 999501 to
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Bacillus subtilis

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MEDLINE
REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur, Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purnelle, B., Rapoport, G., Rey, M., Reynolds, S., Rieger, M., Rivolta, C., Rocha, E., Roche, B., Rose, M., Saddie, Y., Sato, T., Scanlan, E., Schleich, S., Schroeter, R., Scoffone, F., Sekiguchi, J., Secory, S. J., Serror, P., Shin, B. S., Soldo, B., Sorokin, A., Seror, S. J., Serror, P., Shin, B. S., Soldo, B., Sorokin, A., Tacconi, E., Takagi, T., Takahashi, H., Takemaru, K., Takeuchi, M., Tamakoshi, A., Tanaka, T., Terpstra, P., Tognoni, A., Takeuchi, M., Tamakoshi, A., Vandenbol, M., Vannier, F., Vassarotti, A., Vinters, P., Wipat, A., Yamamoto, H., Weitzenegger, T., Winters, P., Wipat, A., Yamamoto, H., Yamane, K., Yasumoto, K., Yata, K., Yoshikawa, H., and Tanaha, K., Yoshikawa, H., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The complete genome sequence of the gram-positive bacterium Bacillus subtilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41,
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369. .1721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aminotransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Bacillus subtilis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: +33 (0)1 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="glpK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="glycerol uptake facilitator"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
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                                                                                                                                                            'db_xref="SWISS-PROT:P18158"
                                                                                                                                                                                                'db_xref="GI:2633265"
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                                                                                                                                                                                                                                                                                                                                                                                    'function="glycerol utilization"
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                                                                                                 GCAATGGACGAATTC 768
                                                                                                                                                                                                                                                              GTGATCATCCCAAACTCGGGGCATTGCGTAATGCTTGAGAGTCCAAGTGAGGTTAATAGA 753
                                                                                                                                                                                                                                                                                                                                               AGAATTGCGCCGTTTGATTTTGCGAAAGAATTGAAGCGCGGCATCAAACAGTCGGAATTG 169736
                                                                                                                                                                                                                                                                                                                                                                                                                               GCACTATTGCCCGTTAGCAAATCAGTTGAGCTGAGCAGGAGGATAGAAAACTCAAAGCTT 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTGAAAATATCTTGGAGAAAATAGACTGTCCAACACTGATTATCGTTGGAGAAGAGGAT 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGCTGGAGGCTTCCTCCTACGGGACGATCCACTCGGGCATCGCATTAAGAGACGAAGAT 169616
                                                                                                                                                                              GTTCCGTTTGCAAACAGCGGGCACGGAGCATTTTATGAGGAAAAAGAGAAGATCAACAGT 169796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCAGAAAGGAACTTGCTGCAATCAAGGTGCCGACGCTGATCCTGCACGGGAGAAAGGAT 169676
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/translation="MSKTRMEKLKTLKTIAETLNOGHDIKATLDEVLKELLSITNLQS
/translation="MSKTRMEKLKTLKTIAETLNOGHDIKATLDEVLKELLSITNLQS
GWIFFLIEEDGSYTLAAANXLPPALSTRKEKVLMCEGECYCLTKFNNGGLRKAANIMNCK
RIESAENLHCFOTEGITHHATVELEDGDRRFGLLNVAAAGKTMEDEEELHILLESVAFQ
IGTAIQRMRLSEYQQKNALLMERNRLAQELHDSVNQMLFSVSLTAKAAKTLTKDENLQ
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GTGGMRGEIGAGTNRMMIYTVBRASAGFARYISKQGEEAKKGFVIPYSHARSPEFA
MEARFLATGGIQTYVFDELRETPELGFAVRGLNAYGGVVVTASHNPPESHYGYKVYGD
DEGGLPFKEADIVIEQVNAIENELTITVVRYDKVYTEKLTSISVHPELSEEVDVKVVF
TPLHGTANKFVRRGLEALGYKNVTVVKEGELPDSNFSTVTSPNEEHAAFEYAIKLGE
EQNADILIATDPDADRLGIAVKNOGOKYTVLFGOTGALLHYLLSKKKKGGILPDNG
VVLKTIYTSEIGRAVASSFGLDTIDTLTGFKFIGEKIKEYEASGQYTFQFGYEESYGY
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QGAEQIEAILASFRQNPPQKMAGKQVVTAEDYAVSKRTLLTESKEEAIDLPKSNVLKY
FLEDGSWFCLRPSGTEPKVKFYFAVKGSSLEDSEKRLAVLSEDVMKTVDEIVESTAK*
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/protein_id="CAB12770.1"
/db_xref="GI:2633266"
/db_xref="SWISS-PROT:P18159"
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6779. .8476
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6655. .6672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DINWVRTYKDAVIDFMSERFQWDEQAKNKHTENLNKLLHDAVVPLEQ'
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RYGSNVDRVPDRVEALKDEAAKRNIPVHILAEAEYSIEEEMTATPADFFVRRTGRLFF
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6779. .8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAB12771.1"
/db_xref="GI:2633267"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="similar to two-component sensor histidine kinase
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47.58;
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AUTHORS
TITLE
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VERSION
KEYWORDS
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Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McCwan, P., McGurk, A., McKernan, K., Mcheeters, R.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigiilo, J.,
Vassiliev H., Viel, B., Vo. A., Wilson, B., Wilson, B., Wilson, D., Ve, W. J.
* NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (30-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 9, 2000 this sequence version replaced g1:7671347. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., De
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 197196)
Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens chromosome SEQUENCE, 18 unordered p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC068272.2 GI:8389603
                                                                                                                                                                                                                                                                                                                                                                        Chemistry: Dye-terminator Big Dye; 100% of romsembly program: Phrap; version 0.960731 Consensus quality: 185286 bases at least Q40 Consensus quality: 191641 bases at least Q30 Consensus quality: 194150 bases at least Q20 Insert size: 194000; agarose-fp Insert size: 195496; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center clone name: 640_B_6

Center clone name: 640_B_6

Sequenoing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads
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                                                                                                                                                                                                                                                                                            Quality coverage: 4.4 in Q20 bases; Quality coverage: 4.3 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: L9936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: WIBR
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Primates;
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sum-of-contigs agarose-fp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
                                                note="assembly_fragment"
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'note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34428: gap of 100 bp
44805: contig of 10377 bp in length
44905: gap of 100 bp
44907: contig of 9102 bp in length
54107: gap of 100 bp
68486: contig of 14379 bp in length
68586: gap of 100 bp
89801: contig of 12115 bp in length
89901: gap of 100 bp
111726: contig of 21825 bp in length
11826: gap of 100 bp
11826: gap of 100 bp
11826: gap of 100 bp
1182783: contig of 19957 bp in length
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Direct Submission

Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

seqreétégenoscope.cns.fr - Web: www.genoscope.cns.fr)

This STS is part of a random genomic sequencing program of thirteen

yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces

exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces

lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia

angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
                                                                                                                                                                                                                                                    2 (bases 1 to 908)
2 (bases 1 to 908)
5 ouclet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
Bolotiny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Ralogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic Exploration of the Hemiascomycetous Yeasts: 1. A set of
yeast species for molecular evolution studies(1)
FFBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNS078EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pichia angusta
Pichia angusta
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T3 end of clone BBOAA020All of library BBOAA from strain CBS of Pichia angusta, sequence tagged site.

AL433892.1 GI:12217306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             angusta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Dujon, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blandin, G., Llorente, B., Malpertuy, A., Wincker, P.,
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1 (bases 1 to 908)
                                                                                                                                                                                                                           Genoscope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEBS Lett. 487 (1),
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                                                                                                                                                                                                                                              (bases 1 to 908)
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of clone BB0AA020All
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/note="assembly_fragment"
131884. .149424
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169493. .197196
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 659 GTAAATAGAACTA 671
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                                                           Center project name: H_NH0810H22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97;
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator B1g Dye; 0% of reads
                                                                                                                                  Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                  Submitted (18-MAY-2000)
University School of Med
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                     MO 63108, 0
                                                                                                                                                                                                                                                                  2 (bases 1 to 184346)
Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG 07-JUL-2000 Homo sapiens chromosome 15 clone RP11-810H22, WORKING DRAFT SEQUENCE, 21 unordered pieces.
                                                                                                                 Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                              AC069138.2 GI:8469088
HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                 The sequence of Homo sapiens clone
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/strain="CBS 4732"
/db_xref="taxon:4905"
/clone="BB0AA02A11"
/clone_lib="BB0AA"
/note="end : T3"
                                                                                                                                                                   ----- Genome Center
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228 c
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Pred. No. 5.
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Quality coverage: 4.54 in Q20 bases; agarose-fp Quality coverage: 4.58 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number will be preserved.
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                         /note-"a
                                                      3296.
                                                                                /note="assembly_name:Contig12"
1336. .3195
                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
                                                                                                                                                                                         Location/Qualifiers
                                                                  /note="assembly_name:Contig14"
            'note="assembly_name:Contig16"
                                                                                                                        /clone="RP11-810H22"
                         "assembly_name:Contig15"
.7155
.10123
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gap of unknown
contig of 1860
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gap of unknown leng
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of 8577
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of 7309
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of 6316
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                 247 AGGGAGA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y Match 4.9%;
Local Similarity 56.7%;
                Homo sapiens chromosome 
Unpublished
                                                 1 (bases 1 to 204302)
Birren, B., Linton, L.,
                                                                                                                     Homo sapiens
                                                                                                                                                       AC021439.6 GI:12658110
HTG; HTGS_PHASE1.
                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                       Homo sapiens chromosome 15 clone RP11-484P15 map IN PROGRESS ***, 7 unordered pieces.
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53844 ...63278
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14239. 18620
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10224. .14138
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36111 c 36782 g 54413 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_name:Contig21"
31342. .37657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="assembly_name:Contig19"
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                                                                                                                                                                                                                                           204302 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 74; Length 184346; Pred. No. 8.5;
                                 Nusbaum, C. and Lander, E. ne 15, clone RP11-484P15
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Db 172638 TTTTCAATGAGGCAAATGATGTTGATTTTTACCAATATTGGTGATAGTAACTTTGATCAC 172579
                                                                                                                                           Query Match
Best Local
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                                         TTTGCAGGCAGGAATATGATGTTTGTTGTCGATAACAGAGGTCATGGCAGGTCCGATAAG 186
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Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K.,
Plerre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
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                                                                                                                                           Similarity
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Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                      64930
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Center clone name: 484_P_15
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------ Project Information
Center project name: L5100
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76487 76586: gap of 100 bp

76587 81413: contig of 4827 bp in length

81414 81513: gap of 100 bp

81514 83674: contig of 2161 bp in length

83675 83774: gap of 100 bp

83775 142002: contig of 5828 bp in length
                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                /clone="RP11-484P15"
/clone_lib="RPCI-11 Human Male BAC"
/41100 c 39057 g 58567 t 648
                                                                                                                                                                                                                                                                                                                                                                               /map="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 8.5;
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                                                                                                             Mismatches
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                                                                                                          0;
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                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-15-1 Kitasato, Sagamihara, Kanagawa 228-855, Japan
(E-mail:hattoriegsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-42-778-9923, Fax:81-42-778-9924)
On Jul 26, 2000 this sequence version replaced gi:8117323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission Massahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Only in DataBase (2000) In press (bases 1 to 172413)
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Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P. Fujlyama,A., Yadd,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 172,413 genomic DNA of 18q22
                                                                                                                                                                                                              preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                     116356
137334
154565
162409
169940
                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: PCR products; 100% of reads chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 169660 bases at least Q40 Consensus quality: 170466 bases at least Q30 Consensus quality: 170710 bases at least Q20 Insert size: 171513; sum-of-contigs Quality coverage: 11.74x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center clone name: RP11-752P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: HumDraft18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: RIKEN Genomic Sciences Center(GSC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------ Project Information
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sapiens DNA, clone:RP11-752P2.
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Primates;
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clone RP11-752P2 map 18q22, WORKING
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hes 112;
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GGCATTTTTCCCTTTCTCTAGAGATTTGTGGAACTTTGAGCATTAGGGAGACGATTTAGA 46087
                                          GTTGTTTGTCGATAACAGAGGTCATGGCAGGTCCGATAAGCCCACTTGGATACGATTTCTA 206
                                                                                         GGAACTTGTTAGGAACTGGAGCAAAGGTGACACTTGTTATATTTTAGCAAAGAGACTGGT
                                                                                                                  AAATATCTATTATGAACTGGTGGATGGACCTGAGCCACCAATTGTCTTGTTCACGGATG
                                                                                                                                                                                                                                                                                                       Similarity
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169940 171161: contty of 1222
171162 171261: gap of 100 k
171262 172413: contty of 1152
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116356 137233: contig of 20878 l
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69939 92558; contig of 22620 bp in length
92559 92658; gap of 100 bp
92659 116255; contig of 23597 bp in length
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41288 41387: gap of 100 bp
41388 69838: contig of 28451 bp in length
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41388. .69838
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30537 c 30035 g 56088 t
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/chromosome="18"
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Pred. No. 9.5;
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye. 100% of reads Consensus quality: 153743 bases at least Q40 Consensus quality: 155127 bases at least Q30 Consensus quality: 155883 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 156403; sum-of-contigs
Insert size: 161992; 1.7% error; agarose-fp
Quality coverage: 4.70x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (20-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coverage: 4.62x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number will be preserved.
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119823 119922: gap of 100 bp
119923 156903: contry of 36981 bp in
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14075 14174: gap of 100 bp
14175 21195: contig of 7021 bp in length
21196 21295: gap of 100 bp
21296 90889: contig of 69594 bp in length
90890 9089: gap of 100 bp
90990 98230: contig of 7241 bp in length
90831 98330: gap of 100 bp
/note="assembly_fragment:00520
clone_end:SP6
                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
                                                                    /clone_lib="RPCI-11.2"
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119822: contig of 21492 bp in length
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Db 122414 ACTTTCAGAAATATTTTTGACATTTAGGTGCTGTATTTTACGTAGATGTAGACTACAGAA 122355
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nes 72; Conserv
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Sequencing vector: M13, 86%
Sequencing vector: plasmid; 14%
Chemistry: Dye-primer ET; 86% of reads
Chemistry: Dye-terminator Big Dye; 14% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 164208 bases at least Q40
Consensus quality: 169036 bases at least Q30
Consensus quality: 169036 bases at least Q20
                                                                                                                                                                                                                                                                                                                                 Submitted (04-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jun 15, 2000 this sequence version replaced gi:7230857.
                                                                                                                                                                                    Center project name: H_NH0074C03
                                                                                                                                                                                                                                                    Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 177839)

Waterston,R.H.
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HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens chromosome
24 unordered pieces.
                                                                                                                                                                                                                               Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence of Homo sapiens clone
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/note="assembly_fragment:00953
clone_end:T7
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90990. .98230
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29074 c 27600 g
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, 2000 this sequence version replaced gi:7230857
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21296. .90889
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/note="assembly_fragment:01365"
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Pred. No. 12;
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9 clone
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DRAFT SEQUENCE,
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Quality coverage: 3.92 in Q20 bases; agarose-fp Quality coverage: 3.84 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                    66334
72895
72995
72995
85601
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98374
112656
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1750
                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
                                                                                                                                                                         Location,
'note="assembly_name:Contig8"
                            note-"assembly_name:Contig7"
                                                                                                        /clone="RP11-74C3"
                                                   note="assembly_name:Contig6"
                                                                                note-
                                          .6069
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1749:
3894:
3994:
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                                                                                                                                                                                   contig of 16931
gap of unknown 1
contig of 29399
                                                                                                                                                                                                                                                   gap of unknown length contig of 14182 bp in gap of unknown length
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gap of unknown length
contig of 2145 bp in length
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contig of 18554 bp in
gap of unknown length
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g of 8614
f unknown
g of 6461
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g of 6243
f unknown
g of 8952
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f unknown
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g of 3137
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g of 2397
f unknown
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of 12606 bp in length
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Local Similarity 53.8%;
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Drosophila melanogaster
                        AC019822.1 GI:6665075
HTG: HTGS_PHASE2.
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/note="assembly_name:Contig28
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112756. .131309
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/note="assembly_name:Contig10"
14637. .17798
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|48441. .177839
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35701. .98373
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38351. .42224
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                                                                             113311 bp melanogaster,
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                                                                                                                                                                                                                                                                                                                              Score 37.4;
Pred. No. 22;
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                                                                             SEQUENCING
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                                                                            HTG 03-JAN-2000
IN PROGRESS ***, in ordered
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RESULT 15
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
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TITLE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52899 ATCGAGCTGATAGACCCATTTTGGCAATTCACGGATGGCTGGACAATCTGGGAACCTTCG 52958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53079 TCATACCGAGGGTGATGAAGGAGTTCGGCTGGTCCAAGGTCTCCTTAATGGGTCATTCCC 53138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCGGCTGATTCCCCTGCTTCCCGACTACATAGGCGTGCTGTGCATCGACCTACCCGGAC 53018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCGGAACAATGATCTCTATGAAGTAC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTTAGATGCGGTTGTTAGGGAGACTGGAGTGGAGAAATTTGTTCTCGTCGGACATTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 174555)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burck,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
          Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome 3 clone RP11-46005, PROGRESS ***, 56 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG;
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For more information on this record e-mail to
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC068636.7 GI:11136659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by the finished sequence as soon as it is available and the accession number will be preserved.
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/db_xref="taxon:7227"
24599 c 24514 g 31131 t
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                                                                                                                                                                                                                                                                                                                                          Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 unordered pieces
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Pred. No. 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 66;
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Garcia, A., Garner, T.,
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o fly@celera.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-NOV-2000
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Louiseged, H., Lozado, R.J., Lu, X., Lucler, A., Lucler, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Michell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Nickerson, E., Nwokenkwo, S., Nguyen, A., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oyado, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Tang, H., Wang, S., Ward, Moore, S., Warren, R., Washington, C., Wall, R., Wang, S., Walliams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (06-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 10, 2000 this sequence version replaced gi:11128133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                    be preserved.
                                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number will
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.99029
Consensus quality: 103029 bases at least Q40
Consensus quality: 127633 bases at least Q30
Consensus quality: 141536 bases at least Q20
Consensus quality: 141536 bases at least Q20
Consensus quality: 141636 bases; at least Q20
Estimated insert size: 140921; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: HAZO Center clone name: RP11-46005
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contig of 5705 bp in 1
gap of unknown length
contig of 5754 bp in 1
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COMMENT

AUTHORS TITLE JOURNAL

TITLE JOURNAL REFERENCE

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68458
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Search completed: June Job time: 24254 sec 2 2001, 20:32:36

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Listing first 45 summaries
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ALIGNMENTS

NAME/KEY: unsure LOCATION: (1)..(1116) OTHER INFORMATION: unsure US-09-739-449-589 Sequence 589, Application US/09739449
GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Statter, Steven C.
TITLE OE INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR TILING DATE: 2000-02-23
SQUID NO 589
LENGTH: 1116
TYPE: DNA
TYPE: DNA Query Match 8.2%; Best Local Similarity 44.9%; Matches 367; Conservative ORGANISM: Agrobacterium FEATURE: 436 CTGGCCCGGGAGCTCGTGGAGTGGGGGGGTACCCGGGTGGTTGTGTTCGACTTCCGGGGCCAC 136 GGGGTGGCTCGGGTGGCTCGGCCGGCGCGCGTAAGAGGCTGCTCCTGGCCGCTGTG 195 361 301 ACCGCGGAGGATGGCTTGGTGGTTCGGGGCCTGGGTGCTGGGCCCCCGGCGCTGGGGCAAC CACCCGGAGAGCTGTCGGCCCGTTGCGCCGGAGGGGCTCACCTACAAAGAGTTCAGCGTG 315 GCTGTCTTGGCGCTTGTTGTCCCGTTGTTGTCCCCGGCTTATGTGGCGTATAGTAGTCTG CCGGTGTTCGTTTTGATGCACGGGTATACTGGGTGCCGCTCGGCGCCCTACATGGCTGTG tumefaciens at all Score 85.4; DB 5; Pred. No. 4e-09; Mismatches 446; Indels n locations Length 1116; 4; Gaps 435 540 375 480 255 600 ۲,

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PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 2506
LENGTH: 1163
TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
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                                                                                                                                                                                                                                                                                          Sequence 2506, Application US/09739449
GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slatter, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens
FILE REFERENCE: 38-10(15490)C
                                                                                                         Query Match
Best Local Sim
Matches 362;
                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
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                                                                                                                  Similarity
                                                                                                         Conservative
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                                                                                                        Score 83; DB 5;
Pred. No. 1.2e-08;
0; Mismatches 558
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US-09-739-449-591
                              PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 591
LENGTH: 974
                                                                                                                                                                                                                 Sequence 591, Application US/09739449 GENERAL INFORMATION:
                                                                                                               APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens
FILE REFERENCE: 38-10(15490)C'
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
ORGANISM: Agrobacterium
                  TYPE: DNA
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US-09-739-449-2277; Sequence 2277, Application US/09739449; GENERAL INFORMATION:
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; LOCATION: (1)..(974)
; OTHER INFORMATION: unsure
US-09-739-449-591
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                                NUMBER OF SEQ ID NOS:
SEQ ID NO 2277
LENGTH: 1204
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Best Local Similarity
Matches 296; Conserv
                                                                                        APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
                                                                   PRIOR APPLICATION NUMBER: US 09/514,000 PRIOR FILING DATE: 2000-02-23
        TYPE: DNA
ORGANISM: Agrobacterium
FEATURE:
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Pred. No. 5e-08;
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APPLICANT: HINKLE, Gregory J.

APPLICANT: Slater, Steven C.

TITLE OF INVENTION: Agrobacterium tumefaciens Ge
FILE REFERENCE: 38-10(15490)C

CURRENT APPLICATION NUMBER: US/09/739,449

CURRENT FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: US 09/514,000

PRIOR FILING DATE: 2000-02-23

NUMBER OF SEQ ID NOS: 13351

SEQ ID NO 1199
                                                                                                                           RESULT 5
US-09-739-449-1199/c
Sequence 1199, Application US/09739449
GENERAL INFORMATION:
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; LOCATION: (1)..(1204)
; OTHER INFORMATION: unsure
US-09-739-449-2277
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RESULT 6
US-09-739-449-2284

Sequence 2284, Application US/09739449

GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
FILE OF INVENTION: Agrobacterium tumefaciens Ger
FILE REFERENCE: 38-10(15490)C

CURRENT APPLICATION NUMBER: US/09/739,449

CURRENT FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: US/09/514,000

PRIOR FILING DATE: 2000-02-23

NUMBER OF SEQ ID NOS: 13351
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ORGANISM: Agrobacterium to
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(782)
OTHER INFORMATION: unsure
US-09-739-449-1199
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; LOCATION: (1)..(1271)
; OTHER INFORMATION: unsure
US-09-739-449-2284
                                                                                                            RESULT
Sequence 2285, Application US/09739449
GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TIFLE OF INVENTION: Agrobacterium tumefaciens Genome
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
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Best Local Similarity
Matches 299; Conserv
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ORGANISM: Agrobacterium
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RESULT 8
US-09-739-449-2273
; Sequence 2273, Application US/09739449
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1125)
; OTHER INFORMATION: unsure at all n locations
US-09-739-449-2285
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Best Local Similarity
Matches 268; Conserv
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PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 2285
LENGTH: 1125
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                                                                                                                                                                                             GGCTTCGGCCCCGCTGGGTGGAGGCGCCTGGATAAGCCGTTGCTGGTGTATGGGCCCC
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pred. No. 1.4e-07;
0; Mismatches 451;
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; NAME/KEY: unsure
; LOCATION: (1)..(990)
; OTHER INFORMATION: unsure
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CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 2273
LENGTH: 990
TENGTH: 990
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Agrobacterium tumefaciens FEATURE:
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                                                               CGGGACCCGCTGGTGACGCGGGACGAGGCGAGCCTGGCGTCCCGTAGCCCCGTGTGGC
                      CGTCTCGTCGAGGTTCCTGGGGCTGGCCACGTGGAGGCCGTGGATGTGCTCGGGCCGGG 977
                                                                                                            GGCTTCGGCCCCGCTGGGAGGGCGCGTGGATAAGCCCGTTGCTGGTGTATGGGCCCC
                                                                                                                                                           GGCGCTGTAGCGATGGTGGAGGGTGCTGGAT
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Pred. No. 2.7e-07;
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US-09-739-449-385
; Sequence 385, Application US/09739449
; GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.

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LENGTH: 919

TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(919)
OTHER INFORMATION: unsure at all n lo
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PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity 41.1%;
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TATGTCTCGGAGCGGTTCCCCGGCCGGCCGGATAATATTGGTGGGGGTTCAGTATGGGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGATGGCTTGGTTCGGGGCTGGGGTGCTGGGCCCCGGGGGCTGGGGGCAACCCGGTG 381
                       CTCGTCGAGGTTCCTGGGGCTGGCCACGTGGAGGCCGTGGATGTGCTCGGGCCGGG
                                             GACCCGCTGGTGACGCGGGACGAGGCGAGGAGCCTGGCGTCCCGTAGCCCGTGTGGCCGT
                                                                                              TTCGGCCCCGCTGGGTGGAGCGCGTGGATAAGCCGTTGCTGGTGGTGTATGGGCCCCGG
                                                                                                                                            CCGTACTATAGGCTCCGGGACGTCATACCCCGGTGGCTGGAGTACAAGACGCCGCTGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294;
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RESULT 10 US-09-739-449-622

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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Seq
FILE REFERRICE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 622
LENGTH: 1150
                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: unsure
; LOCATION: (1)..(1150)
; OTHER INFORMATION: unsure
US-09-739-449-622
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Best Local Similarity 41.7%;
Matches 381; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Agrobacterium tumefaciens EEATURE:
                                                                                                                                                                                                                                           545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 GTGGACACAGGGGTGGCTCGGGTGCCTGGGCTCGGCCGCGGTAAGAGGCTGCTCCTG
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CGGGCGTTGACCTCGGCTTCGGCCCCCGCTGGGGTGGAGCGCGTGGATAAGCCGTTGCTGG
                                                                                                                                  CGGTGGCTGCTGATAGCCCCGTACTATAGGCTCCGGGACGTCATACCCCGGTGGCTGGAGT
                                                                                                                                                                                                                                          ACATGGCTGTGCTGGCCCGGGAGCTCGTGGAGTGGGGGTACCCGGTGGTTGTTCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTAGTCTGCACCCGGAGAGCTGTCGGCCCGTTGCGCCGGAGGGGGCTCACCTACAAAGAG
                                                   GGTTCAGTATGGGCGGCGCTGTAGCGATCGTGGAGGGTGCTGGGGACCCGGGGTCTACG
                                                                                                                                                                                                               GCCGCTGTGGCTGTTGGCGCTTGTTGTGTCCGTTGTTGTCCCGGCTTATGTGGCGTAT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACAAGACGCCGCTGCCGGGCTGGGTGGTGTGCTGCCGGGTTCTACGGGAGGCTGATGG
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Pred. No. 2.9e-07;
0; Mismatches 531;
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NUMBER OF SEQ ID NOS: 13351

SEQ ID NO 2276

LENGTH: 1089

TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
FEATURE:
NAME/KEY: unsure
LOCATION: (1). (1089)
OTHER INFORMATION: unsure at all n locations
US-09-739-449-2276
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US-09-739-449-2276
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                    Matches
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APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(13490)C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
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                                                                                                                                                                                                                                                                     189 CGCTGTGGCTGTTTGGCGCTTGTTGTCCGTTGTTGTCCCGGCTTATGTGGCGTATAG
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity hes 311; Conserv
                                                                                                                                    GGGCAACCCGGTGTTCGTTTTGATGCACGGGTATACTGGGTGCCGCTCGGCGCCCTACAT
                                                                                                                                                                           CAGCGTGACCGCGGAGGATGGCTTGGTGGTTCCGGGCTGCTGGGCCCCGGCGCCTGG
GGGCCACGGGGAGAGCGGGGGCTCGACGACGATTGGGCCCCGGGAGGTGCTGGATGCCCG
                                                    GGCTGTGCTGGCCCGGGGAGCTCGTGGAGTGGGGGGTACCCGGTGGTTGTTCTGACTTCCG
                                                                                                        cgggggggggggc 921
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                                                                                                                                                                                                                                                                                                                                                                                Score 75.2; DB 5;
Pred. No. 4.7e-07;
0; Mismatches 538;
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; ORGANISM: Agrobacterium tumefaciens FEATURE: FEATURE: NAME/KEY: unsure ; LOCATION: (1)..(827) ; OTHER INFORMATION: unsure at all n US-09-739-449-1144
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US-09-739-449-1144
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NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 1144
LENGTH: 827
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                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
                                                                                                                                                                     Matches
                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                       274 CCCGTTGCGCCGGAGGGCTCACCTACAAAGAGTTCAGCGTGACCGCGGAGGATGGCTTG
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394 CACGGGTATACTGGGTGCCGCTCGGCGCCCTACATGGCTGTGCTGGCCCGGGAGCTCGTG
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                                                                                                                                                                    Local Similarity
nes 265; Conserv
                                                                       GTGGTTCGGGGCCTGGGGCCCCCGGCGCTGGGGGCAACCCGGTGTTCGTTTTGATG
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                                                       CCCGTGTGGCCGTCTCGTCGAGGTTCCTGGGGCCTGGCCACGTGGAGGCCGTGGATGTGCT
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                                                                                                                                                                    Conservative
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                                                                                                                                                                               7.2%;
                                                                                                                                                                    0,
                                                                                                                                                                  Score 74.8; DB 5;
Pred. No. 5.7e-07;
0; Mismatches 502;
                                                                                                                                                                                                                                                     locations
                                                                                                                                                                                              Length
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Gereile Reference: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 2507
LENGTH: 968
TYPE: DNA
                                                                                                                        ; FEATURE:

, NAME/KEY: unsure

; LOCATION: (1)..(968)

; OTHER INFORMATION: unsure

US-09-739-449-2507
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US-09-739-449-2507
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                                                        Matches
                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       Sequence 2507, Application US/09739449 GENERAL INFORMATION:
                                                                                                                                                                                           ORGANISM: Agrobacterium
               319 GCGGAGGATGGCTTGGTGGTTCGGGGCTTGGGTGCTGGGGCCCCCGGCCCTGGGGGCAACCCG 378
  303
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CTGATAGAGCTGGCGCACGAGGAGTGCCCTCCGGGGGCCCGGTGGCTG 1040
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                                                        285;
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                                                       Conservative
                                                                  7.18;
                                                                                                                                                                                              tumefaciens
                                                                                                                                     at all
                                                    Score 73.8; DB 5; Length 9 Pred. No. 9e-07; 0; Mismatches 358; Indels
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                                                                                                            ; OTHER INFORMATION: unsure at all n locations US-09-739-449-1003
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US-09-739-449-1003
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                                                                                                                                                                                                                                                                               Sequence 1003, Application US/09739449
GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
CURRENT FILING DATE: 2000-12-19
                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 1003
LENGTH: 925
                                   Query Match
Best Local Similarity
Matches 267; Conserv
                                                                                                                                      FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(925)
                                                                                                                                                                              ORGANISM: Agrobacterium tumefaciens
                                                                                                                                                                                                   TYPE: DNA
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                                      Conservative
                                                  6.9%;
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                                                  Score 72; DB 5;
Pred. No. 2.1e-06;
                                      Mismatches
                                      544;
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                                                                Length 925
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
FITLE OF INVENTION: Agrobacterium tumefaciens Genome Sec
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US/09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 974
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US-09-739-449-974
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                               FEATURE:
                                                   ORGANISM: Agrobacterium tumefaciens
                                                                                   LENGTH: 1171
TYPE: DNA
NAME/KEY: unsure
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; OTHER INFORMATION: unsure at all n
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Search completed: June 3, 2001, 00:58:56 Job time: 16955 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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221: gb_est50: *
222: gb_est53: *
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240: gb_est60: *
250: gb_est60: *
260: gb_est60: *
270: gb_est60: *
280:
| Query Match 7.7%; Score 80.6; DB 161; Best Local Similarity 39.1%; Pred. No. 3.2e-08; Matches 281; Conservative 0; Mismatches 438; | rce | TITLE Functional Genomics of Plant Stress Tolerance JOURNAL Unpublished (2000) COMMENT Contact: Michalowski.C.B. University of Arizona Bio Sciences West room 513, Tucson, AZ 85721, Tel: 520-621-7982 Fax: 520-621-1697 Email: cbm@u.arizona.edu An open reading frame exists. FEATURES FEATURES | Eukaryota; Viridiplantae; Embryophyta; Eukaryota; Viridiplantae; Embryophyta; Magnoliophyta; eudicotyledons; core euc Caryophyllales; Aizoaceae; Mesembryanth CE 1 (bases 1 to 1006) RS Bohnert, H. J., Borchert, C., Brazille, S., H., Kawasaki, S., McCollough, A., Michal Scara, G., Wheeler, M. and Zepeda, G.R. | BE034822 1006 ML04H02 ML Mesemb BE034822 BE034822,1 GI:83 EST. Common ice plant. | ALIGNMENTS | 70.4 6.8 1122
70.2 6.7 766
70.2 6.7 1186
70.6 7 780
70 6.7 888
70 6.7 892
69.8 6.7 1135 | 71.8 6.9 741 217 71.6 6.9 1016 231 71.6.8 764 217 70.6 6.8 915 217 70.6 6.8 1325 145 70.4 6.8 740 217 70.4 6.8 924 167 70.4 6.8 965 211 | 8 7.1 1035 145 BB2 6 7.1 1035 145 BB2 6 7.1 1035 213 AZ2 7.0 872 217 AZ2 7.0 1291 145 BB2 7.0 1290 1290 BB2 7.0 1290 1290 BB2 7.0 1280 7.0 BB2 7.0 BB2 7.0 BB2 7.0 BB2 7.0 BB2 7.0 BB2 7.0 BB2 7.0 BB2 7.0 BB2 7.0 BB2 7.0 BB2 7.0 BB2 7.0 BB2 7.0 AZ2 7.0 1039 146 BB2 7.0 1039 146 B | 73.8 7.1 821 213 AQ8
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Indels 0; Gaps 0; | llinum"
ng seedpods"
others | ce
L, USA | Tracheophyta; Spermatophyta; licots; Caryophyllidae; nemum. Brooks,J., Eaton,M., Ferrea owski,C.B., Palacio,C., | 07-JUN-2000
NA 5', mRNA sequence. | | SP_
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HVS | AZ194927 SP_1029 A A1249930 Tetraodon AZ199325 SP_1039 A AZ195437 SP_1030 A BP256543 HVSMEf001 AZ195718 SP_1030 B BE455162 HVSMEfb009 AC748706 Hz 5540 A | MEF00
4832_
1029_
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37183
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050H1
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1002_
1006_ | HS_48 |
| TITLE Development of a genetically and physically anchored EST resource for barley genomics JOURNAL Unpublished (2000) COMMENT Contact: Wing RA Clemson University Genomics Institute | SOURCE barley. SOURCE CORGANISM Hordeum vulgare ORGANISM Hordeum vulgare Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum. 1 (bases 1 to 1050) AUTHORS: Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu , Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo , T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and | N 00 62 | Oy 919 CGFCTCGFCGAGGTTCCCFGGGCCACGTGGAGGCCGTGGATGTGCTCGGGCCGGCC 978 Do | 799 GCTTCGGCCCGCTGGGGTGGAGCGCGTGGATAAGCCGTTGCTGGTGTGTATGGGCCC | Qy 739 CCGGGCTGGGTGGTGTGCCGGGTTCTACGGGAGGCTGATGGCGGGGGGTTGACCTC 798 | Qy 619 GGCGCTGTAGCGATCGTGGAGGGTGCTGGGGACCCCGCGGGTCTACGCGGTGGCTGAT 678 | Qy 499 GAGACCGGGGCTCGACGACGACGACGACGACGACGAGGTGCTGGATGCCCCGGGCTGTGGTG 558 1 1 1 1 1 1 1 1 1 1 | GGGGGNGNGGGTTTGNGGGNGGGGGGGGNGNGGGGGGGG | |

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              CGCTACGCAGACATGCTGATAGAGCTGGCGCACGAGGAGTGCCCTCCGGGGGCCGGTGG 1037
                                       CGTCTCGTCGAGGTTCCTGGGGCTGGCCCACGTGGAGGCCGTGGATGTGCTCGGGCCGGGC 978
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100 Jordan Hall, Cl
Tel: 864 656 7288
Fax: 864 656 4293
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Seq primer: ANTTAACCCTACTAAAGGG
High quality sequence stop: 926.
High quality sequence stop: 926.
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/clone_lib="Hordeum vulgare seedling green leaf EST library HVcDNA0004 (Erysiphe infected & control)"
/tissue_type="seedling green leaf"
/tissue_type="seedling green leaf"
/lab_host="TyC121"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhc 825 c 0 g 38 t 187 others
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/cultivar="CI16155 (Mla13)"
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 GGAGAGCTGTCGGCCCGTTGCGCCGGAGGGGCTCACCTACAAAGAGTTCAGCGTGACCGC
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start ???
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 1299)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Ram,
T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF267681 1299 bp mRNA EST 17-NOV-2000 HV_CEA0018J13f Hordeum vulgare seedling green leaf EST library HVcDNA0004 (Erysiphe infected & control) Hordeum vulgare cDNA (**PV_CEA0018J13f, mRNA sequence.**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 864 656 7288 Fax: 864 656 4293
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100 Jordan Hall, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for barley genomics 
Unpublished (2000)
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/cultivar="CI16155 (Mla13)"
/db_xref="taxon:4513"
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Pred. No. 8.2e-08;
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Fax: (206) 616-3887

Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.edu web Server: http://www.htsc.washington.edu plate: 3183 row: P column: 1

Seq primer: M13 Reverse
                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 884)
Cmith K Swartzell, S., Holzman, T.,
                                                                                                                                                                                                                                                                                                                                                       AQ782679.1 GI:5685639 GSS.
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                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.
                                                                                                                                                     Contact: Mahairas GG, Wallace
                                                                                                                                                                      99380589
                                                                                                                                                                                                               Sequence-tagged connectors: A sequence approach to
                                                                                                                                                                                                                                           Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
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RESULT BE421615

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DEFINITION LOCUS

BE421615 1504 bp mRNA ES HWM011cH.01r ITEC HWM Barley Leaf Library clone HWM011cH.01, mRNA sequence.

Hordeum

24-JUL-2000 vulgáre cDN

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/db_xref="taxon:9606"
/clone="Plate=3183 Col=1
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Location/Qualifiers
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/sex="male"
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Pred. No. 1.5e-07;
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GGCGCTGTAGCGATCGTGGAGGGTGCTGGGGACCCGCGGGTCTACGCGGTGGCTGCTGAT 678
                                                                                                                                                                             GGCTATGTCTCGGAGCGGTTCCCCCGGCCGCCGGATAATATTGGTGGGGTTCAGTATGGGC
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                                                                  AGCCCGTACTATAGGCTCCGGGACGTCATACCCCGGTGGCTGGAGTACAAGACGCCGCTG 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Clouti, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Laro, G.R., Lin, J.J., McGuire, P., Oghhara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.
International Triticeae EST, Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hordeum vulgare
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae;
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BE421615.1 GI:9419458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        International Triticeae EST Cooperative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: wenzel@mm.pbz.agrar.tu-muenchen.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wenzel G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Munchen, Lehrstuhl fur Pflanzenbau und Pflanzenzuchtung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Hordeum vulgare"
/cultivar="Barke"
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Pred. No. 1.7e-07;
0; Mismatches 454;
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Qy

261 GGAGAGCTGTCGGCCCGTTGCGCCCGGAGGGGCTCACCTACAAAGAGTTCAGCGTGACCGC 320

Query Match Best Local Similarity Matches 300; Conserv

Conservative

0;

Indels Length

0; Gaps

0

7.4%;
38.5%;

Score 77.4; DB 146; Pred. No. 1.7e-07; Mismatches 480;

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                                                                                                                                                                                                                                                                                   Clemson University
100 Jordan Hall, Cl
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hordeum vulgare
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; (
Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF267199 1551 bp mRNA EST 17-NOV-2000 HV_CEa0017D19f Hordeum vulgare seedling green leaf EST library HVcDNA0004 (Erysiphe infected & control) Hordeum vulgare cDNA clone
                                                                                                                                                                                                                Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 533
High quality sequence stop: 950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 1551)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., F
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palme
,Y., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W.,
                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
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              29
          /tissue_type="seedling green
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39 c 763 g 67 t
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/clone_lib="Hordeum vulgare seedling glibrary HVcDNA0004 (Erysiphe infected
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3 others
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Clemson University
Clemson University
                                                                                            Gossypium arboreum Gossypium arboreum Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                               AW727475 1049 bp mRNA EST 16-NO
GA_Ea0012I02 Gossypium arboreum 7-10 dpa fiber library
arboreum cDNA clone GA_Ea0012I02, mRNA sequence.
                                     Malvales; Malvaceae; Gosspium.

1 (bases 1 to 1049)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T.,
D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, developm of the cotton fiber
                                                                                                                                       Gossypium
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                               Unpublished (2000)
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                                                                       Simmons, J.,
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Query Match
Best Local Similarity 45.4
Matches 313; Conservative
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                                   TTCCTGGGGCTGGCCACGTGGAGGCCGTGG 961
                                                                                    TGACGCGGGACGAGGCGAGGAGCCTGGCGTCCCGTAGCCCGTGTGGCCGTCTCGACG
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                                                                                                                                 CGGCCGGCCGGCCGGGGGGGGGGGGGGGGGTCGGGG--CGGGGGCGCGCGGGG
                                                                                                                                                            CTGGGGTGGAGCGCGTGGATAAGCCGTTGCTGGTGTATGGGCCCCGGGACCCGCTGG
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                                                                     GGCTCCGGGACGTCATACCCCGGTGGCTGGAGTACAAGACGCCGCTGCCGGGCTGGGTGG
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Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
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quality sequence stop:
Location/Qualifiers
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/clone="GA_Ea0012102"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
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Pred. No. 3.4e-07;
0; Mismatches 375
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AW731157 16-NOV-2000 MRNA sequence.
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
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An integrated analysis of the genetics, development, of the cotton fiber
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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Gossypium arboreum
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864 656 4293
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Location/Qualifiers
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/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/clone_tib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
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/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
    642 c    299 g    74 t    9 others
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/strain="AKA"
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Best Local
    Best Local Similarity Matches 303; Conserv
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                                                                                                                                                                                                                                                                                                       Clemson University Genomics Institute Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
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AW727527 MRNA Sequence.
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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    Conservative
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                                                                                         /lab_host="E. coli"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
/ 726 c 192 g 64 t 8 others
                                                                                                                                                   /db_xref="taxon:29729"
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/strain="AKA"
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Score 75.6; DB 119;
Pred. No. 4.2e-07;
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                                                                                         Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

1 (bases 1 to 12/7)
Wing.R.A., Frisch.D., Yu.Y., Main.D., Rambo,T., Simmons,J., Henry, D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                               GA
                                                                                                                                                                                       Gossypium arboreum
                                Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
                                                                                                                                                                                                                  EST
                                                                                                                                                                                                                                                  BF280850 1277 bp mRNA EST 17-NOV GA_Eb0041L16 Gossypium arboreum 7-10 dpa fiber library arboreum cDNA clone GA_Eb0041L16, mRNA sequence.
                                                                                                                                                                                                    Gossypium arboreum.
                                                                               Unpublished (2000)
        864 656 7288
864 656 4293
rwing@clemson.edu
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                                 29634, USA
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GGGCAGGGGGGGTGGGGGGAGGA
                    GCCCTCCGGGGGGCCGGTGGCTGA
                                                                                                           CGTCCCGTAGCCCGTGTGGCCGTCTCGTCGAGGTTCCTGGGGGCTGGCCACGTGGAGGCCG
                                                                                                                                                       TGCTGGTGGTGTATGGGCCCCCGGGACCCCGCTGGTGACGCGGGACGAGGCGAGGCCTGG
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88 c 1022 g 51 t 10 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:29729"
/clone="6A_EB0041L16"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-1
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                                                                        CGCGTGGTCCGCTTCTKGTGTGGGGGGGGGGGGGGGTTGCTKCTCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
Submitted (29-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genome survey sequence SP6 end of BAC BACN04P24 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL099352
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN04P24"
/note="end : SP6"
a 439 c 135 g
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/ɒlasmid="ɒBeloBAC11"
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Pred. No. 5.1e-07;
3; Mismatches 371;
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Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                          California Institute of Technology Pasadena California 91125, USA
                                                                                                                                                                                                                                                                                                                                                                                    Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS
                                                                                                                                                                      Seq primer: T7
Class: BAC end
                                                                                                                                                                                                   Email: acameron@caltech.edu
Plate: 1038 row: N column
                                                                                                                                                                                                                               Tel: (626) 395-8421 Fax: (626) 793-3047
                                                                                                                                                                                                                                                                                   Contact: Cameron, RA, David
Division of Biology 156-29
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Location/Qualifiers
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                             DH10B"
                                                    /clone="Plate=1038 Col=6 Row=N"
/clone_lib="Strongylocentrotus purpuratus,
urchin, sperm genomic BAC library"
                                                                                                  /db_xref="taxon:7
                                         /note="Organ: sperm;
                                                                                                  /organism="Strongylocentrotus
/db_xref="taxon:7668"
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                                                                                                                                                                                                                                                                    GGACCCGCTGGTGACGCGGGACGAGGCGAGGAGCCTGGCGTCCCGTAGCCCGTGTGGCCG
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                                                                                                                                           AQ788449 877 bp DNA GSS 03-AUG-1999
HS_3130_A1_D11_T7C CIT Approved Human Genomic Sperm Library D
sapiens genomic clone Plate=3130 Co1=21 Row=G, DNA sequence.
AQ788449
scanning the human genome Proc. Natl. Acad. Sci. U. 99380589
                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 877)
                                                                                                    Homo sapiens
                           Sequence-tagged connectors: A sequence approach to
                                                  Mahairas,G.G., Wallace,J.C.,
Keller,A., Shaker,R., Furlon
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                                        lood, L.
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                                                Furlong, J., Youn
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         P.
         96
                                                 Young, J.,
         (17),
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                                                 Swartzell,S.,
g,J., Zhao,S.,
          9739-9744
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                                                            Holzman, T.,
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                               CGTCTCGTCGAGGTTCCTGGGGCTGGCCACGTGGAGGCCGTGGATGTGCTCGGGCCGG 976
                                                                 GGCGCTGTAGCGATCGTGGAGGGTGCTGGGGGACCCCGCGGGTCTACGCGGTGGCTGCTGAT
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                                                                                                                                   GGCTTCGGCCCCGCTGGGAGCGCGTGGATAAGCCGTTGCTGGTGTATGGGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3130 row: G column: 21
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E-Coli DH10B"
a 603 c 32 g 84 t 117 others
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/db_xref="taxon:9606"
/clone="plate=3130 Col=21 Row=G"
/clone_lib="CIT Approved Human Genomic Sperm
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38.0%;
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Pred. No. 6.3e-07;
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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__Ea0012010 Gossypium arboreum 7-10 dpa fiber library Gossypium
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: 762 c 97 g 43 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:29729"
/clone="GA_Ex0012010"
/clone_11b="Gossypium arboreum
/tissue_type="Fibers isolated f
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Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T.,
D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, developm of the cotton fiber
                                                                                                                                                                                                                                Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                          Clemson University Genomics Institute Clemson University
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                                                                                                                                                                                                                                                                                                        Contact: Wing RA
                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
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Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
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                                                                                                                                                                                                                Email: rwing@clemson.edu
                                                                                                                                                                                                                                                              100 Jordan Hall,
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                                                        dpa"
          /lab_host="E. coli"
/note="Vector: pBK-CMV;
828 c 293 g
                                                                    /db_xref="taxon:29729"
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/clone_lib="Gossypium arboreum
/tissue_type="Fibers isolated 1
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/strain="AKA"
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                                               TGTGGCCGTCTCGTCGAGGTTCCTGGGGCTGGCCCACGTGGAGGCCGTGGATGTGCTCGGG 972
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Maximum DB seq length: 2000000000
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1: /cgn2_6/ptodata/2/pna/US

2: /cgn2_6/ptodata/2/pna/US

3: /cgn2_6/ptodata/2/pna/US

4: /cgn2_6/ptodata/2/pna/US

5: /cgn2_6/ptodata/2/pna/US

6: /cgn2_6/ptodata/2/pna/US

6: /cgn2_6/ptodata/2/pna/US

8: /cgn2_6/ptodata/2/pna/US

8: /cgn2_6/ptodata/2/pna/US

9: /cgn2_6/ptodata/2/pna/US
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1446.900 Million cell updates/sec
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1041
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'cgn2_6/ptodata/2/pna/US0906C_COMB.seq: *
'cgn2_6/ptodata/2/pna/US0006_COMB.seq: *
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/2/pna/US080_COMB.seq:*
/cgn2_6/ptodata/2/pna/US081_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US6015_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6016_COMB.seq:*
/cgn2_6/ptodata/2/pna/US6016_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US6026_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US6013_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US6027_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	c c c 2222222222323232323232323232323232		Result No. 1 1 4 5 5 6 6 7 7 7 7
72.8 72.8 72.8 72.8 71.6 71.6	1	66667777887	Score 1041 85.4 84.6 83.8 83.8 83.8 79.8
6.6.6.6.7.0.0 6.9.9.9.00	177777777777777 500000000000000000000000	7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,	Query Match 100.0 8.2 8.1 8.0 7.7 7.7 7.7
1449 1449 1449 1449 600 600 600 600	1150 728 1089 1089 827 857 661 661 1000 1218 1749	947 865 1271 1127 1527 1527 1475 1475 770 990	Length 1041 1116 868 942 1163 974 1204 717 782
22 28 48 48 50 22 22 29 117 118 25 25 25	529 529 529 527 527 527 527	144 188 29 29 18 19 19 22 22 22 29 29 29 29	DB 17 29 22 28 29 29 29 29 29 29
US-04-209-830-516/8 US-09-565-240-24459 US-09-703-708-4024 US-60-164-320-4024 US-60-183-791-4024 US-09-553-094-5304 US-09-533-094-5304 US-09-304-517A-246031 US-09-304-517A-246031 US-09-440-687-8289 US-09-654-617-61513 US-09-654-016-61513 US-09-664-016-61513	-09-739-449-622 -09-739-449-622 -60-209-830-2548 -09-739-449-1124 -09-698-013-3579 -09-698-013-2507 -09-53-094-1003 -09-553-094-2507 -09-313-292-2475 -09-313-292-2475 -09-313-292-2475	-60-129-391-160 -60-129-391-160 -93-40-22809-739-449-228 -09-739-449-228 -09-524-038-202 -09-524-038-202 -09-575-004-42 -09-565-306-687 -09-739-449-227 -09-739-449-2778 -09-553-094-100	ID US-09-382-242-24 US-09-739-449-589 US-09-765-240-24958 US-09-702-134-43124 US-09-739-449-2506 US-09-739-449-227 US-09-739-449-2316 US-09-739-449-1199
Sequence 24959, A Sequence 24959, A Sequence 4024, Ap Sequence 4024, Ap Sequence 4024, Ap Sequence 5304, Ap Sequence 5304, Ap Sequence 246031, Sequence 8289, Ap Sequence 61513, A Sequence 61513, A Sequence 61513, A Sequence 339097, A	385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385, App 385	160, F 579, F 2284, 2285, 202, F 202, F 42, Ap 68748, 7782, 10051,	Description Sequence 24, Appl Sequence 589, App Sequence 43124, A Sequence 2506, Ap Sequence 591, App Sequence 591, App Sequence 5316, Ap Sequence 5316, Ap Sequence 5316, Ap

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                                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1041; Conservative 0,
                                                                                                                                                                                                                                                                                                                   TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS:
LENGTH: 1041 NUCLEOTIDES
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 INCH DISKETTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF
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 181
                                                121
                        181
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ZIP: 920
                                                                                               61
                                                                                                                                                                                                                                                                                  TYPE: NUCLEIC ACID STRANDEDNESS: SINGLE TOPOLOGY: LINEAR
                                                                                                                      61
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LENGTH: NUCLEIC ACID
SING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
SOFTWARE: WORD PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                            TTTGCATTTTACTGGTTTCTGGCCGTGTATACGTGGTTACCCGGTGTCCTAGTCCGGGGC 120
CTCCTGGCCGCTGTGGCTGTTGTGGCGCTTGTTGTCCCGGCTTATGTG
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4225 EXECUTIVE SQUARE, STE 1400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYSTEM: MS-DOS
WORD PERFECT 6.0
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REID, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PS/2
                                                                                                                                                                                                                                                                      GENOMIC DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anthony
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                                                                                                                                                                                              Score 1041; DB 17;
Pred. No. 2.6e-188;
); Mismatches 0;
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                                                                                                                                                                                                                      Length 1041;
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefacien
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 589
LENGTH: 1116
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                                                                                                                                                                                    Sequence 589, Application US/09739449 GENERAL INFORMATION:
TYPE: DNA
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US-09-565-240-24958; Sequence 24958, Application; GENERAL INFORMATION:
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Best Local Similarity
Matches 367; Conserv
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FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(1116)
OTHER INFORMATION: unsure
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nilarity 44.9%;
Conservative
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Pred. No. 9.7e-07;
0; Mismatches 446;
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US/09565240

RESULT 4
US-09-702-134-43124
Sequence 43124, Application
GENERAL INFORMATION:

US/09702134

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SEQ ID NO 24958
LENGTH: 868
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3106-115-Q1-K1-D4.
US-09-565-240-24958
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Matches
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CURRENT FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS:
1EQ ID NO 3/050
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TITLE OF INVENTION: NO
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21
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mes 297; Conserv
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                                                       CGTCTCGTCGAGGTTCCTGGGGCTGGCCACGTGGAGGCCGTGGATGTGCTCGGGCCGGGC 978
                                                                                      CGGGACCCGCTGGTGACGCGGACGAGCGAGGAGCCTGGCGTCCCGTAGCCCGTGTGGC 918
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                                           AGCCCGTACTATAGGCTCCGGGACGTCATACCCCGGTGGCTGGAGTACAAGACGCCGCTG
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La Rosa, Thomas J.
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Pred. No. 1.4e-06;
0; Mismatches 365;
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CURRENT FILING DATE: 200
NUMBER OF SEQ ID NOS:
SEQ ID NO 43124
LENGTH: 942
LENGTH: 942
TYPE: DNA
ORGANISM: OTYZA SATÍVA
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Best Local Similarity 44.8%;
Matches 322; Conservative
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APPLICANT:
APPLICANT:
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CGTCTCGTCGAGGTTCCTGGGGCTGGCCACGTGGAGGCCGTGGATGTGCTCGGGCCGGGC 978
                                                                                          CGGGACCCGCTGGTGACGCGGGCGACGAGGCGAGGCCTGGCGTCCCGTAGCCCGTGTGGC 918
                                                                                                                                                                                      AGCCCGTACTATAGGCTCCGGGACGTCATACCCCCGGTGGCTGGACGTACAAGACGCCGCTG
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                                            GGCTTCGGCCCCGCTGGGTGGAGCGCGTGGATAAGCCGTTGCTGGTGGTGTATGGGCCC
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Kovalic, David K.
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RESULT 5 US-09-739-449-2506

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; LOCATION: (1)..(1163)
; OTHER INFORMATION: unsure
US-09-739-449-2506
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SEQ ID NO 2506
LENGTH: 1163
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Best Local
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APPLICANT: Slater, Steven C.
FITLE OF INVENTION: Agrobacterium tumefaciens
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Agrobacterium tumefaciens FEATURE:
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                        GGCTGATGGCGGGCGTTGACCTCGGCTTCGGCCCCCGCTGGGGTGGAGCGCGTGGATAAGC
                                                                                                 GGGTCTACGCGGTGGCTGCTGATAGCCCCGTACTATAGGCTCCGGGACGTCATACCCCGGT
                                                                                                                                                  TATTGGTGGGGTTCAGTATGGGCGGCGCTGTAGCGATCGTGGAGGGTGCTGGGGACCCCGC
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pred. No. 2.8e-06;
pred. Mismatches 558;
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US-09-739-449-591; Sequence 591, Application US/09739449; GENERAL INFORMATION:
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NAME/KEY: unsure

: LOCATION: (1)..(974)

: OTHER INFORMATION: unsure

US-09-739-449-591
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Best Local Sin
Matches 296;
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SEQ ID NO 591
LENGTH: 974
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CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens
FILE REFERENCE: 38-10(15490)C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                              GGCGCTGTAGCGATCGTGGAGGGTGCTGGGGGACCCGCGGGTCTACGCGGTGGCTGCTGAT 678
                                                                                             GGCTATGTCTCGGAGCGGTTCCCCCGGCCGGCCGGATAATATTGGTGGGGGTTCAGTATGGGC
                                                                                                                                               GAGAGCGGGGCTCGACGACGATTGGGCCCCCGGGAGGTGCTGGATGCCCGGGCTGTGGTG
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1204)
; OTHER INFORMATION: unsure
US-09-739-449-2277
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; Sequence 2277, Appli
; GENERAL INFORMATION:
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SEQ ID NO 2277
LENGTH: 1204
TYPE: DNA
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Best Local Similarity 45.1
Matches 319; Conservative
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APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens
EILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILLING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/514,000 PRIOR FILING DATE: 2000-02-23
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                                                                                                                                                                                                                                                        451
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                                                                                                                            GAGCGGTTCCCCGGCCGGCCGGATAATATTGGTGGGGGTTCAGTATGGGCGGCGCGCTGTAGCG
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AGGCTCCGGGACGTCATACCCCGGTGGCTGGAGTACAAGACGCCGCTGCCGGGCTGGGTG
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                                                      ATCGTGGAGGGTGCTGGGGACCCGCGGGGTCTACGCGGTGGCTGCTGATAGCCCCGTACTAT
                                                                                                             GGCTTCGGCCCCGCTGGGGTGGAGCGCGTGGATAAGCCGTTGCTGGTGGTGTATGGGCCC
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45.18;
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Pred. No. 1e-05;
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RESULT 8
US-09-553-094-5316
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; GENERAL INFORMATION:
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SEQ ID NO 5316

LENGTH: 717

TYPE: DNA
ORGANISM: Zea mays
OTHER INFORMATION: Clone ID: LIB3061-092-Q1-N6-H2
US-09-553-094-5316
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Best Local Similarity
Matches 270; Conserv
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CURRENT APPLICATION NUMBER: US/09/553,094
CURRENT FILING DATE: 2000-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fisher, Dane K.
TITLE OF INVENTION: NA
TITLE OF INVENTION: Plants
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   386
                      679
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                                         326
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AGCCCGTACTATAGGCTCCGGGACGTCATACCCCGGTGGCTGGAGTACAAGACGCCGCTG
                                      GGCGCTGTAGCGATCGTGGAGGGTGCTGGGGACCCGCGGGTCTACGCGGTGGCTGCTGAT 678
                                                                           GGCTATGTCTCGGAGCGGTTCCCCGGCCGGCCGGATAATATTGGTGGGGGTTCAGTATGGGC 618
                                                                                                                    GAGAGCGGGGCTCGACGACGATTGGGCCCCCGGGAGGTGCTGGATGCCCCGGGCTGTGGTG 558
                                                                                                                                                       GCCCGGGAGCTCGTGGAGTGGGGGTACCCGGGTGGTTGTGTTCGACTTCCGGGGGCCACGGG
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                                                                                                                                                                                                                                                                                     Score 79.8; DB 22; Pred. No. 1.1e-05;
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APPLICANT: HINKLE, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
FITLE OF INVENTION. Agrobacterium tumefaciens Ger
FILE REFERENCE: 38-10(1549))C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 1199
LENGTH: 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(782)
OTHER INFORMATION: unsure
US-09-739-449-1199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                        429 GGCTGTGCTGGCCCGGGAGCTCGTGGGAGTGGGGGGTACCCGGGTGGTTGTGTTTCGACTTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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CAGTATGGGCGCGCTGTAGCGATCGTGGAGGGTGCTGGGGACCCGCGGGTCTACGCGGT
                                                                                                                                                                                                                                                                                                                                                    CGTCTCGACGTTCCTGGGGCTGGCCACGTGGAGGCCGTGGATGTGCTCGGGCCCGGGC
                                GACGCCGCTGCCGGGCTGGGTGGGTGTGCTGGCCGGGTTCTACGGGAGGCTGATGGCGGG
                                                                    GGCTGCTGATAGCCCGTACTATAGGCTCCGGGACGTCATACCCCGGTGGCTGGAGTACAA 728
                                                                                                                                        CGGGACCCGCTGGTGACGCGGGACGAGGCGAGGAGCCTGGCGTCCCGTAGCCCCGTGTGGC
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US-60-129-391-160
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GENERAL INFORMATION:
APPLICANT: Keith et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: RESPIRATORY DISEASES
FILE REFERENCE: 107196.138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 3674
SEQ ID NO 160
LENGTH: 947
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure LOCATION: (31),(32),(36) LOCATION: (31),(32),(36) OTHER INFORMATION: Identity of nucleotide sequences at the above locations are -60-129-391-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/60/129,391
CURRENT FILING DATE: 1999-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                            344 GCTGGGTGCTGGGCCCCCGGCGCTGCGGGCAACCCGGTGTTCGTTTTGATGCACGGGTATA
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                                    CGGGCCGGGCCGCTACGCAGACATGCTGATAGAGCTGGCGCACGAGGAGTGCCCTCCGGG
GGCCCCGGGAGGTGCTGGATGCCCCGGGCTGTGGTGGGCTATGTCTCGGAGCGGTTCCCCG
                     CCCGTGTGGCCGTCTCGTCGAGGTTCCTGGGGGCTGGCCACGTGGAGGCCGTGGATGTGCT
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43.0%;
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Pred. No. 1.6e-05;
0; Mismatches 498
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319 GCGGAGGATGGCTTGGTGGTTCGGGGCTGGGTGCTGGGCCCCGGCGCTGGGGGCAACCCG 378

Query Match
Best Local Similarity
Matches 314; Conserv

Conservative

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44.18;

Score 78.2; DB 18; Pred. No. 2.3e-05; 0; Mismatches 398;

Indels Length

Gaps

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865; 0;

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NAME/KEY: source
LCCATION: (1).(865)
OTHER INFORMATION: /clone="nbxb0005aF11.g"
NAME/KEY: misc_feature
LCCATION: (345)..(403)
OTHER INFORMATION: High quality region
NAME/KEY: misc_feature
LCCATION: (1).(865)
OTHER INFORMATION: n = a, t, c or g
US-09-406-292A-579
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US-09-406-292A-579
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GENERAL THEORMATION:
APPLICANT: Wing, Rod A.
APPLICANT: Dean, Ralph A.
                                                                                                                                                                                                            SOFTWARE: P
                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/406,292A CURRENT FILING DATE: 1999-09-24 PRIOR APPLICATION NUMBER: 60/101,712 PRIOR FILING DATE: 1998-09-25
                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: A-30646A
                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: GENOMIC THEREOF
                                                                                                                                                         TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                    FEATURE:
                                                                                                                                                                                              LENGTH:
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                                                        PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 2284
LENGTH: 1271
TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
                                                                                                                                                                                                                     Sequence 2284, Application US/09739449 GENERAL INFORMATION:
                                                                                                                                        APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
09-739-449-2284
        NAME/KEY: unsure LOCATION: (1)..(1271)
OTHER INFORMATION: unsure at all n locations
                                               FEATURE:
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Query Match

7.5%;

Score

78.2;

DB 29;

Length 1271;

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RESULT 13
US-09-739-449-2285
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                                                                                  PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 2285
LENGTH: 1125
                                                                                                                                                                                                                                   Sequence 2285, Application US/09739449 GENERAL INFORMATION:
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                                                                                                                                                     APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens
ETLE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
NAME/KEY: unsure
LOCATION: (1)..(1125)
OTHER INFORMATION: unsure at all n locations
                                            ORGANISM: Agrobacterium tumefaciens FEATURE:
                                                                       TYPE: DNA
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0; Mismatches 370;
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US-09-739-449-2285

Query Match Best Local Similarity Matches 268; Conserv

Conservative

0; Mismatches 451; Indels Score 77.8; DB 29; Pred. No. 2.7e-05;

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Length 1125;

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RESULT 14
US-09-404-284-202
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                                  CURRENT APPLICATION NUMBER: US/09/404,284
CURRENT FILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 4670
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 202
LENGTH: 1527
                                                                                                                                                     Sequence 202, Applicati
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
                                                                                                                 TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained TITLE OF INVENTION: From Various Libraries FILE REFERENCE: 20411-780
         ORGANISM: Homo sapiens
                        TYPE: DNA
FEATURE:
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RESULT 15
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; LOCATION: (1)...(1527)
; OTHER INFORMATION: n =
US-09-404-284-202
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                                                                                            Sequence 202, Application US/09524038 GENERAL INFORMATION:
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Best Local Similarity 36.8%;
Matches 270; Conservative
APPLICANT: Drmanac, Radoje T.
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Dickson, Mark C.
APPLICANT: Jones, Lee w.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
                                                                                                                                                                                      1291 ggggnnggggnggg 1304
                                                                                                                                                                                                                      1021 CCTCCGGGGGCCGG 1034
                                                                                                                                                                                                                                                                                                          424 TACATGGCTGTGCTGGCCCGGGAGCTCGTGGAGTGGGGGTACCCGGTGGTTGTGTTCGAC
                                                                                                                                                                                                                                                                               961 GATGTGCTCGGGCCGGGCCGCTACGCAGACATGCTGATAGAGCTGGCGCACGAGGAGTGC
                                                                                                                                                                                                                                                                                                                                 901 TCCCGTAGCCCGTGTGGCCGTCTCGTCGAGGTTCCTGGGGCTGGCCACGTGGAGGCCGTG
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CURRENT APPLICATION NUMBER: US/09/524,038
CURRENT FILING DATE: 2000-03-13
EARLIER APPLICATION NUMBER: 09/404,284
EARLIER FILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 4670
SOFTWARE: Hypatent.pl Version 3.1
SEQ ID NO 202
LENGTH: 1527
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1527)
OTHER INFORMATION: n = A,T,C or G
US-09-524-038-202
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Best Local Similarity 36.8%;
Matches 270; Conservative
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                                                                                 961 GATGTGCTCGGGCCGGGCGGCTACGCAGACATGCTGATAGAGCTGGCGCGCACGAGGAGTGC 1020
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                         TCCCGTAGCCCGTGTGGCCGTCTCGTCGAGGTTCCTGGGGCCTGGCCCACGTGGAGGCCGTG
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Search completed: June Job time: 39305 sec 3, 2001, 00:43:27

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

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US-09-130-114-2
US-09-130-145-2
US-09-010-928B-3
US-07-915-246-1
US-08-485-568A-11
US-08-89-740A-4
US-08-89-740A-1
US-08-89-740A-1
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US-08-9103-429A-1
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15, Appl 16, Appl 16, Appl 3, Appl 3, Appl 3, Appl 3, Appl 1,
ALIGNMENTS

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DEDNESS:
; LENGTH: 1041 NUCLEOTIDES ; TYPE: NUCLEIC ACID
; SEQUENCE CHARACTERISTICS:
619-678-5099
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TELECOMMUNICATION INFORMATION:
MIMPER: 38,3
HAILE, LISA A.
; ATTORNEY/AGENT INFORMATION:
; APPLICATION NUMBER:
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SIFICATION: 435
; FILING DATE: February 16, 1996
CATION DATA:
; SOFTWARE: WORD PERFECT 6.0
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R: IBM PS/2
: COMPUTATE BETTE TOTAL:
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225 EXECUTIVE SQUARE
ADDRESSEE: FISH & RICHARDSON P.C.
DENCE ADDRESS
: NIMBER OF SECTIONS: 42
CANT: KOSMOTKA,
WARREN, Patrick
SWANSON; Ronald
LINK, St
MAFFI?
: APPLICANT: REID, John
: ROBERTSO
AL INFORMATION:
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US-08-602-359A-24
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Pred. No. 1.9e-222;
; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 152331
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NAME/KEY: misc_feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A
US-09-128-155-16
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Best Local Similarity
Matches 194; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
 21873
                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                                                                       22173
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                                                                    GCGTTGACCTCGGCTTCGGCCCCGCTGGGGTGGAGCGCGTGGATAAGCCGTTGCTGGTGG
                                                                                                                                                                              TGGCTGCTGATAGCCCGTACTATAGGCTCCGGGGACGTCATACCCCGGTGGCTGGAGTACA 727
                                                                                                                                                                                                                                TCAGTATGGGCGGCGCTGTAGCGATCGTGGAGGGTCTGGGGGACCCGGGGTCTACGCGG
                                                                                                                                                                                                                                                                                                                                         GGGGCCACGGGGAGAGGGGGGGGGGGGTGCTGGATGCCC
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 NNNGTNNNACCNCCCACCC
                                                                                                           AGACGCCGCTGCCGGGCTGGGTGGGTGGCTGGCCGGGTTCTACGGGAGGCTGATGGCGG
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                         TGTATGGGCCCCGGGACCC
                                                     5.1%;
ilarity 44.2%;
Conservative
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Pred. No. 0.0025;
0; Mismatches 245;
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RESULT 3 US-09-130-114-2/c Sequence 2, Application US/09130114

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; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EBNA
US-09-130-114-2
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SEQ ID NO 2
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APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/1D903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 332; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCGGGCCGCTACGCAGACATGCTGATAGAGCTGGCGCACGAGGAGTGCCCTCCGGGGG
                                          TGGGCCCCGGGACCCGCTGGTGACGCGGGACGAGCCGAGCCTGGCGTCCCGTAGCCC
                                                                                                                                                           TGACCTCGGCTTCGGCCCCGCTGGGGTGGAGCGCGTGGATAAGCCGTTGCTGGTGGTGTA 851
                                                                                                                                                                                                                     GGACGGGGAGGACGGGAGGACGAGGACGGGGGAGGAGGACGAGGACGGGGA
                                                                                                                                                                                                                                                                                                           TGATAGCCCGTACTATAGGCTCCGGGACGTCATACCCCGGTGGCTG---GAGTACAAGAC 731
                                                                                                                                                                                                                                                                                                                                      GGGCGCCCTGTAGCGATCGTGGAGGGTGCTGGGGGACCCGCGGGTCTACGCGGTGGCTGC 674
                                                                                                                                                                                                                                                                                                                                                                                                  GGTGGGCTATGTCTCGGAGCGGTTCCCCCGGCCGCCGGATAATATTGGTGGGGGTTCAGTAT 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGGGAGAGCGGGGCTCGACGACGATTGGGCCCCGGGAGGTGCTGGATGCCCGGGCTGT 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACCGCGGAGGATGGCTTGGTGGTTCGGGGCCTGGGGTGCTGGGGCCCCCGGCGCTGGGGGCAA 374
                                                                       GTGTGGCCGTCTCGTCGAGGTTCCTGGGGCTGGCCACGTGGAGGCCGTGGATGTGCTCGG 971
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Pred. No. 0.0019;
0; Mismatches 444;
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US-09-010-928B-3
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                                                                                                                                                                                                                                                                                                     Query Match 4.8%;
Best Local Similarity 44.0%;
Matches 396; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lewis, Randolph V
APPLICANT: Hayashi, Cheryl Y
TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28977
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE
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                                                                                                                                                                       353
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 361
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LOCATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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GGCGCTGGGGGCAACCCGGTGTTCGTTTTGATGCACGGGTATACTGGGTGCCGCTCGGCG
                                 GTGGTTTTTGGACCTGGTGGTGCTGGACCCGGTGGAGCTGGTGGTGGTGGTCCTG 532
                                                                                                                                  GCGTATAGTAGTCTGCACCCGGAGAGCTGTCGGCCCGTTGCGCCCGGAGGGGCTCACCTAC
                                                                                                                                                                   GTGGATACGGACCTGGTGGTTCTGGACCTGGCGGTTTTTGGACCTGGCGGTTCTGGACCTG
                                                                                                                                                                                                                                                                      CTCCTGGCCGCTGTGGCTGTTGTGGCGCTTGTTGTGTCCCGGCTTATGTG 240
                                                                                                                                                                                                                                      GTGGTTCTGGACCCGGCGGATACGGACCTGGTGGTTCTGGACCTGGCGGTTCTGGACCTG 352
                                                                                                  GTGGATACGGACCTGGTGGCTCTGGACCCGGTGGTGCTGGTCCCGGTGGTGTTGGACCCG
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8110 GATEHOUSE RD.
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taken from 3' region. Stop codon begins at position 2722
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Pred. No. 0.0061;
D; Mismatches 496;
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SUITE 500E
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                                                                                                                                                                                                                                                                                                         496;
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                                                                                                                                                                                                                                                                                                                                     Length 2824;
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US-07-915-246-1
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Patent No. 540183
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APPLICANT: Baszczynski, Chris L.
APPLICANT: Ballis, Lynne
APPLICANT: Bellmare, Guy
APPLICANT: Bolvin, Rodolphe
TITLE OF INVENTION: A BRASSICA REGULATORY SEQUENCE
TITLE OF INVENTION: ROOT-SPECIFIC OR ROOT-ABUNDANT
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                       STREET: Chicago
CITY: Chicago
TMATE: Illinois
                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                          CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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   ATTORNEY/AGENT INFORMATION:
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                     FILING DATE: 19920716
CLASSIFICATION: 435
                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                               SOFTWARE:
                                                                                                                                                                                           COUNTRY: USA
ZIP: 60661
                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                             PatentIn Release #1.0, Version
                                                          US/07/915,246
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Floor
                                                                                               #1.25
                                                                                                                                                                                                                                                                                                                                            GENE EXPRESSION
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US-08-458-568A-11/c; Sequence 11, Application; Patent No. 5821339; GENERAL INFORMATION:
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Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 707-8889
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HYPOTHETICAL:
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                                      ATGGGCCCCGGGACCCGCTGGTGACGCGGGACGAGGCG
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CGGTGGTGGAGCTGGAGGTGGCGGAGGAGGAGGGG 1356
                                                                              TGGAGCTGGAGAGGATACGGTGGTGGTGGTGGAGAAGGACACGGTGGTGGAGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Herpes simplex virus
STRAIN: Herpes Simplex Virus Type
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INFORMATION FOR SEQ ID NO: 1
                                                                                                                    2161
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                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                 548 GGGCTGTGGTGGGCTATGTCTCGGAGCGGTTCCCCGGGCCGCCGGATAATATTGGTGGGGT 607
                                                                                                                                                                                                                                                                                488 GGGGCCACGGGGAGAGCGGGGGCTCGACGACGATTGGGCCCCGGGAGGTGCTGGATGCCC 547
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728 AGACGCCGCTGCCGGGCTGGGTGGTGCTGGCCGGGTTCTACGGGAGGCTGATGGCGG
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OPERATING SYSTEM:
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nes 243; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & STREET: One Liberty Place, 46th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ropology: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                 TGGCTGCTGATAGCCCGTACTATAGGCTCCGGGACGTCATACCCCGGTGGCTGGAGTACA 727
                                                                                                                                              TCAGTATGGGCGGCGCTGTAGCGATCGTGGAGGGTGCTGGGGGACCCGCGGGTCTACGCGG
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RESULT 7
US-09-320-878-19/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                           Matches 232;
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APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622002120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER FILING DATE: 1998-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1997-04-30
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER FILING DATE: 1999-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: CIP OF 09/141,908 EARLIER FILING DATE: 1998-08-28 EARLIER PPLICATION NUMBER: CIP OF 09/073,538 EARLIER FILING DATE: 1998-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/320,878A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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6714 GGTGCGCATGGCGTGGGGGTCGGCGACGTCGCAGGCGGCGATGGTGACGCGGGCGCCCGA
                                                                                 6774 CGCGCCGGCGGTGTGGACGACGCCGGTGAGGGGCGTCTCGGCGGGGATGGCGTCGAGGAG
                                                                                                                                                                                                                                                       6894 GAACGCGTCGAGGTCCAGGTCCCGGGTCAGCTCGAGCACCGAGGCCCCGACGGCCTT 6835
                                     625 GTAGCGATCGTGGAGGGTGCTGGGGGACCCGGGGGTCTACGCGGTGGCTGCTGATAGCCCG
                                                                                                                                                                                                             505 GGGGGCTCGACGACTTGGGCCCCGGGAGGTGCTGGATGCCCCGGGCTGTGGTGGGCTAT 564
                                                                                                                                                                                                                                                                                              445 GAGCTCGTGGAGTGGGGTACCCGGTGGTTGTGTTCGACTTCCGGGGGCCACGGGGAGAGC 504
                                                                                                                         GTCTCGGAGCGGTTCCCCGGCCGGCCGGATAATATTGGTGGGGTTCAGTATGGGCCGCGCT 624
                                                                                                                                                                     CGCACGGTGGGCCCGCCGGACCTGCTCGGCGGTCAGCGTGTCCACGATGCCGTCGTCGAG
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RESULT 8
US-08-804-227C-1
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                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/804,227C FILING DATE: February 21, 1997 CLASSIFETCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION UNMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 1:
                             FEATURE:
NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCI(DOS) Text only CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 15:
STREET: LILLY CORPORATE CENTER
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                  FEATURE:
                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy
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                                                                                                                                                                              OLECULE TYPE:
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                                                                                                                                NAME/KEY:
LOCATION:
NAME/KEY:
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                                                                                                                                                                                                STRANDEDNESS: Si
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
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                                                                                                                                                                                                                                                CENGTH:
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Kuhstoss, Stuart A.
Rosteck, Paul R., Jr.
Sutton, Kimberly L.
Sutton, Kimberly L.
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816..14234
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14351..19945
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                                                                                                                                                                  Sequence 1, Application Patent No. 5986077
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Best Local Similarity
Matches 302; Conserv
                                                                                                                                                   GENERAL INFORMATION:
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                                    CORRESPONDENCE ADDRESS: ADDRESSEE: Evenson,
                                                                                           TITLE OF INVENTION:
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                                                                                                                                  APPLICANT:
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                                                                          NUMBER OF SEQUENCES:
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                      STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGACGATTGGGCCCCGGGAGGTGCTGGATGCCCGGGCTGTGGTGGGCTATGTC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACGGGTATACTGGGTGCCGCCTCGGCGCCCTACATGGCTGTGCCTGGCCCGGGAGCTCGTG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGGAGGGTGCGAAGGCTCCTGGCAGTCCCGAAGAGGCACAGCCTGCTGTGGGTGTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                           CTGGTGACGCGGGACGAGGCGAGGCCTGGCGTCCCGTAGCCCGTGTGGCCGTCTCGTC
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Washington
                   1200 G Street,
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                                      Evenson, McKeown,
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                                                                                         Process for producing anthracyclines and intermediates thereof
                                                                                                                                                                                   US/08809740A
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                     Edwards and Lenahan 700
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                                                                      RESULT
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Sequence 4, Application US/08809740A Patent No. 5986077 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.6%;
Best Local Similarity 51.2%;
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 30-SEP-1995
APPLICATION NUMBER: FI 944556
FILING DATE: 30-SEP-1994
ATTORNEY_AGENT INFORMATION:
NAME: H. Thomas Anderton, Jr.
REGISTRATION NUMBER: 40,895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                     2373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 27-MAR-PRIOR APPLICATION DATA:
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LOCATION: 359..1651
                                                                                                                         2553 CACCCCGGACGAGGACGCGGAGGCCGACGCGGTG 2589
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                  798 CGGCTTCGGCCCCGCGGGGTGGAGCGCGTTGGATAAGCCGTTGCTGGTGGTGTATGGGCC 857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: 1648..1651
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                                                                                                                                                                                                                                                                                                                                   GTCGGCCCGGGCGCGGGTGACGCGGTGGTACGGGCGCATCGATGGGTACGCCGCCAC 2432
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2937..3197
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SYSTEM: PC-DOS/MS-DOS
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                                                                                        RESULT
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              Sequence 1, Application US/08403852D Patent No. 5891695 GENERAL INFORMATION:
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Best Local Similarity
Matches 111; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/F195/
FILING DATE: 30-SEP-1995
APPLICATION NUMBER: FI 944556
FILING DATE: 30-SEP-1994
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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LENGTH: 3252 base pair
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MEDIUM TYPE: Floppy
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OTHER INFORMATION:
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LOCATION: 1648..2877
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TOPOLOGY: 111
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                                                                                                                                                                                                                                                                                                      CGGCTTCGGCCCCGCTGGGGTGGAGCGCGTGGATAAGCCGTTGCTGGTGGTGTATGGGCC
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51.2%;
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Best Local Similarity
Matches 200; Conserv
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/
FILING DATE: 10-MAY-199
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5392 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/FF
FILING DATE: 25-SEP-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/
FILING DATE: 25-SEP-192
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
                                                                 3416
                                                                                                                                   3476
                                                                                                                                                                                                 ORIGINAL SOURCE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meyers, Kennet REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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GCGGGCAGTTCGGCGGCCGGGCCGGCAGCGGCAGGAGGATCTTGGCGTGCCGGTGCCTGC 329:
                               GCCAGGACCGGGTCGTCGGAGCCGGTGAGCGCCACCGTGAAGCCGTCCGCGGGGCTGTCG 3357
                                                                                                ATAGGCTCCGGGACGTCATACCCCGGTGGC-----TGGAGTACAAGACGCCGCTG 738
                                                                                                                                20005-3315
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1300 I Street, N.W., Suite 700
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Thibaut,
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                                                                                                                                                                                                                                                                 Score 45.4; DB 2;
Pred. No. 0.089;
0; Mismatches 206
                                                                                                                                                                                                                                                                   206;
                                                                                                                                                                                                                                                                                                 Length 5392;
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APPLICATION NUMBER: PCT/FR 93/009
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                    TELEFAX: (202) 408-44
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
              MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 10-MAY-1995
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                                                      TOPOLOGY:
                                                                    TYPE: nucleic acid
STRANDEDNESS: doub
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                                                                                                                                                                                                                                REGISTRATION NUMBER: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                            LENGTH:
                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                  NAME: Meyers, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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VENTION: Polypeptides Involved In The
VENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
VENTION: Coding For These Polypeptides And Their Use
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Best Local Similarity 48.0
Matches 200; Conservative
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APPLICANT: Blanc, Veronique
                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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ORGANISM: S.p
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TITLE OF INVENTION:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                    STREET: 1300 - CITY: Washington
                                                                                                                                                                              COUNTRY: USA
ZIP: 20005-3315
APPLICATION NUMBER:
                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                       ADDRESSEE:
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1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                De Crecy-Lagard, Valerie
VENTION: Polypeptides Involved In The
VENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
VENTION: Coding For These Polypeptides And Their Use
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Crouzet, Joel
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US/08/403,852
                                                     US/09/231,818
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Pred. No. 0.089;
0; Mismatches 206; Indels
                                                                                       Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 5392;
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GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
ITILE OF INVENTION: GENES F
FILE REFERENCE: 4-30582A
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                                                                                                                                                                                              US-09-335-409-1
                                                                                                                                                            Sequence 1, Application Patent No. 6121029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.48;
Best Local Similarity 48.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 408-44 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
ORGANISM: S.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 5392 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J
                                                                                                                                                                                                                                                                3177 GGGGCCGGCCACGTCGAAGTGCCTGCCCTGGTGGTCGAGTTGGTGGACGGCGGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                      3296 TGCTTCACCGAGGCGGCGTCGGCCGCCTCGTCGAGCAGGACGAGGTCGGCGGCCGCCGCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                919 CGTCTCGTCGAGGTTCCTGGGGGCTGGCCACGTGGAGGCCGTGGATGTGCTCGGGCCG 975
                                                                                                                                                                                                                                                                                                                                                        859 CGGGACCCGCTGGTGACGCGGACGAGCCGTGGCGTCCCGTAGCCCGTGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 25-SEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                     AGGGCGGGGCCGGTGACG-GCGACGACGGGGGGGGGGCGGCGGGCGGCGGCGACGTTGAG 3178
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                     BIOSYNTHESIS OF
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                     EPOTHILONES
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LENGTH: 68750
TYPE: DNA
ORGANISM: Sorangium cellulosum
                                                                                                                                                                                               Sequence 1, Application US/09103429A Patent No. 6187558
                                                                               GENERAL INFORMATION:
APPLICANT: Granados, Robert R
APPLICANT: Wang, Ping
APPLICANT: Wang, Ping
TITLE OF INVENTION: A NO. 6187558el Invertebrate Intestinal
TITLE OF INVENTION: cDNA and Related Products and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.3%;
Best Local Similarity 44.2%;
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CURRENT FILING DATE: 199-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Pinnisi & Michaels,
STREET: 118 No. 6187558th Tioga
                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                 872 TGACGCGGGACGAGGCGAGGAGCCTGGCGTCCC 904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGAGTGGGGGTACCCGGTGGTTGTGTTCGACTTCCGGGGCCACGGGGAGAGCGGGGGCT 511
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Pred. No. 0.21;
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Search completed: June Job time: 23015 sec

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; IMMEDIATE SOURCE: ; CLONE: IIM14 US-09-103-429A-1
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Best Local Similarity
Matches 124; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Michaels, Christopher
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: BTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 14850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Rel-
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                               669 GGCTGCTGATAGCCCGT 685
                                                                                                                                                                                                                                                                      429 GGCTGTGCTGGCCCGGGAGCTCGTGGAGTGGGGGTACCCGGTGGTTGTGTTCGACTTCCG 488
                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 24-JUI CLASSIFICATION: 80
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
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                                                                                                                                                                                                GGCCCACGGGGAGAGCGGGGGGCTCGACGATTGGGCCCCGGGAGGTGCTGGATGCCCG
GGTTGTGGTTGGGGCCT 417
                                                           CTGAGTGGTAGTTGGGGCCTGGGTGGTTGGGGCCTGGGTGGTTGGGGCCTGGGT
                                                                                      CAGTATGGGCGGCGCTGTAGCGATCGTGGAGGGTGCTGGGGACCCGGGGTCTACGCGGT
                                                                                                                      GGTGGTTGTGGTAGGGGCCTGAGTGGTTGTGGTTGGGGGCCTGAGTGGTAGTAGTAGGGGC
                                                                                                                                                GECTGTGGTGGGCTATGTCTCGGAGCGGTTCCCCCGGCCGCCGGATAATATTGGTGGGGTT 608
                                                                                                                                                                                 GGCCTGAGTGGTAGTTGGGGCCTGGGTGGTAGTTGGGGCCCTGGGTGGTTGGGGCCCTG
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                                                                                                                                                                                                                                                                                                                Score 44.2; DB Pred. No. 0.14;
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Result
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                                                                                                                                                                                                                                                                                                                                                                                         Score
         1041
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1: /SIDS2/gcgdat
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/SIDS2/gcgdata/geneseq/geneseqn/Na1981.DAT:

/SIDS2/gcgdata/geneseq/geneseqn/Na1981.DAT:

/SIDS2/gcgdata/geneseq/geneseqn/Na1983.DAT:

/SIDS2/gcgdata/geneseq/geneseqn/Na1984.DAT:

/SIDS2/gcgdata/geneseq/geneseqn/Na1984.DAT:

/SIDS2/gcgdata/geneseq/geneseqn/Na1987.DAT:

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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Comp
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1280.130 Million cell updates/sec
Human gene express
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Human adenosine Al
Human adenosine Al
Human colon cancer
Arabidopsis thalia
                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                        DNA encoding Pyrod
Human colon cancer
Human colon cancer
                                                                                                                                                                                            Human gene express
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Human ovarian tumo	Z77506	20	2188	4.5	47	45	O
3	Z87299	21	4689	4.5	47.2	44	o
Wheat starch synth	C86411	21	2842	4.5	47.2	43	
Wheat starch synth	C86435	21	2807	4.5	7	42	
Human gene express	217479	20	1523	4.5	47.2	41	
Human gene express	217507	20	1523			40	
Streptomyces nogal	X25480	17	3252		47.4	39	
Tylactone synthase	T80413	18	43280	4.6	47.8	38	
AC004449 cDNA clon	C90085	22	38186	4.6	47.8	37	o
Human METH1 relate	Z32028	20	38186		47.8	36	ი
Recombinant cosmid	Z56001	21	38506		48	3 5	O
Nucleotide sequenc	A75633	21	38506	4.6	48	34	a
S. venezuelae pik	287285	21	37948	4.6	48	3 3	o
Œ	Z87318	21	36778	4.6	48	32	O
	V25925	19	24379	4.6	48	31	a
Streptomyces freno	T93095	18	24379	4.6	48	30	ი
ma	Z87297	21	13842	4.6	48	29	o
HSV-2 strain SB5 C	V62152	19	10211	4.6	8	28	
HSV-2 strain SB5 C	V62170	19	3698	4.6	8	27	
Herpes simplex vir	V12286	19	2480	4.6		26	
HSV L/ST region.	Q76213	16	12001	4.6	8	25	O
Genomic clone G11F	Q55750	15	1505	4.6	8	24	
	A01833	21	1059	4.6	48.4	23	
Wheat raffinose sy	D00338	21	2653	4.7		22	
HSV-2 strain SB5 C	V62176	19	117213	4.7	8	21	
Nucleotide sequenc	A14651	21	77536	4.7	49	20	a
S. avermitilis ave	A92302	21	31422	4.7	49.4	19	
Streptomyces prist	T59268	17	2888	4.8	49.6	18	O
Streptomyces prist	T59269	17	888	4.8	49.6	17	
Human gene express	Z17264	20	1312	4.8	49.8	16	a
c DNA encoc	A53800	21	7720	4.8	50	15	O
	X02974	20	3198	5.0	52	14	O
Human gene express	75	20	1103	5.1	52.6	13	ი
Streptococcus olea	A09469	21	50937	5.2	54	12	

ALIGNMENTS

RESULT T79322

T79322;

T79322 standard; DNA; 1041 BP

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WPI; 1997-425035/39.
P-PSDB; W23088.
                                                  Callen W, Kosmotka A, Reid J, Robertson DE,
                                                                                                                                                                                        pulp; paper; lignin removal; su
disease resistance; feedstuff;
                                                                                                                                                                                                                           DNA encoding Pyrodictium sp. esterase TAG11-17LC
                                                                                                                                                                                                                                             16-FEB-1998 (first entry)
                                                                                                16-FEB-1996;
                                                                                                                11-FEB-1997;
                                                                                                                                   21-AUG-1997
                                                                                                                                                     W09730160-A1
                                                                                                                                                                      Pyrodictium sp.
                                                                                                                                                                                                          Esterase; thermostable enzyme; ester; chiral compound; cheese;
                                                                              (RECO-) RECOMBINANT BIOCATALYSIS INC.
                                                                                                96US-0602359.
                                                                                                                97WO-US02039
                                                                                                                                                                       strain TAG11.
                                                 Link S, Maffia AM, M
Swanson RV, Warren PV;
                                                                                                                                                                                                sugar; lignocellulose;
                                                            Murphy D;
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Nucleic acid encoding heat stable esterase from thermophilic bacteria - which is active in organic solvents, useful in cheese

or P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 1041;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1041 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This DNA sequence codes for thermostable esterase TAG11-17LC (W23088) of Pyrodictium TAG11, a thermophilic sulphur archae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    paper manufacture, and to study plant resistance
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                                                             GATGCCCGGGCTGTGGTGGGCTATGTCTCCGGAGCGGTTCCCCCGGCCGCCGGATAATATTG
                                                                                                                           GACTTCCGGGGCCACGGGGAGAGCGGGGGCTCGACGACGATTGGGCCCCCGGGAGGTGCTG
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                GTGGGGTTCAGTATGGGCGGCGCTGTAGCGATCGTGGAGGGTGCTGGGGACCCGCGGGTC
                                             gacttccggggccacggggagagcgggggctcgacgattgggccccggggaggtgctg
                                                                                                                                                                         ccctacatggctgtgctggcccgggagctcgtggagtgggggtacccggtggttgtgttc
                                                                                                                                                                                           CCCTACATGGCTGTGCTGGCCCGGGAGCTCGTGGAGTGGGGGTACCCGGTGGTTGTTCTTC
                                                                                                                                                                                                                                     ggcgctgggggcaacccggtgttcgttttgatgcacgggtatactgggtgccgctcggcg
                                                                                                                                                                                                                                                     GCCGCTGGGGGCAACCCGGTGTTCGTTTTGATGCACGGGTATACTGGGTGCCCCTCGGCG
                                                                                                                                                                                                                                                                                                   AAAGAGTTCAGCGTGACCGCGGAGGATGGCTTGGTGGTTCGGGGCTGGGTGCTGGGCCCC
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Pred. No. 2
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.4e-208;
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                                                                                                                                                   14-MAY-1998;
15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
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probe;
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Claim

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CC detecting at least one differentially expressed gene product in a test con of the differentially expressed gene product in a test concerous state of the cell suspected of being cancerous, where detection concerous state of the cell from which the test sample was derived. CC The polynucleotides sequences can be used in a method for detecting cd differentially expressed genes correlated with a cancerous state of a cc mammalian cell. The polynucleotides can also be used as probes for cd detecting and mapping related genes. They can be used in diagnosis and corremetastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-positive breast cancer.
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79; Conservative
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15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
                                                                  detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for
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                  detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of
                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
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Lamson G, Drmanac R,
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HYSEQ I
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Crkvenjakov R,
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R, Dickson M, Drmanac
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TCTCGTCGAGGTTCCTGGGGCCTGGCCACGTGGAGGCCGTGGATGTGCTCGGG
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                                                                        GGACCCGCTGGTGACGCGGGACGAGGCGAGGAGCCTGGCGTCCCGTAGCCCGTGTGGCCG
                                                                                               CTTCGGCCCCGCTGGGTGGAGCGCGTGGATAAGCCGTTGCTGGTGGTGTATGGGCCCCG
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                                                 CCCGTACTATAGGCTCCGGGACGTCATACCCCGGTGGCTGGAGTACAAGACGCCGCTGCC
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217263/c
ID 217263 standard; cDNA; 1337 BP
XX
AC Z17263;
XX
DT 12-OCT-1999 (first entry)
XX
DE Human gene expression product
XX
KW Human; gene; gene expression p
KW detection; mapping; tissue typ
KW genetic analysis; colorectal c
XX
PN w09938972-A2.
XX
PN w09938972-A2.
XX
PD 05-AUG-1999.
XX
PF 28-JAN-1998; 98US-00806666.
PR 03-APR-1998; 98US-00806666.
PR 03-APR-1998; 98US-00806666.
8XCCCCCCCCCCCCCCCCCX8XXTHHHHHHXXXXXAHHHHHHXXXXXX
                                                   cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell cuspected of being cancerous, where the gene product is encoded by one cf the 5248 polynucleotide sequences given in 212532 to 21779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer. The polynucleotides of the invention are especially used in the diagnosts, prognosis and management of colorectal cancer, breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
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(HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a library of human polynucleotides comprising the sequences given in Z12532 to Z17779. Also described method of detecting differentially expressed genes correlated with cancerous state of a mammalian cell, comprising detecting at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escobedo J, Garcia PD,
Jones WL, Kassam A, Ken
Lamson G, Leshkowitz D,
Stache-Crain B, Sudduth-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 2250-2251; 2479pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human genes and their differentially expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-494092/41.
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on; mapping; tissue typing; profiling; forensic; cancer;
analysis; colorectal cancer; breast cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHIRON CORP. HYSEQ INC.
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arcia PD, Garcia V, Giese K, Innis
sam A, Kennedy GC, Kita D, Labat I;
hkowitz D, Pot D, Randazzo F, Reinh
, Sudduth-Klinger J, Williams LT;
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98US-0080515
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117 GGGCGTAGCTGTGGACACAGGGGTGGCTCGGGTGCCTCGGCCCGGCGGGGTAAGAG 176

Matches

Conservative

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Mismatches

Query Match
Best Local Similarity

6.7%;

Score 70.2; DB 20; Pred. No. 3.3e-06;

Length Indels

2;

Gaps

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Sequence 1337 BP; 42 A; 577 C;

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22 T; 669 other;

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                                  Human colon cancer cell line polynucleotide sequence SEQ ID NO:2468
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detection; cancerous state; metastasis; identific
cancer; oestrogen receptor-positive breast cancer
                                                                                         standard; cDNA;
                                                      (first entry)
                                                                                         1127
                                                                                         BP.
         identificati
                  product;
therapy;
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14-MAY-1998;
15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
                                                                                                                                                                                                                                                         A00010 to A02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.
                                                                                                         The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of pre-metastatic or metastatic cancerus states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-negative breast cancer, oestrogen receptor-negative breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Williams LT, Escobedo
Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
                                                                                Sequence 1127
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
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                                                                                BP; 3 A; 214 C; 505 G;
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98US-0105234.
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               6.2%;
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Crkvenjakov R, Dickson M, Drmanac
Garcia V, Jones LW, Stache-Crain
                                                                                                                                                                                                                                                                                                                                                                                                         English
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   0;
Score 64.2; DB 21;
Pred. No. 5.7e-05;
0; Mismatches 468;
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Best Local Similarity 31.1
Matches 212; Conservative
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 ATTGGTGGGGTTCAGTATGGGCGCGCTGTAGCGATCGTGGAGGGTGCTGGGGGACCCGCG
                              gngggggngggggggggcncgcgggggcgntttnttnggtggnggcgggggncgnngngcc
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 Novel human gen differentially
                                                           Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard
Stache-Crain B, Sudduth-Klinger J, Williams LT;
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24-FEB-1998;
31-MAR-1998;
03-APR-1998;
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                                     WPI; 1999-494092/41.
                                                                                                                                                                                                                                                                                                                                                 Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer;
                                                                                                                                      (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
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                                                                CC cancerous state of a mammalian cell, comprising detecting at least one conditions of the State of being cancerous, where the gene product is encoded by one CC of the State polynucleotide sequences given in 212532 to 21779. The CC polynucleotides can be used as a source of primers and probes, which can CC be used for a variety of purpose, e.g. detection of expression levels, CC mapping, tissue typing or profiling, forensics, genetic analysis and CC detection of polymorphisms. Polypeptides encoded by the polynucleotides CC can be used for raising antibodies for experimental, diagnostic and CC therapeutic purposes. The polynucleotides may also be used to construct CC arrays for diagnostics (which may be used to detection elevels between CC cells (e.g. to identify abnormal or diseased tissue in a human, to C cidentify a genetic predisposition or susceptibility to a disease such as C cancer). The polynucleotides of the invention are especially used in the C diagnosis, prognosis and management of colorectal cancer, breast cancer, C appriled analogues and antagonatics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           method of detecting differentially expressed genes correlated with cancerous state of a mammalian cell, comprising detecting at least
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Sequence 1359 BP; 85 A; 424 C; 29 <u>ი</u> 15 T; 806 other

В δõ 밁 20 밁 Š δÃ 밁 Ωy B Ş В Ş 밁 Ş 망 δÃ 밁 ΩV В Qγ Query Match Best Local Matches 170; 363 243 GTATAGTAGTCTGCACCCGGAGAGCTGTCGGCCCGTTGCGCCCGGAGGGGCTCACCTACAA 302 GGTGGTGTATGGGCCCCCGGGACCCGCTGGTGACGCGGGACGAGGCGAGGAGCCTGGCGTC GTACAAGACGCCGCTGCCGGGCTGGGTGGGTGTGCTGGCCGGGTTCTACGGGAGGCTGAT NGGGGNNNGNNGNGGNGNGNGNGNTNNGNGTNGNNGGGNNNNGGTNNGNGNNNNGGN GGCGGGCGTTGACCTCGGCTTCGGCCCCCGCTGGGAGCGCGTGGATAAGCCGTTGCT NNGNNNGNUNGGGNNNGGGNNNNNNGGTNNNNNNNGGGGNNNNNNNGGGGNGNNN NNGNGNNNNNNNNGNNTNNGNNGNNGNNNNNNGNNNNNNGGNNGGNNGNGGGNNNGGGN CGCGGTGGCTGATAGCCCGTACTATAGGCTCCGGGACGTCATACCCCGGTGGCTGGA CTTCCGGGGCCACGGGGAGAGCGGGGGCTCGACGACGATTGGGCCCCCGGGAGGTGCTGGA GTGNNTGGNNNNGGNNGNGGGGGNG-GNGTGNGNNNNNGNNNNNNGGGGNGNGNNNNGNG CGCTGGGGGCAACCCGGTGTTCGTTTTGATGCACGGGTATACTGGGTGCCGCTCGGCGCC GGGNNGNNGNGNGNNNGNGTGNTGNNGNNNTGNGGNGGGNNNGGGNGNNNGNNNNTNT AGAGTTCAGCGTGACCGCGGAGGATGGCTTGGTGGTTCGGGGCCTGGGTGCTGGGCCCCGG GGGGTTCAGTATGGGCGGCGCTGTAGCGATCGTGGAGGGTGCTGGGGACCCGCGGGTCTA 662 CTACATGGCTGTGCTGGCCCGGGAGCTCGTGGAGTGGGGGTACCCGGTGGTTGTTTCGA Similarity Conservative 5.9%; 21.3%; 0; Score 61.2; DB 20 Pred. No. 0.00025 Mismatches DB 20; 627; Length 1359; 1; Gaps 1060 1239 722 940 602 542 422 ۲.

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Reinhard C, Giese K,
Cron G, Drmanac R,
Kita D,
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21-OCT-1998;
27-OCT-1998;
                                    correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a
                                                                                                                A00010 to A02716 represent polynucleotides isolated from cDNA constructed from human colon cancer cell lines. The present in also describes a method of detecting differentially expressed correlated with a cancerous state of a mammalian cell, comprise
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(HYSE-)
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               detecting
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Randazzo F, F
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                                                                                                                  TGGCCCGGGAGCTCGTGGAGTGGGGGTACCCGGTGGTTGTGTTCGACTTCCGGGGCCACG
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                            GCCGTCTCGTCGAGGTTCCTGGGGCTGGCCACGTGGAGGC
                                                       nggngcacngggggncnnnncgcngnncgcggggtgagagggtncggnnacgggggg
                                                                                       CCCGGGACCCGCTGGTGACGCGGGACGAGGCGAGGAGCCTGGCGTCCCGTAGCCCGTGTG
                                                                                                                                                   TCGGCTTCGGCCCCGCTGGGGTGGAGCGCGTGGATAAGCCGTTGCTGGTGGTGTATGGGC
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68; Conservative
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30.5%;
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Pred. No. 0.00036;
0; Mismatches 608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    744 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 other;
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C directed against at least 2 mRNAs selected from target genes, coding and conor-coding regions of RNAs corresponding to target genes, gene

C initiation codons, genomic flanking regions, intron-exon borders, the

C 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one

C or more diseases, conditions or mixtures. The antisense oligonucleotides

C may be derived from sequences X55272-74. These multiple target

C oligonucleotides (specifically X55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions

C are those associated with impaired respiration and inflammation,

C allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,

C respiratory distress syndrome, pain, cystic fibrosis, pulmonary vasconstriction.
                                                           Best Loc
Matches
                                                                                                                                                                                   cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                            hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymorhemas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic
                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             colon cancer; breast cancer; lung cancer, hepatocellular carcinoma; kidney cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense oligonucleotide; multiple target; antisense treatm impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X53491 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 37; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vasoconstriction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-229400/19
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17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-1998;
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103 GGTGTCCTAGTCCGGGGGGTAGCTGTGGGACACAGGGGTGGCTCGGGTGCCTGGGCTCGGC
                                                         Loçal Similarity 29.1 nes 272; Conservative
                                                                                                                                                        114955
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                                                                                                                                                    29417 C;
                                                         Score 58.6; DB 20;
Pred. No. 0.0014;
0; Mismatches 562;
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                   Human adenosine Al receptor antisense oligonucleotide fragment.
                                                    05-JUL-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACCCGGTGGTTGTTCGACTTCCGGGGGCCACGGGGAGAGCGGGGGCTCGACGACGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dnnccgcbggccbgggcgcgccgccgggsnnndnnccgcbggccbgggcgcgccgc 104404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTGGGTGCCGCTCGGCGCCCTACATGGCTGTGCTGGCCCGGGAGCTCGTGGAGTGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gcgcgccgccggccgggccsnnndnnccgcbggccbgggcgcgccgccggccgggcsnnn 104344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCTGGGTGCTGGGCCCCCGGCGCTGCTGGGGGCAACCCCGGTGTTCGTTTTGATGCACGGGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggccgggcsnnndnngtcgggccgggcsnnndnntcgggccgggcsnnndnncgggccgg
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                                                                                                                             DNA; 114955
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive
                                                                                                                                                                                                                                                                                                                                                                                   carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pulmonary vasoconstriction; inflammation; allergic rhinitis;
acute asthma; allergy; asthma; impeded respiration;
respiratory distress syndrome; pain; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUN-1998;
                                                                                                                                                                                                                                                                                                                               Sequence 114955 BP; 6071 A; 29417 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                              pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense oligonucleotides used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-229400/19
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                                                                                                                                                                                            318
                                                                                                                                                                                                                                                                                                                                                                 metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    impaired respiration; inflammation; lung disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense oligonucleotide; multiple target; antisense treatment;
                                        438
GGGCGGCAAGCCGGGGCCGCGGGCCCAGGCGAGCCCNNHNNNSVGCGGAGCCVGCGC
                                                                                                                GGTGTTCGTTTTGATGCACGGGTATACTGGGTGCCGCTCGGCGCCCCTACATGGCTGTGCT 437
                                                                                                                                                      CCCNNHNNNSGGGCCGGGCGGGCCAAGCCGGGCCGGGGCCGAGCCCANGGGGCCCNNHNNN 105621
                                                                                                                                                                                            GGCCCGGGAGCTCGTGGAGTGGGGGTACCCGGTGGTTGTTCGACTTCCGGGGCCACGG 497
                                                                                                                                                                                                                                   241;
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                                                                                                                                                                                                                                   Conservative
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97US-0059160.
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                                                                                                                                                                                                                                                     5.6%;
33.3%;
                                                                                                                                                                                                                                 43;
                                                                                                                                                                                                                                                 Score 58.4; DB 2 Pred. No. 0.0015;
                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                 36712 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                       DB 20;
                                                                                                                                                                                                                                   437;
                                                                                                                                                                                                                                                                                                                                 21328 T;
                                                                                                                                                                                                                                                                     Length 114955
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                                             15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
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          (CHIR )
(HYSE-)
                                                                                                                                                                                                                                                                                                                                                  A02504 standard;
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                                                                                                                                                                                                                breast cancer; oestrogen receptor-positive breast cancer;
oestrogen receptor-negative breast cancer; lung cancer; s
                                                                                                                                                                                                                                                                          Human colon cancer cell line polynucleotide sequence SEQ ID NO:2495
                                                                                                                                                                                                                                                                                                    19-MAY-2000
                                                                                                                                                                                                                                                                                                                            A02504;
                                                                                            14-MAY-1998;
                                                                                                                   13-MAY-1999;
                                                                                                                                           18-NOV-1999
                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                         probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGCGCGCCCVGGCCVNNHNNNSCGGCCCGGCCGGCCGCCCCVGGCCVGNNHNNNSC 104961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNNHNNNSCGGCCCGGCCGGCGCGCCCVNNHNNNSCGGCCCGGCCGGCGCGCCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                             GGC 104958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCCGCTACGCAGACATGCTGATAGAGCTGGCGCACGAGGAGTGCCCTCCGGGGGCCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGGGACCCGCTGGTGACGCGGGACGAGGCGAGGAGCCTGGCGTCCCCGTAGCCCGTGTGG
                                                                                                                                                                                                                                        detection; cancerous state; metastasis; identification;
                                                                                                                                                                                                                                                   colon cancer; tumour;
                     CHIRON
                                                                                                                                                                                                                                                                                                    (first entry)
                                                                   98US-0085426.
98US-0085537.
98US-0085696.
                      CORP
                                             98US-0105234
98US-0105877
                                                                                                                   99WO-US10602
                                                                                                                                                                                                                                                                                                                                                    CDNA;
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                                                                                                                                                                                                                                                  diagnosis; gene expression
                                                                                                                                                                                                                           therapy;
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Query Match
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Reinhard (
Lamson G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor negative breast cancer, lung cancer, and colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A00010 to A02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leshkowitz
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TTCAGTATGGGCGGCGCTGTAGCGATCGTGGAGGGTGCTGGGGACCCGCGGGTCTACGCG
                                                                                                                                                                       GCCGCTGTGGCTGTTGGCGCTTGTTGTGTCCGTTGTTGTCCCGGCTTATGTGGCGTAT 246
                                                                                                                                 CGGGGCCACGGGGAGAGCGGGGGGGCCCCGACGACGATTGGGCCCCCGGGAGGTGCTGGATGCC
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                                                                                                                                                                                                                                                                                                           ATGGCTGTGCTGGCCCGGGAGCTCGTGGAGTGGGGGTACCCGGTGGTTGTGTTCGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                GGGGGCAACCCGGTGTTCGTTTTGATGCACGGGTATACTGGGTGCCGCTCGGCGCCCCTAC
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D, Kita
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Randazzo F, Kennedy GC, Pot D; Kass
Crkvenjakov R, Dickson M, Drmanac S,
Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54.6; D
Pred. No. 0.00
0; Mismatches
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                                                                                                                                                                              CDS
                                                                                                                                                                                                              Streptococcus
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                                                                                                           complement (2658..4967)
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/product= 8,8a-deoxyoleandolide_synthase_2
          'label- ORF2
                                /product= 8,8a-deoxyoleandolide_synthase_1
.8267..29717
                                                                                                                       'label - olen2
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Pred. No. 0.0065;
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This is part of the Streptococcus antibioticus oleandomycin gene cluster. CC The oleandolide polyketide synthase (PKS), also known as CC 8,8a-deoxyoleandolide synthase, is encoded by three open reading frames CC (ORF), designated oleAI, oleAII and oleAIII. The PKS is a type I carrier protein (ACP) domain. The oleandolide PKS is a type I carrier protein (ACP) domain. The oleandolide PKS loading module contains an inactivated KS, called KS-Q, where Q is the abbreviation for CC activity. The large multifunctional PKS enzymes catalyze the biosynthesis of polyketide macrolactones through multistep pathways involving CC decarboxylative condensations between acylthicesters followed by cycles of varying beta-carbon processing activities. The macrolide product of the PKS, 8a-deoxyoleandolide, is further modified by epoxidation and CC glycosylation to yield oleandomycin, an antibacterial polyketide. The CC invention concerns an isolated recombinant DNA compound, comprising a coding sequence for a domain of loading module PKS in which the CC module 1 KS domain is inactivated by deletion or other mutation. In CC particular, the inactivation is mediated by a change in the KS domain CC coleandolide PKS in which the inactivation in the codon for the active site cysteine. The CC coleandolide PKS is useful for synthesizing polyketides, which are useful cleandolide PKS is useful for synthesizing polyketides, which are useful coleandolide PKS is useful for synthesizing polyketides, which are useful coleandolide PKS is useful for synthesizing polyketides, which are useful coleandolide PKS is useful for synthesizing polyketides, which are useful coleandolide PKS is useful for synthesizing polyketides, which are useful coleandolide PKS is useful for synthesizing polyketides, which are useful coleandolide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant DNA compound encoding oleandolide polyketide synthase for synthesizing polyketides comprising a coding sequence for a domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Betlach MC,
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16-FEB-1999;
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DB; Y92707, Y92708, Y92709
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   12-OCT-1999
                                         Z17584;
                                                                             Z17584 standard; cDNA; 1103 BP
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Score 52.6; DB 20; Pred. No. 0.015; 0; Mismatches 526;

Length Indels

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Gaps

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Sequence 1103

BP; 131 A; 274 C; 48 G; 18 T;

632 other;

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The present invention describes a library of human polynucleotides CC comprising the sequences given in 212532 to 217779. Also described is a CC method of detecting differentially expressed genes correlated with the CC cancerous state of a mammalian cell, comprising detecting at least one CC differentially expressed gene product in a test sample from a cell. CC suspected of being cancerous, where the gene product is encoded by one CC suspected of being cancerous, where the gene product is encoded by one CC of the 5248 polynucleotides equences given in 212532 to 21779. The CC mapping, tissue typing or profiling, forensics, genetic analysis and CC mapping, tissue typing or profiling, forensics, genetic analysis and CC mapping, tissue typing or profiling, forensics, genetic analysis and CC can be used for raising antibodies for experimental, diagnostic and CC can be used for raising antibodies for experimental, diagnostic and CC can be used for raising antibodies for experimental, diagnostic and CC carrays for diagnostics (which may be used to determine function of an CC carrays for diagnostics (which may be used to determine function of an CC cancer); and to detect differences in expression levels between CC dientify a genetic predisposition or susceptibility to a disease such as CC cancer). The polynucleotides of the invention are especially used in the CC cancer. The polynucleotides can also be used to screen for cancer, and lung cancer. The polynucleotides can also be used to screen for cancer.
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28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
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Lamson G, Leshkowitz D,
Stache-Crain B, Sudduth
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M68; tumour necrosis factor; TNF; programmed cell death; apoptosis; receptor; immune response; cell differentiation; ligand; cancer; bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;
                                                               Genomic DNA encoding M68 TNF receptor related protein.
                                                                                                                              A53800;
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roles in immune responses, cell death, cell proliferation and stimulation of cell differentiation. M68 lacks a transmembrane domain and is a secreted factor suggesting that it functions as a natural inhibitor for its ligand. The altered expression pattern of M68 in a multitude of tissues suggests that M68 may play a role in cancer by binding to its ligand and blocking apoptotic cell death induced by such a ligand. This anti-apoptopic role of M68 suggests that modulators of M68 will be useful in treatment of apoptosis-related modulators of M68 will be useful in treatment of apoptosis-related
              atherosclerosis, aplastic anaemia, myelodisplastic syndromes, osteoporosis, Alzheimers disease, Parkinsons disease, stroke, myocardial infarction.
                                                                            apoptosis including systemic lupus erythematosus, Hashimoto's thyroiditis, Grave's disease, idiopathic mysodema, autoimmune diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis, liver diseases, autoimmune gastritis, ulcerative colitis,
                                                                                                                                              diseases such as various forms of cancer and various bone disorders. M68 nucleic acids and proteins are therefore useful for treating conditions involving atypical apoptosis and for identifying modulators of M68. Modulators of M68 are useful for treatment of cancer and other diseases associated with abnormal levels of
                                                               liver diseases, aut
glomerulonephritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated human M68 nucleic acids and proteins which are part of the tumor necrosis factor receptor (TNFR) family, useful for identifying modulators that may be used to treat various diseases e.g. cancer, osteoporosis, Alzheimer's disease
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Search completed: June 2, 2001, 21:59:41 Job time: 29479 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Estimated insert size: 198300; agarose-fp estimation
Estimated insert size: 293091; sum-of-contigs estimation
Quality coverage: 4.85 in Q20 bases; agarose-fp estimation
Quality coverage: 3.28 in Q20 bases; sum-of-contigs estimation
Quality coverage: 3.28 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 101 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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773 GGAGGCTGATGGCGGGGTTGACCTCGGCTTCGGCCCCGCTGGGATGGAGCGCGTGGATA 832	713 GGTGGCTGGAGTACAAGACGCCGCTGCCGGGCTGGGTGGG	653 CGCGGGTCTACGCGGTGGCTGCTGATAGCCCGTACTATAGGCTCCGGGACGTCATACCCC 712	593 TAATATTGGTGGGGTTCAGTATGGGCGGCGCTGTAGCGATCGTGGAGGGTGCTGGGGACC 652	533 AGGTGCTGGATGCCCGGGCTGTGGTGGGCTATGTCTCGGAGCGGTTCCCCGGCCGCCGGA 592	473 TIGTGTTCGACTTCCGGGGCCACGGGGGAGAGCGGGGGGCTCGACGACGATTGGGCCCCGGG 532	413 GCTCGGCGCCCTACATGGCTGTGCTGGCCCGGGAGCTCGTGGAGTGGGGGTACCCGGTGG 472	353 TGGGCCCCGGCGCTGGGGGCAACCCGGTGTTCGTTTTGATGCACGGGTATACTGGGTGCC 412	293 TCACCTACAAAGAGTTCAGCGTGACCGCGGAGGATGGCTTGGTGGTTGGT	233 CTTATGTGGCGTATAGTCTGCACCCGGAGAGCTGTCGGCCCGTTGCGCCGGAGGGGC, 292	173 AGAGGCTGCTCCTGGCCGCTGTGGCTGTTGGCGCTTGTTGTTG	113 TCCGGGGCGTAGCTGTGGACACAGGGGTGGCTCGGGTGCCTCGGCCGCGCGCG	Query Match 9.2%; Score 96.2; DB 77; Length 303091; Best Local Similarity 35.7%; Pred. No. 1.6e-07; Matches 309; Conservative 0; Mismatches 553; Indels 3; Gaps 1;	* 85.48 865.21 contig of 10/4 bp in length * 85.52 86.21 gap of unknown length * 87.45 87.44 contig of 1123 bp in length * 87.45 87.45 gap of unknown length * 87.45 88.965 contig of 1121 bp in length * 88.966 89.055 gap of unknown length * 89.066 90.76 contig of 1121 bp in length * 90.77 91.279 contig of 1003 bp in length * 90.277 91.279 contig of 1003 bp in length * 91.280 91.79 gap of unknown length * 91.280 92.563 contig of 1184 bp in length * 92.664 92.663 gap of unknown length * 92.664 93.688 contig of 10.25 bp in length * 93.689 93.788 gap of unknown length * 93.689 93.788 gap of unknown length * 93.69 94.934 contig of 11.46 bp in length * 95.035 96.111 contig of 10.75 bp in length * 96.112 96.211 gap of unknown length * 96.212 98.352 contig of 21.41 bp in length * 98.453 99.645 contig of 11.93 bp in length * 98.453 99.645 contig of 11.93 bp in length * 99.646 99.745 gap of unknown length * 99.646 99.74

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                                                                                                                                                                     Consensus quality: 154414 bases at least Q40
Consensus quality: 183510 bases at least Q30
Consensus quality: 194836 bases at least Q20
Estimated insert size: 222300; agarose-fp estimation
Estimated insert size: 233130; sum-of-contigs estimation
Quality coverage: 3.27 in Q20 bases; agarose-fp estimation
Quality coverage: 3.12 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 61 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACU79420 239130 bp DNA
Mus musculus chromosome 16 clc
SEQUENCE, 61 unordered pieces.
ACU79420
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Center: Joint Genome Institute
Center Code: JGI
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Submitted (01-SEP-2000) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
1 (bases 1 to 239130)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                          Summary Statistics
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                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Project Information
Center Project Name: 0
Center clone name: RPCI-23_111E8
                                                                  Center: Joint Genome Institute
Center Code: JGI
                                                                                                         Submitted (01-SEP-2000) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
                                                                                                                                                2 (bases 1 to 209887)
DOE Joint Genome Institute
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DOE Joint Genome Institute
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                                                     Web site:
                                                                                                                                     Direct Submission
                                                                                                                                                                                          Sequencing of Mouse
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Summary Statistics

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Consensus quality: 116537 bases at least Q40
Consensus quality: 149032 bases at least Q30
Consensus quality: 164980 bases at least Q30
Consensus quality: 164980 bases at least Q30
Estimated insert size: 153300; agarose-fp estimation
Estimated insert size: 205287; sum-of-contigs estimation
Quality coverage: 3.52 in Q20 bases; agarose-fp estimation
Quality coverage: 2.63 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a "vorking draft' sequence. It currently
* consists of 47 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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/db_xref="taxon:10090"
/chromosome="16"
/clone="RP23-111E8"
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Center
Summary Statistics
Consensus quality: 135394
Consensus quality: 159082
Consensus quality: 170477
                                                                                                                                                  Genome Institute, 20
                                                                                                                                                                                                                                                                                                                                                                     AC087227 205691 bp DNA HTG 19-DEC-20 Mus musculus chromosome 16 clone RP23-124B17, WORKING DRAFT SEQUENCE, 31 unordered pieces.
                                                                                                                             Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                Submitted (19-DEC-2000) Production Sequencing Genome Institute, 2800 Mitchell Drive, Walnut
                                                                                                                                                                                                                                                           1 (bases 1 to 205691)
DOE Joint Genome Institute.
                                                                                         Project Information
                                                                                                                                                                                               Direct Submission
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DOE Joint Genome Institute.
                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                               Sequencing
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                                                                                                                site: http://www.jgi.doe.gov
                                                                Project Name:
clone name: R
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Estimated insert size: 197300; agarose-fp estimation
Estimated insert size: 202691; sum-of-contigs estimation
Quality coverage: 3.42 in Q20 bases; agarose-fp estimation
Quality coverage: 3.33 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 31 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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/chromosome="16"
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                                                                                                                                                                                                                                                                                                     Consensus quality: 151438 bases at least Q40
Consensus quality: 173959 bases at least Q20
Consensus quality: 185196 bases at least Q20
Estimated insert size: 220300; agarose-fp estimation
Estimated insert size: 226885; sum-of-contigs estimation
Quality coverage: 3.77 in Q20 bases; agarose-fp estimation
Quality coverage: 3.21 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 72 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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                                                                    Mammalla; Eutheria; Rodent:
1 (bases 1 to 252689)
DOE Joint Genome Institute
Sequencing of Mouse
                                                                                                                                                                                                 AC079433 252689 bp DNA HTG 01-SEP-2000 Mus musculus chromosome 16 clone RP23-76F18, WORKING DRAFT SEQUENCE, 68 unordered pieces.
                                                                                                                     Eukaryota; Metazoa;
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HTG; HTGS_PHASE1; HTGS_DRAFT
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* NOTE: This is a 'working draft' sequence. It currently consists of 68 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus quality: 136458 bases at least 040 Consensus quality: 163599 bases at least 030 Consensus quality: 177476 bases at least 020
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Center Code: JGI
Web site: http://www.jgi.doe.gu
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JOURNAL REFERENCE

Jnpublished

TITLE

AUTHORS

TITLE

JOURNAL AUTHORS

Submitted Direct REFERENCE

KEYWORDS SOURCE ORGANISM

Mus musculus

touse mouse.

VERSION ACCESSION RESULT AC079433

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DEFINITION

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contig gap of contig

unknown of 1365 unknown of 1032 unknown of 1658 unknown of 1159

bp in 1 length

47601:
48760:
48860:
50518:
50618:
51750:
53115:
53215:
53205:
54409:

gap of contig gap of contig gap of

length bp in l

length

length

contig gap of contig

unknown of 1336 unknown of 1081

bp in length length bp in length

length

gap of contig

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gap of contig gap of contig gap of contig gap of contig gap of gap of gap of gap of

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length

t bp in length to in length

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63101 65183 65283 66388 66488 66174 70061 70161 70161 71207 71307 75030 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130 75130

contig gap of contig

unknown of 1105 unknown of 1686

p length
bp in length
length
bp in length
hi length
length
length
bp in length

gap

contig gap of contig gap of contig gap of contig

bp in length hp in length

length

unknown of 1035 unknown of 1227 unknown of 1147

bp in length length bp in length

length

unknown of 1886 unknown of 2082

contig gap of contig gap of

n length
bp in length
n length
n length
7 bp in length
n length

gap of contig

of 1094 unknown of 1098 unknown of 1699

length length length

bp in 1 length

gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig contig

i unknown length g of 1787 bp in le g of 1787 bp in le g of 1046 bp in le g of 1046 bp in le g of 3723 bp in le g of 3723 bp in le g of 8636 bp in le g of 8636 bp in le g of 5466 bp in le g of 10700 bp in le g of 10700 bp in le g of 6977 bp in le

length length

length

length

in length

length

f unknown length g of 11341 bp in f unknown length

length

-	REFERENCE AUTHORS TITLE TOURNAL REFERENCE AUTHORS TITLE TOURNAL COMMENT	Qy 1036 G Db 8196 G RESULT 7 ACOB7228 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Oy 796 C Db 7956 G Oy 856 C Oy 916 O Oy 916 G Oy 916 G Oy 916 G Oy 976 G Oy 976 G Ob 8136 G
Consensus quality: 162494 bases at least Q40 Consensus quality: 190921 bases at least Q30 Consensus quality: 204528 bases at least Q30 Consensus quality: 204528 bases at least Q30 Estimated insert size: 249300; agarose-fp estimation Estimated insert size: 260337; sum-of-contigs estimation Quality coverage: 3.18 in Q20 bases; agarose-fp estimation Quality coverage: 3.04 in Q20 bases; sum-of-contigs estimation ** NOTE: This is a 'working draft' sequence. It currently ** consists of 53 contigs. The true order of the pieces ** is not known and their order in this sequence record is ** runs of N, but the exact sizes of the gaps are unknown. ** This record will be updated with the finished sequence ** as soon as it is available and the accession number will ** be preserved. 1359: contig of 1359 bp in length ** 1360 1359: gap of unknown length ** 2661 2760: gap of unknown length ** 2661 2760: gap of unknown length ** 2761 4056: contig of 1296 bp in length	Manmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 265537) DOE Joint Genome Institute. Sequencing of Human Chromosome 16 Unpublished 2 (bases 1 to 265537) DOE Joint Genome Institute. Direct Submission Submitted (19-DEC-2000) Production Sequencing Facility, DOE Joint Genome Institute. Direct Submission Submitted (19-DEC-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USAGenome Center Center: Joint Genome Institute Center Code: JGI Web site: http://www.jgi.doe.gov Project Information Center Project Name: 0 Center Clone name: RPCI-23_125D15	265537 bp DNA HTG 19 13 chromosome 16 clone RP23-125D15, WORKII 53 unordered pieces. 6I:11890790 PGI:11890790 PGI:11890790 SI:1890790	CTCGGCCTTCGGCCCCGCTGGGGTGGAGCGCTGGATAAGCCGTTGCTGGTGATATGGG 855
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37464 39124 40579 40679 42877 42877 42877 42877 42887 45468 45468 4859 511099 511099 511099 511099 51109 52848 52848 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 57248 572	25176. 2634. 2634. 27414. 27414. 2756. 286.5. 287.5. 287.5. 29802. 29902. 29902. 31019. 31119. 32266. 32266. 3236. 33417. 33417. 34816. 34816. 35885.	16183 176283 17623 17623 17623 18729 18829 19912 20012 20012 21485 21485 21485 22584 22584 22584 23841 23941	4156 5449 5549 6645 6645 6945 8472 8472 9614 10804 10804 12111 12111 12111 12111 13433 13533 14784
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BASE COUNT
ORIGIN
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Best Local Similarity
Matches 275; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                      23314
                                                                                                                                                                                23134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 GGGGTGGCTCGGGTGCCTGGGCTCGGCCGGCGGTAAGAGGCTGCTCCTGGCCGCTGTG 195
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                                                                                                                                                                         CCGGTGTTCGTTTTGATGCACGGGTATACTGGGTGCCGCTCCGGCGCCCTACATGGCTGTG 435
                                                                                                                                                                                                                                                                    ACCGCGGAGGATGGCTTGGTGGTTCGGGGCCTGGGTGCTGGGGCCCCCGGCGCTGGGGGCAAC
GTGGGCTATGTCTCGGAGCGGTTCCCCCGGCCGGCTAATATTGGTGGGGTTCAGTATG
                                                         GGGGAGAGCGGGGCTCGACGACGATTGGGCCCCGGGAGGTGCTGGATGCCCGGGCTGTG
                                                                                                                                             CTGGCCCGGGAGCTCGTGGAGTGGGGGTACCCGGTGGTTGTTCTGTTCCGACTTCCGGGGCCAC
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189245
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79405
79505
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/db_xref="taxon:10090"
/chromosome="16"
/chone="RP23-125D15"
/clone=lib="RPCI mouse BAC library
/clone=lib="RPCI mouse BAC library
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177104: contig of 12596 bp in 16
177204: gap of unknown length
189144: contig of 11940 bp in 16
189244: gap of unknown length
206994: contig of 17750 bp in 16
207094: gap of unknown length
227754: contig of 20660 bp in 16
2277854: gap of unknown length
2277854: gap of unknown length
265537: contig of 37683 bp in 1
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32.7%;
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9: contig
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Pred. No. 2.3e-05;
0; Mismatches 567; Indels
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of unknown length
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Best Local Similarity
Matches 402; Conserv
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Fragment Name Begin
CEY39B6_0 1
CEY39B6_1 100001
CEY39B6_2 200001
CEY39B6_3 300001
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                   463 TACCCGGTGGTTGTGTTCGACTTCCGGGGGCCACGGGGAGAGCGGGGGGCTCGACGACGATT
                                                                                                       343 GECTGEGTGCTGEGCCCCCGGCGCTGGGGGCCAACCCGGTGTTCGTTTTGATGCACGGGTAT 402
                                                                                                                                          283 CCGGAGGGCTCACCTACAAAGAGTTCAGCGTGACCGCGGAGGATGGCTTGGTGGTTCGG 342
                                                                                                                                                                                                                                      103 GGTGTCCTAGTCCGGGGCGTAGCTGTGGACACAGGGGTGGCTCGGGTGCCTGGGCTCGGC 162
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                                                                                  GTTGTCCCGGCTTATGTGGCGTATAGTAGTCTGCACCCGGAGAGCTGTCGGCCCGTTGCG
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                                                                                                                                                                                                                                                                                                     Score 82.2; DB 83;
Pred. No. 5.5e-05;
0; Mismatches 533;
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                                                                          Assembly program: XGAP4; version 4.5 Sequencing vector: M13; M77815; 3% of reads Sequencing vector: plasmid; L08752; 96% of reads Chemistry: Dye-terminator ABI; 1% of reads Chemistry: Dye-terminator ET-amersham; 11% of reads Chemistry: Dye-terminator ET-amersham; 11% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 12, 2000_this sequence version replaced gi:9799973.
        Consensus
                                  Consensus
                                                      Dye-terminator Big Dye; 87% of reads
                                                                                                                                                                                                                                                       Center project name: dJ1166H10
                                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                        Center code:
                                                                                                                                                                                                                                                                                                                                                                                               Center: Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pavitt, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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141517 bases at least Q30
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*, 13 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be preserved.

11347 11446: gap of 100 bp 111447 27540: contig of 11394 bp in length 27541 27640: gap of 100 bp 27541 27640: gap of 100 bp 27541 27640: gap of 100 bp 27541 32586: contig of 12895 bp in length 27547 32586: gap of 100 bp 32587 32586: gap of 100 bp 45582 45581: contig of 12895 bp in length 45582 45681: gap of 100 bp 45582 45681: gap of 100 bp 611447 61546: gap of 100 bp 611447 61548 87587: contig of 11807 bp in length 75388 75487: gap of 100 bp 611807 bp in length 87295 87394: contig of 1407 bp in length 87295 90801: contig of 3407 bp in length 90802 90901: gap of 100 bp 90902 95339: contig of 4438 bp in length 95340 95439: gap of 100 bp 95440 104017: contig of 8578 bp in length 104118 104117: gap of 100 bp 104118 104117: gap of 100 bp 104118 104117: gap of 100 bp 104118 104117: gap of 100 bp 104118 104117: gap of 100 bp 104118 104117: gap of 100 bp 104118 104117: gap of 100 bp 104118 104117: gap of 100 bp 104118 104117: gap of 100 bp 104118 104117: gap of 100 bp 104118 104117: gap of 100 bp 104118 104117: gap of 100 bp 104118 104117: gap of 100 bp 104118 104117: gap of 100 bp 104118 104117: gap of 100 bp 104118 104117: gap of 100 bp 104118 104118 104117: gap of 100 bp 104118 104117: gap of 100 bp 104118 104117: gap of 104118 104118 104117: gap of 104118 104118 104117: gap of 104118 104117: gap of 104118 104118 104117: gap of 104118 104118 104117: gap of 104118 104118 104117: gap of 104118 104118 104117: gap of 104118 104118 104117: gap of 104118 104118 104118 104118 104118 104118 104118 104118 104118 104118 104118 104118 104118 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 10418 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currentl consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record
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  /note="assembly_fragment:00660'
                                                      /note="assembly_fragment:00499"
                                                                                                             /note="assembly_fragment:00231'
                                                                                                                                                                 note="assembly_fragment:00123"
                                                                                                                                                                                                                        /note="assembly_fragment:00132
fragment_chain:2"
                                                                                                                                                                                                                                                                                                        /note="assembly_fragment:00820
fragment_chain:2"
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fragment_chain:1"
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/db_xref="taxon:9606"
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'ragment_chain:1"
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127850. .139713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Consensus quality: 90425 bases at least Q40
Consensus quality: 105247 bases at least Q30
Consensus quality: 115624 bases at least Q30
Consensus quality: 115624 bases at least Q30
Estimated insert size: 164311; agarose-fp estimation
Estimated insert size: 184321; sum-of-contigs estimation
Quality coverage: 3.02 in Q20 bases; sum-of-contigs estimation
Quality coverage: 3.02 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 65 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (01-APR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Sep 24, 2000 this sequence version replaced gi:9090643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Primates; C
1 (bases 1 to 187738)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
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Center Project Name:
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DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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Best Local Similarity 35.9%;
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/chromosome="16"
/clone="CTD-2012K14"
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a 40396 c 52911 g 40853 t
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contig of 11014 bp in length
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Pred. No. 5.1e-05;
D; Mismatches 533;
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gap of contig

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of 1202
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Summary Statistics Consensus quality: 189570 bases at least Q40 Consensus quality: 207567 bases at least Q30 Consensus quality: 217222 bases at least Q30 Consensus quality: 217222 bases at least Q20 Estimated insert size: 290766; sum-of-contigs estimation Estimated insert size: 290766; sum-of-contigs estimation Quality coverage: 8.11 in Q20 bases; agarose-fp estimation Quality coverage: 6.44 in Q20 bases; sum-of-contigs estimation. * NOTE: This is a 'working draft' sequence. It currently * consists of 75 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will	PHE PHE PHE PHE PHE PHE PHE PHE PHE PHE	F1000	Db 38111 GGGGGNGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
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Best Local Similarity 29.8%;
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243479
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79 243478: gap of unknown length
79 298166: contig of 54688 bp in length.
Location/Qualifiers
1. .298166
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/db_xref="taxon:9606"
/chromosome="16"
/clone="repl1-358F6"
/clone_lib="RPCI human BAC library 11"
         971
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Pred. No. 4.7e-05;
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104002 105901 106001 109703

895

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955

16128

16188

94174 98665 98765 101608 101708 103902

91566 91666 94074

81480 82829 82929 86818 86918 89153

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Consensus quality: 197223 bases at least Q30
Consensus quality: 214345 bases at least Q30
Consensus quality: 214345 bases at least Q30
Estimated insert size: 257300; agarose-fp estimation
Estimated insert size: 293095; sum-of-contigs estimation
Quality coverage: 3.01 in Q20 bases; agarose-fp estimation
Quality coverage: 2.65 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 77 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 300695)
DOE Joint Genome Institute.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Joint Genome Institute Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (01-SEP-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
1 (bases 1 to 300695)
DOE Joint Genome Institute.
Sequencing of Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center Project Name: 0
Center clone name: RPCI-23_1J12
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 222707)
DOE Joint Genome Institute.
2 (bases 1 to 222707)
DOE Joint Genome Institute.
Direct Submission
Submitted (01-SEP-2000) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
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COMMENT
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Consensus quality: 188237 bases at least Q30
Consensus quality: 197123 bases at least Q20
Consensus quality: 197123 bases at least Q20
Estimated insert size: 198300; agarose-fp estimation
Estimated insert size: 218807; sum-of-contigs estimation
Quality coverage: 4.06 in Q20 bases; agarose-fp estimation
Quality coverage: 3.68 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 40 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Joint Genome Institute
Center Code: JGI
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Center clone name: RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.jgi.doe.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                         GGGTACCCGGTGGTTGTGTTCGACTTCCGGGGGCCCACGGGGAAGAGCGGGGGGCTCGACGACG
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/db_xref="taxon:10090"
/chromosome="16"
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/clone_lib="RPCI mouse BAC library 23"
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Consensus quality: 102018 bases at least 040 consensus quality: 120321 bases at least 020 consensus quality: 120321 bases at least 020 consensus quality: 130817 bases at least 020 Estimated insert size: 138300; agarose-fp estimation Estimated insert size: 159688; sum-of-contigs estimation Quality coverage: 3.79 in 020 bases; agarose-fp estimation Quality coverage: 3.28 in 020 bases; sum-of-contigs estimation.*
* NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACUB/190 162388 bp DNA
Homo sapiens chromosome 16 clo
SEQUENCE, 28 unordered pieces.
ACOR7100
                                                                                                                                                                                                                                                             Submitted (13-DEC-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                          Summary Statistics
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Sequencing of Human Chromosome
                                                                                                                                                       Center clone name: RPCI-11_473I1
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DOE Joint Genome Institute.
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Mammalia; I
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                                                                                                                                                                                                                                                                                                                                                                                                                 ; Metazoa;
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Primates;
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WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record
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                 /clone_lib-"RPCI human BAC library 35790 c 38554 g 38910 t 6967
                                                       /chromosome="16"
/clone="RP11-47311"
                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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65: gap of unknown length 128: contig of 13863 bp in length 828: gap of unknown length 1371: contig of 23543 bp in length 1371: contig of 31840 bp in length 143311: contig of 31840 bp in length 1570                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of contig
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                                                                        CCCGCTGGGGTGGAGCGCGTGGATAAGCCGTTGCTGGTGTGTATGGGCCCCGGGACCCG
                                                                                                                                                                                                                         project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage CP 5706 91057 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.ir)
The cDNA library to be analyzed within the framework of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Botryotinia fuckeliana
Eukaryota; Fungi; Ascomycota; Euascomycetes; Discomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope.
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Bitton, F., Levis, C., Fortini, D., Pradier, J.M.
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700 c 75 g 33 t 8 othe
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Searc Job t	ф	Qy	Ф	Qy	Db
Search completed: June 2, 2001, 20:25:15 Job time: 23813 sec	180 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	988 GACATGCTGATAGAGCTGGCGCACGAGGAGTGCCCTCCGGGGGCCCGTGG	240 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	928 GAGGTTCCTGGGGCTGGCCACGTGGACGCCGTGGATGTGCTCGGGCCCGGCCCGCCTACGCA 987	300 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
	GGG 131	GTGG 1037	GGGCGGGCGGGG 181	CGGGCCGCTACGCA 987	eeeeeeeeeee 241